

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 133719

To: Jeffrey Parkin Location: rem/3d39/3c18

Art Unit: 1648

Wednesday, September 29, 2004

Case Serial Number: 10/084813

From: Beverly Shears Location: Remsen Bldg.

RM 1A54

Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes				
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us-10-084-813-13.rai

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                                                                                                         September 28, 2004, 09:00:23; Search time 16.2 Seconds (without alignments) 57.362 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lssued_patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08 466-33D-2
US-08 466-33D-2
US-08 -466-33D-2
US-08 -575-967A-2
US-08 -575-967A-2
US-09 -514-185-52
US-09 -514-185-52
US-09 -534-185-52
US-09 -534-185-52
US-09 -796-202-1
US-09 -796-202-1
US-09 -796-202-1
US-09 -796-202-1
US-09 -907-468-11
US-09 -686-319A-13
US-09 -686-319A-13
US-09 -686-319A-13
US-09 -686-319A-13
US-09 -594-185-5
US-08 -681-192-2
US-08 -681-192-2
US-08 -932-6593
US-09 -534-252-991A-25052
US-09 -489-00126-318-4
US-09 -540-216-77-2
US-09 -540-218-70-216-77-2
US-09 -134-001C-5171
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                                                                                                                                                                                                                                                                                                                  389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       - protein search, using sw model
                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                   US-10-084-813-13
96
1 SQYQFWKNFQTLKIVILG 18
                                                                                                                                                                                                                                                                                                                                                                                          seq length: 0
seq length: 200000000
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Match
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Perfect score:
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US-08-833-752-11
US-08-833-752-11
US-08-833-752-11
Sequence 11, Application US/08833752
Patent No. 6448375
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: VASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
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                                                          Sequence 5, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 14, Appli
Sequence 5, Appli
INFORMATION FOR
Sequence 10, Appl
Sequence 26013, A
Sequence 5538, Ap
Sequence 57794, Ap
Sequence 67794, Ap
Sequence 6731, Ap
Sequence 6731, Ap
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                                Sequence
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ZIP: 92660

ZIP: 92660

COMPUTER READABLE FORM:

MEDLUM TYPE: Floppy disk

COMPUTER: PROPY disk

COMPUTER: 
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US-09-489-039A-8904

US-08-45-039A5-5

US-08-45-669-5

US-08-239-938-1

US-08-833-152-9

US-08-88-313A-14

PCT-US95-00476-5

US-09-165-92A-10

US-09-165-92A-10

US-09-165-92A-10

US-09-153-93A-26013

US-09-134-00CC-3794

US-09-134-00CC-6031

US-09-134-00CC-6031

US-09-134-00CC-6031

US-09-134-00CC-6031

US-08-134-00CC-6031

US-08-134-00CC-6031

US-08-134-00CC-6031

US-08-134-00CC-6031

US-08-134-00CC-6031

US-08-134-00CC-6031
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Best Local Similarity 100."
Matches 18, Conservative
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1 SQYQFWKNFQTLKIVILG 18
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TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-087-232A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
                                                                                                                                                                                                                                                                                     amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
US-08-861-105-14
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CITY: Ha
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1 Sequence 13 Application US/09087232A

2 Sequence 15.3431

3 GENBRAL INFORMATION:

APPLICANT: Oulllent et al.

TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR

TITLE OF INVENTION: VALIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.

NUMBER OF SEQUENCES:

ADBRESSEE: Baker & Bocts, L.L.P. attn. Lisa Kole

STREET: 30 Rockefeller Plaza

CITY: New York

COUNTRY: USA

INEW YORK

COUNTRY: USA

SOFTWARE: FLORDY disk

COMPUTER: IBM PC compatible

OMPUTER: IBM PC compatible

OMPUTER: IBM PC compatible

OMPUTER: SACHARE: PatentIn Release #1.0, Version #1.30 (BPO)

CURRENT APPLICATION DATA:

SPILING DATE: 28 MAY 1998

CLASSIFICATION: 435
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Patent No. 6025154
GABERAL INFORMATION:
FAPRILICANT: Li, Yi
TITLE OF INVENTION:
TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSE:
STRRE, KESSLER, GOLDSTEIN & FOL.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
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                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MUDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,343D
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1488.1150000/EKS/KLM
                                       Sequence 2, Application US/08466343D Patent No. 6025154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION UNDRER: 36,68
REPERENCE/DOCKET UNDRER: 1488
TELECOMMUNICATION INFORMATION:
TELEFONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 SQYQFWKNPQTLKIVILG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SOYOFWKNPOTLKIVILG 18
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-466-343D-2
                                                                                                                                                                                                                                                                                            COUNTRY:
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PRIOR APPLICATION DATA.

APPLICATION WRENES: 60046,027

APPLICATION WRENES: 60046,027

APPLICATION WRENES: 60046,027

APPLICATION WRENES: 60046,027

REFERENCE/DOCKER WRENES: 35,225

REFERENCE/DOCKER WRENES: A 31115

TELECOMMULICATION MARRIES: A 31115

TELECOMMULICATION REPRESENTATION: 11,1115

TELECOMMULICATION REPRESENTATION: 11,1115

DESCRIPTION REPRESENTATION: 11,1115

TELECOMMULICATION REPRESENTATION: 11,1115

DESCRIPTION REPRESENTATION: 11,1115

DESCRIPTION: 11,1115

TOTAL STRAIN REPRESENTATION: 11,1115

TOTAL STRAIN REPRESENTATION: 11,1115

TITLE OF THE STRAIN REPRESENTATION: 11,1115

THE STREET: 411 HACKARRAGE FORM: 11,1115

THE STREET: 411 HACKARRAGE FORM: 11,1115

THE STREET: 411 HACKARRAGE FORM: 12,1115

THE STREET: 411 HACKARRAGE FORM: 13,1115

THE STREET: 411 HACKARRAGE FORM: 14,115

THE STREET H
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The Sep 28 IS:49:56 2004
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18-10-084-818-12:181

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Sequence 52, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805e1 Molecules of the G Protein-Coupled NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STRIE: Assachusetts
COUNTY: Boston
STRIE: Assachusetts
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFTCATION NUMBER:
FILING PATICATION NUMBER:
FILING PATICATION NUMBER:
FILING DATE: 20-MAR-98
FILING PATICATION NUMBER:
FILING DATE: POTATE:
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Patent No. 6265184
GENERAL INFORMATION:
FARM CARAY et al.
TITLE OF INVENTION: Chemokine Receptor Materials and Methods NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 4300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 96; DB 3; Length 352; Best Local Similarity 100.0%; Pred. No. 3.8e-08; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 96; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels
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COUNTRY: USA
CONDUIRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER LEM PC compatible
COMPUTER PERCENT: TEM PC compatible
COMPUTER PERCENT: TEM PC compatible
COMPUTER: PERCENT: PC-DOS/MS-DOS
SOFTWARE: PERCENT: Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/575,967A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 2555184and, Greta E.
REFERRORE/DOCKET NUMBER: 32918
TELEFRATION NUMBER: 35,302
REFERRORE/DOCKET NUMBER: 32918
TELEFRAX: 206-485-1900
TYPE: AMINO acid
TOPOLOGY: linear
MOMESTULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) NAME/KEY: misc_feature
); OTHER INFORMATION: /= "88C amino acid sequence"
US-08-575-967A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 SQYQFWKNFQTLKIVILG 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SOYOFWKNFOTLKIVILG 18
                                                                                                                                               ; STRANDEDNESS: single
; POPOLOGY: linear
MOLECTULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-861-105-14
                          SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 6300 Sear
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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US-08-575-967A-2
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US-09-517-605-5

US-09-517-605-5

Sequence 5, Application US/09517605

Sequence 5, Application US/09517605

Beneral INFORMATION:
APPLICANT: Littman, Dan R.
APPLICANT: Warn, Douglas S.
APPLICANT: Warn Kooyk, Yvette
APPLICANT: Geijtenbeck, Theo
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
TITLE TENTREBRICE: 1049-1-017

CURRENT APPLICATION NUMBER: US/09/517,605

CURRENT APPLICATION NUMBER: US/09/517,605

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 5

LENTRE ALENTRE SEQ ID NOS: 17

SEQ ID NO 5

LENTRE ALENTRE SEQ ID NOS: 17

LENTRE ALENTRE SEQ ID NOS: 17
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                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 96; DB 3; I
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                              185 SQYQFWKNFQTLKIVILG 202
                                                                                                                                                                                                                                                                                                                                                                                   1 SQYQFWKNFQTLKIVILG 18
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
                                                                                       : 352 amino acids
amino acid
                                                                                                                                                              MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-045-583-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CRGANISM: Homo sapiens
US-09-517-605-5
                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MANDEAGOURES, AMY E.
REGISTRATION NUMBER: 36,207
REPERENCE/OCCET UNBER: MAITELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400

DB 4; 100.0%; Score 96;

185 SQYQFWKNFQTLKIVILG 202

RESULT 6 US-09-045-583-52

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US-005-02-783A-2
US-005-502-783A-2
US-005-502-783A-2
Sequence 2, Application US/09502783A
Sequence 2, Application US/09502783A
Sequence 2, Application US/09502783A
Setent No. 6511826
GENERAL INFORMATION:
APPLICANT: Li, Yi
APPLICANT: Li, Yi
TITLE OF INVENTION: PLONRIO POLYMUCHEOLIGES Encoding Human G-Protein Chemokine Receptor (CCRS);
TITLE OF INVENTION: PLONRIO POLYMUCHER: 1886.115006
CURRENT PAPLICATION NUMBER: 2081-995-96
CURRENT PILING DATE: 2001-08-23
PRIOR PILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOOFWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
STREET: Knobbe, Martens, Olson & Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                   ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATE: 9-APR-1997
FILING DATE: 9-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 96; DB 4; I
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 96; DB 4; 1
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-09-796-202-1
; Sequence 1, Application US/09796202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 SQYQFWKNFQTLKIVILG 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SOYOFWKNFOTLKIVILG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SOYOFWKNFOTLKIVILG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 352 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                   U.S.A.
                                                                                                                                                                COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-502-783A-2
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US-09-534-185-52

; Sequence 52, Application US/09534185

; Patent No. 6403767

; GENERAL INPORMATION:

; APPLICANT: GRAHAM, Gerard J. et al.

APPLICANT: GRAHAM, Gerard J. et al.

APPLICANT: TILE OF INVENTION: No. 640376761 Molecules of the G Protein-Coupled

; TILE OF INVENTION: No. feptabelical Receptor Superfamily and Uses

Therefor
                                       Gaps
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Patent No. 6448375
CENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: FASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOXINES RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                  Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CEMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                Pred. No. 3.8e-08;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,583
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 7227-7400
TELEFAX: (617) 742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
100.08; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 352 amino acids TYPE: amino acid
                                                                                                             185 SQYQFWKNFQTLKIVILG 202
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                                                                               1 SOYOFWKNFOTLKIVILG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 18; Conservative
                                       18; Conservative
             Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-534-185-52
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US-08-833-752-5
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Patent No. 6548636
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCRS PEPTIDES FOR HIV-1 INFECTION
FILE REFERRINCE: 2048/61011/JPW/SHS
CURRENT APPLICATION NUMBER: US/09/796,202
CURRENT FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 96; DB 4; Length 352; 100.0%; Pred. No. 3.8e-08; Dect. 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: 10/601

COMPUTER: ELADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30

CURSTENT APPLICATION DATA:
APPLICATION NUMBER: US/08/907,468
FILING DATE:
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REGISTRATION INFORMATION:
TELEPHONE: 201-447-5800
TELEFAX: 201-33-1684
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 SQYQFWKNFQTLKIVILG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SOYOFWKNFOTLKIVILG 18
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Best Local Similarity 100.
Matches 18; Conservative
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HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-08-907-468-11
                                                                                                                                                                                                                                                                                                                ; SEQ ID NO 1
| LENGTH: 352
| TYPE: PRT
| ORGANISM: human
US-09-796-202-1
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85.4%; S

Query Match Best Local Similarity

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US-08-745-9844.2

| US-08-745-9844.2
| Sequence 2, Application US/08724984A
| Patent No. 63805551
| Patent No. 6380551
| Patent No. 63805551
| Patent No.
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Gaps

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Mismatches

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15; Conservative

Matches

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CITY: Boston
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US-09-489-039A-13500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 53, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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46.9%; Score 45; DB 3; Length 355;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 8; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                 49.0%; Score 47; DB 4; Length 355; ilarity 61.5%; Pred. No. 5; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OFBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/045,583
CURRENT APPLICATION NUMBER: US/09/886,319A;
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 60/222,081
PRIOR FILING DATE: 2000-08-01
PRIOR APLICATION NUMBER: DE 10030149.5
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 84
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 20-WAR-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING: PAICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MANDEAGOURES, AMY E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 YOFWICHFOTLKIVILG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 355 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                            195 WKRFQALKLNLLG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                  6 WKNFOTLKIVILG 18
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internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                         TYPE: PRT
CORGANISM: Mus musculus
US-09-886-319A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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Matches 8; Conserv
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FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-045-583-53
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US-09-045-583-53
                                                                                                                                                                                        352
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                                                                                                                                                                                                                                                                                         Query Match
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192 FQQWKLFQALKLNLFG 207

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Sequence 1350, Application US/09489039A
Fatent No. 6610836
GENERAL INFORMATION:
APPLICANT: GATY BECTON et. al
APPLICANT: ATTLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT PILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13500
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0
S-09-534-185-53
Sequence 53, Application US/09534185
Sequence 53, Application US/09534185
Batent No. 6403767
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 640376701 Molecules of the G Protein-Coupled
TITLE OF INVENTION: Heptahelical Receptor Superfamily and Uses
Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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CONDITER: 102109

COMPUTER READABLE FORM:
MEDITUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC Compatible
COMPUTER: 1BM PC Compatible
COMPUTER: 1BM PC COMPA: DC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: CANANOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,583
FILING DATE: CUNKNOWN>
ATTORNEY/AGENT INPERMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.9%; Score 45; DB 4; Length 355; 50.0%; Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207 REGISTRATION NUMBER: MNI-044 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 53:
                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD,
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 355 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 FQQWKLFQALKLNLFG 207
                                                                                                                                                                                                                                                                                                                                                       STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617)742-42
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 YOFWKNFOTLKIVILG 18
                                                                                                                                                                                                                NUMBER OF SEQUENCES: 56
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Best Local Similarity 50.0°
Matches 8; Conservative
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RESULT 20
US-08-935-263-4

§ Sequence 4, Application US/08935263A

§ Patent No. 6117669

§ GENERAL INFORMATION;

§ APPLICANT: Brunich, Yasuhiro

§ APPLICANT: Hoshino, Tatsuo

§ APPLICANT: Kimura, Hitoshi

§ APPLICANT: Biotin Genes

© URRENT APPLICATION NUMBER: US/08/935,263A

© URRENT PILING DATE: 1997-09-27

§ SOFTWARE: PALENT: RILING DATE: 1996-09-27

§ SOFTWARE: PALENT: PALENT: NUMBER: PALENT: 
                                                PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Schreck, Patricia A.
REGISTRATION NUMBER: 33,777
REFERENCE/DOCKET NUMBER: ATG50014
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5031
TELEFAX: 610-270-4026
TELEX
                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 344 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.8%;
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Best Local Similarity 66.7
Matches 8; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 YQYWKNIDPVK 137
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                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Kurthia sp.
US-08-935-263-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FRAGMENT TYPE: 1, ; ORIGINAL SOURCE: US-08-681-192-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 21
US-09-594-185-4
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                                                                                                                       Query Match
45.3%; Score 43.5; DB 4; Length 352;
Best Local Similarity 43.5%; Pred. No. 19;
Matches 10; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-681-192-2
; Sequence 2, Application US/08681192
; Patent No. 6287801
; Patent No. 6287801
; Patent No. 6287801
; APPLICANT: BERGSMA, DERK
; APPLICANT: ELSHOURBAGY, NABIL
; APPLICANT: SALAU, HENRY
; APPLICANT: STEVEN
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR HNPDS78
; VUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithfilm Beecham Corporation
; STRRET: 709 Swadeland Road
; CITY: Ring of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.8%; Score 43; DB 4; Length 172; llarity 57.1%; Pred. No. 11; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-61-976-4131

Sequence 4131, Application US/09621976

Fatent No. 6639063;
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
ITILE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICANTON NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SEQ ID NO 4131
LENGTH: 172
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COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM: DAS
APPLICATION NUMBER: US/08/681,192
                                                                                                                                                                                                                                                                                         2 QYQFW-----KNFQTLKIVIL 17
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 QFWKNFQTLKIVIL 17
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) NAME/KEY: SIGNAL
; LOCATION: -30..-1
US-09-621-976-4131
                                                             US-09-489-039A-13500
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44.8%; Score 43; DB 3; Length 344; 66.7%; Pred. No. 22; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 3; Length 460;
Pred. No. 45;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09594185
Patent No. 6365388
GENERAL INFORMATION:
APPLICANT: Furuichi, Tatsuo
APPLICANT: Hoshino, Tatsuo
APPLICANT: Kimura, Hitoshi
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Sequence 25024, Application US/09252991A
| Sequence 250262, Application US/09252991A
| Sequence 25027, Application US/09252991A
| Patent No. 6551795
| GENERAL INFORMATION:
| APPLICANT: Marc J. Rubenfield et al.
| APPLICANT: Marc J. Rubenfield et al.
| APPLICANT: Marc J. Rubenfield et al.
| TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
| FILE REPERENCE: 107196.136
| CURRENT PILING DATE: 1999-02-18
| PRIOR APPLICATION NUMBER: US 60/074,788
| PRIOR FILING DATE: 1999-02-18
| PRIOR FILING DATE: 1998-02-18
| PRIOR FILING DATE: 1998-07-27
| SEQ ID NO 25022
| LUBGGH: 363
| LUBGGH: 363
| LUBGGH: 363
| LUBGGH: 363
                                                                                                                                                                                                                                                           Sequence 2, Application US/09491577
Sequence 2, Application US/09491577
Sequence 2, Application US/09491577
GENERAL INFORMATION:
APPLICANT: Vale University
APPLICANT: Carlson, John R.
APPLICANT: Clyne, Peter J.
APPLICANT: Clyne, Peter J.
APPLICANT: Clyne, Peter J.
APPLICANT: Wim, Hunhyong
APPLICANT: Wim, Hunhyong
APPLICANT: Wim, Hunhyong
APPLICANT: Wim, WimsBR: US/09/991,577
CURRENT APPLICATION NUMBER: US/09/991,577
CURRENT FILING DATE: 1200-01-25
EARLIER APPLICATION NUMBER: US 60/117,132
BARLIER FILING DATE: 1999-01-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patentin Ver. 2.1
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                               Gaps
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Best Local Similarity 53.3%; Pred. No. 35;
Matches 8; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
42.7%; Score 41; DB 4; Length 363;
Best Local Similarity 60.0%; Pred. No. 51;
Matches 9; Conservative 2; Mismatches 0; Indels
                               1; Indels
     Best Local Similarity 75.0%; Pred. No. 21; Matches 6; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Drosophila melanogaster
US-09-491-577-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 YOFWKNFOTLKIVIL 17
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                                                                                                                                   146 YVFWKNYQ 153
                                                                                  3 YOFWKNFQ 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 25
US-09-252-991A-25052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-252-991A-25052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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Patent No. 6673910
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR IDAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: POR IDAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 3023
LENGTH: 227
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Fatent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRESENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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Pred. No. 45;
2; Mismatches 3; Indels
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43.8%; Score 42; DB 4; Length 727;
Best Local Similarity 37.5%; Pred. No. 74;
Matches 6; Conservative 5; Mismatches 5; Indels
APPLICANT: Kiyasu, Tatsuya
APPLICANT: Nagahashi, Yoshie
TILE OPT INVENTION: BIOTIN BIOSYNTHETIC GENES
FILE REFERRNCE: BIOCIN BOSYNTHETIC GENES
FILE REFERRNCE: BIOCIN GENES
CURRENT APPLICATION NUMBER: US/09/594,185
CURRENT FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: 08/335,263
PRIOR PILING DATE: 1997-09-22
PRIOR PILING DATE: 1996-09-27
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PATENTIN OF 1996-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 6593
LENGTH: 160
LYPE: PRT
ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 OLEYWKNOTTLSLITI 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 YOFWKNFOTLK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: M.catarrhalis
US-09-540-236-3023
                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Kurthia sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-540-236-3023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-328-352-6593
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42.7%; Score 41; DB 4; Length 160;

Query Match

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APPLICANT: Murphy, Philip M.

APPLICANT: Murphy, Philip M.

TITLE OF INVENTION: Cloning and Expression of Human

TITLE OF INVENTION: Macrophage Inflammatory Protein-1 alpha (MIP-1

TITLE OF INVENTION: alpha)/RANTES Receptor.

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSED: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California
                                                                                                                                                                                                                                                 Score 40; DB 4; Length 316;
Pred. No. 64;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.7%; Score 40; DB 1; Length 355; 53.8%; Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/012,988A
FILING DATE: 19930128
CLASSIFICATION: 435
ATTORNEY/AGBNT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 15280-118
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08450393A; Patent No. 5707815.
GENERAL INFORMATION:
APPLICANT: Charo, Israel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-012-988A-2; Sequence 2, Application US/08012988A; Patent No. 5652133
                                                                                                                             TYPE: PRT;
CRGANISM: Klebsiella pneumoniae
US-09-489-039A-8904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
                1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                               226 WINVÖGLKVEILG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 WKLFQALKLNLFG 207
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Best Local Similarity 53.84
....hes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                        6 WKNFQTLKIVILG 18
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            PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
SEQ ID NO 8904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94610
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US-09-134-001C-4582
Sequence 4582, Application US/09134001C
Sequence 4582, Application US/09134001C
Sequence 4582, Application US/09134001C
Sequence 4582, Application US/09134001C
SEQUENCE SEQUENCES RELATING
TITLE OF INVENTION: WOLZEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
NUMBER: OF SEQ ID NOS: 5674
SEQ ID NO 4582
LENGTH: 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: LYAIN DOUGETEE-Stamm et al
APPLICANT: LYAIN DOUGETEE-STAMM et al
APPLICANT: LYAIN DOUGETEE-STAMM AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: REPLERANDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPDERANDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PRIOR APPLICATION NUMBER: US 60/065,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR SEQ ID NOS: 5674
SEQ ID NO 5171
LENGTH: 311
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; Sequence 8061, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
    APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: NUMBER: 2004001
; CURRENT APPLICATION NUMBER: US 60/117,747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 27
2.09-134-001C-5171
; Sequence 5171, Application US/09134001C
; Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5171
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Matches
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E: Knobbe, Martens, Olson & Bear
620 Newport Center Drive 16th Floor
                  ATTORNEY/AGENT INFORMATION:
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amino acid
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Best Local Similarity 53.00
Best Local 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapien
US-09-239-938-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        355
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US-09-239-938-1
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41.7%; Score 40; DB 1; Length 355;
Best Local Similarity 53.8%; Pred. No. 73;
Matches 7; Conservative 2; Mismatches 4; Indels
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| Parent No. 612287
| GENERAL INFORMATION:
| APPLICANT: Cauchlin, Shaun
| TITLE OF INVENTION: NAMMALIAN MONOCYTE CHEMOATTRACTANT
| TITLE OF INVENTION: PROTEIN RECEPTORS
| NUMBER OF SEQUENCES: 14
| CORRESPONDENCE ADDRESS: Cooley Godward Castro Huddleson & Tatum
| STREET: 5 Palo Alto Square
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MANWALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
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MEDIUM TYPE: FLODBY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARE-ORDER #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,669
FILING DATE: MAY 25, 1995
CLASSIFFICATION: 435
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
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NO
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STATE: California
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California
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STATE: CALL.
COUNTRY: USA
TP: 94306-2155
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US-08-450-393A-5
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HYPOTHETICAL: A
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CITY: Pa
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Patent No. 6448375

GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: LIBERT, REDESIC
APPLICANT: LIBERT, REDESIC
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSED: Knobbe, Martens, Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Best Local Similarity 53.8%; Pred. No. 73; 4; Indels
Matches 7; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Oin, Shixin
APPLICANT: Oin, Shixin
APPLICANT: Assam, Walter
APPLICANT: Rassam, Nasin
APPLICANT: Rassam, Nasin
APPLICANT: Rassam, Nasin
APPLICANT: LavoSite, Inc.
TITLE OF INVENTION: THEREFOR
FILLE BEFERRORE: LKS97-13
CURRENT APPLICATION NUMBER: US/09/239,938
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSEQ for Windows Version 3.0
NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-237/01US
TELECOMMUNICATION INFORMATION:
TELEFRONC: 415-484-5000
TELEFAX: 415-487-663
TELEFAX: 380816CooleyPA
INFORMATION FOR SEQ ID NO: 5:
SECUROR CHARATERISTICS:
LENGTH: 355 amino acids
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41.7%;
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40.0%;
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Best Local Similarity 40.0%
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Best Local Similarity 53.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
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                          COMPUTER READABLE FORM:

MEDLIUM TYPE: Floppy disk
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 34,115
REGISTRATION NUMBER: 34,115
REGISTRATION POR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
CLENGTH: 355 anino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6448375e
US-O8-833-752-9
                                                                                                                                                                                                                                                                                                                41.7%; Score 40; DB 4; Length 355;
53.8%; Pred. No. 73;
tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.7%; Score 40; DB 4; Length 355; 53.8%; Pred. No. 73; tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                         4; Indels
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Best Local Similarity 53.8.
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Best Local Similarity 53.8
Matches 7; Conservative
Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                       U.S.A.
                       COUNTRY: UZIP: 92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JS-09-886-319A-14
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Gaps
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Sequence 5, Application PC/TUS9500476
GENERAL INFORMATION:
THE REQUENCE Of the University of California
TITLE OF INVENTION: MANMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS: 14
CORRESPONDENCE ADDRESS: 14
CORRESPONDENCE ADDRESS: 15
STREET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BR PC compatible
COMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE PATENTIN BATH.

**PLICATION NUMBER: PCT/US95/00476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5; Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 3;
Pred. No. 77;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 73;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 36
US/08/622

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid residue:

TYPE: amino acid residue:

STRANDEDNESS: single

TOPOLOGY: linear

MOLECTUE TYPE: cUnknown:

DESCRIPTION: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US/08/622,679D-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: BETLINEY, ROBERT
REGISTRATION NUMBER: 20.121
REFERENCE/DOCKET NUMBER: 5555
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-977-1001
TELEPHONE: 310-977-1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                319 NQYYFWDDFHPSEVV 333
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Sequence 5538, Application US/09543681A

Sequence 5538, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION:
APPLICANT: GARY BRETON:
APPLICANT: GARY BRETON:
APPLICANT: GARY BRETON:
UTILE OF INVENTION: UNCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001

TITLE OF INVENTION: UNMER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR APPLICATION NUMBER: US 60/128,706

NUMBER OF 553 IN NOS: 8344

SEQ ID NO 5538

LENGHR 2037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 656296

GENERAL INFORMATION:

APPLICANT GATY L. Breton et al.

APPLICANT GATY L. Breton et al.

TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

PILE REPERENCE: GTOS9-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

NUMBER OF SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                             Length 659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 4; I
Pred. No. 4.9e+02;
1; Mismatches 1;
                                                                                               Score 40; DB 4; 1
Pred. No. 1.4e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         core 39; DB 4;
red. No. 25;
Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: September 28, 2004, 09:21:32 Job time : 17.2 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 43.8%; Fred. No.
Matches 7; Conservative 4; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5171
                                      ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 YOFWKNFOTLKIVILG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.7%;
75.0%;
                                                                                                 Query Match
Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                                                                                                                                                              401 OYKTFWKNFGOVLK 414
                                                                                                                                                                                        2 OYO-FWKNF-OTLK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRGANISM: Proteus mirabilis
US-09-543-681A-5538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 75.0°
---- 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283 SAYOYWKN 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SQYQFWKN 8
                                               ; ORGANISM: Pseudo
US-09-252-991A-26013
                                                                                                                                                                                                                                                                                                                     US-09-543-681A-5538
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US-09-328-352-5171
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LENGTH: 92
LENGTH: 659
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US-09-252-991A-26013
; Sequence 26013, Application US/09252991A
; Sequence 26013, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: ABSUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR SPILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
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                                           Sequence 10, Application US/09165922A
Sequence 10, Application US/09165922A
Patent No. 6348641
GENERAL INFORMATION: TITLES, JOHN I.
MOISYADI, ISTEFO
NEUPANE, KABI R.
TITLE OF INVENTION: PURIFIED PROTEINS,
PRODUCING CAFFEINE FREE BEVERAGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSES: JONES, DAY, REAVIS & POGUE
STREET: NORTH POINT, 901 LAKESIDE AVENUE
CITY: CLEVELAND
STATE: OHIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS v. 5.1
SOFTWARE: WordPerfect for Windows v. 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,922A
FILING DATE: 02-OCt-1998
CLASSIFICATION: B00
                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 44114
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: GRIFFITH, CALVIN P.
REGISTRATION NUMBER: 34,831
REFERENCE/DOCKET NUMBER: 26536600003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 566-7050
TELEFAX: (216) 579-0212
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
ENGURY: 371 amino acid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DESCRIPTION: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-165-922A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319 NOYYFWDDFHPSEVV 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SOYOFWKNFOTLKIV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
           RESULT 37
US-09-165-922A-10
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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September 28, 2004, 08:51:21; Search time 52.525 Seconds (without alignments) 118.345 Million cell updates/sec OM protein - protein search, using sw model Run on:

1 QWDFGNTMCQLLTGLYFIGFFS 22 US-10-084-813-12 126 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 Total number of hits satisfying chosen parameters: 1586107 segs, 282547505 residues Searched:

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

A_Geneseq_29Jan04:*

1. geneseqp1980s:*
2. geneseqp2000s:*
4. geneseqp2001s:*
5. geneseqp2001s:*
6. geneseqp2003s:*
7. geneseqp2003bs:*
8. geneseqp2003bs:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aab88994 HIV gp120	Aaw27406 Inactive	Aaw27408 Inactive	Aaw88238 HIV-1 co-	Adc10142 Human NOV	Adc10144 Human NOV	Aaw26766 Human che	Aaw27407 Human CCR	Aaw27123 Human che	Aaw27125 Macaque c	Aaw07602 Human G-p		Aaw88232 HIV-1 co-		Amino	Aae07046 Human G-p	Human	Aag80111 Human CCR		Aae07037 Human G-p		8 Human	Abb56342 Non-endog	Aab83354 Human CCR	Aab82948 Human HIV
ΔΙ	AAB88994	AAW27406	AAW27408	AAW88238	ADC10142	ADC10144	AAW26766	AAW27407	AAW27123	AAW27125	AAW07602	AAW23835	AAW88232	AAY80128	AAG79089	AAE07046	AAE07048	AAG80111	AAE04321	AAE07037	AAE07039	AAB46858	ABB56342	AAB83354	AAB82948
DB	4	Ŋ	N	7	7	7	Ω	7	N	0	N	N	7	m	4	4	4	4	4	4	4	4	4	4	4
Length DB	22	8	-	н	9	9	3	S	വ	S	S	S	ນ	ഗ	352	M	ហ	ഗ	S	S	S	വ	S	വ	ß
Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0		100.0	100.0	ö	100.0	100.0	100.0		100.0	100.0		100.0
Score	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126
Result No.	н	7	٣	4	C)	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

7150 Human G-p 7152 Human G-p	Human Human	0597 Human G-p	Human	Human		G-prot		5540 Human G-p	8602 Human can	9514 Human C-C	1654 Human G-p	7728 Amino aci	1933 Human C-C	3341 Human che	3359 Macaque c	3834 Human CC
Aau97150 Aau97152	Aam52829 Aam5282	Abg70597	Abg92880	Aae25808	Aae25811	Abb81054	Abb0834	Abg75540	Abr58602	Aa029514	Abu61654	Abp9772	Abp8193.	Adcoa	Adc033	Aaw2383
AAU97150 AAU97152	AAM52829 AAM52828	ABG70597	ABG92880	AAE25808	AAE25811	ABB81054	ABB08343	ABG75540	ABR58602	AA029514	ABU61654	ABP97728	ABP81933	ADC03341	ADC03359	AAW23834
522	352 5	522	22	22	25	52	25	52	22	352 6	25	22		352 7	352 7	371 2
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
126	126 126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126
	28 29	30	32	33	34	35	36	37	38	39		41	42	43	44	45

ALIGNMENTS

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The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCRS. CXCR4 and STR131, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus. The present sequence is an example of a peptide of the invention
                                                                                                                                                              Human chemokine receptor, CD4, HIV, glycoprotein 120, gp120, antagonist, replication, CCR5, CXCR4, CD4, STRL33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gpl20 under physiological conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 126; DB 4; Length 22; Best Local Similarity 100.0%; Pred. No. 1.2e-12; Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                               HIV gp120 protein binding peptide #87.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QWDFGNTMCQLLTGLYFIGFFS 22
                                AAB88994 standard; peptide; 22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 21; Page 38; 114pp; English.
                                                                                                                                                                                                                                                                                                                   25-AUG-2000; 2000WO-US023505.
                                                                                                                                                                                                                                                                                                                                                     27-AUG-1999; 99US-0151270P.
                                                                                                23-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-244398/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22 AA;
                                                                                                                                                                                                                                                  WO200116182-A2.
                                                                                                                                                                                                                   Homo sapiens,
                                                                                                                                                                                                                                                                                  08-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                     Saxinger C;
                                                                AAB88994;
RESULT 1
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AAW27406;

RESULT 2

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AAW27406

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The present sequence is an inactive human CC (Cys-Cys) chemokine receptor 5 (CCR5), which lacks the last 3 transmembrane regions and the regions involved in G protein-coupling. CCR5 or its cDNA can used to diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis, viral infections, especially human immunodeficiency virus type 1 or type 2 (HIV-1) infection, cancer, atherosclerosis and autoimmune disorders. Subjects that express the inactive receptor have a predisposition, or resistance to HIV-1 and/or HIV-2
                                                                                Inactive; human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2; predisposition; resistance; diagnosis; treatment; prevention; inflammatory disease; rheumatorid arthritis; glomerulonephritis; asthma; idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer; atherosclerosis; autoimmune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Active and inactive forms of human CC chemokine receptor CCR-5 - usel to diagnose, prevent and/or treat inflammatory disorders, autoimmune disease and viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIV-1; CCR5; CCR5-delta32; co-receptor; infection; diagnosis; AIDS; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 126; DB 2; Length 215; 100.0%; Pred. No. 1.5e-11; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Libert F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIV-1 co-receptor CCRS variant CCRS-delta32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vassart G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QWDFGNTMCQLLTGLYFIGFFS 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 7; Fig 1d-e; 94pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Samson M, Parmentier M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EURO-) EUROSCREEN SA.
                                   Inactive human CCR5.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                               WO9732019-A2.
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       S X C C C C C C C C X S X L L L X X B X X 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is an inactive human (C (Cys-Cys) chemokine receptor S (CCRS), which is not a receptor of human immundeficiency virus type 1 or type 2 (HIV-1 or HIV-2), CCRS or its CDNA can used to diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer, atherosclerosis and autoimmune disorders. Subjects that express the inactive receptor have a predisposition, or resistance to HIV-1 and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inactive; human Cys-Cys chemokine receptor-5; CCR5; human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2; predisposition; resistance; diagnosis; treatment; prevention; inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma; idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer; atherosclerosis; autoimmune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Active and inactive forms of human CC chemokine receptor CCR-5 - useful to diagnose, prevent and/or treat inflammatory disorders, autoimmune disease and viral infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vassart G, Libert F;
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                                                                                                                                                                                                    AAW27406 standard; protein; 184 AA.
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QWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OWDFGNTMCQLLTGLYFIGFFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 1a; 94pp; English.
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96EP-00870102
                                                                                                                                                                                                                                                                                                                               14-APR-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  Inactive human CCR5.
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06-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mac
Local Sim
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Gaps

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32. .56 /note= "transmembrane domain 1"

Location/Qualifiers

Domain

14-APR-1998 (first entry)

AAW27408;

Query Match

Matches

93

g

RESULT 3

AAW27408

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This is the amino acid sequence of a CCR5 variant protein, designated CCR5-delta12, that includes the first 4 transmembrane domains of wild-type CCR5 (see AAW88121), but lacks transmembrane domains of wild-type CCR5 (see AAW88122), but lacks transmembrane domains 5-7. CCR5 serves as a co-receptor for infection by macrophage-tropic (M-tropic) strains of HIV-1. Individuals homozygous for the CCR5-delta23 mutation are resistant to HIV-1 infection, but heterozygous individuals are susceptible. The invention additionally relates to the identification of variant CCR5mil (See AAW88211), which lacks transmembrane domains 3-7 of CCR5. The detection of CCR5 variants may be used to identify individuals at lower risk of infection relative to the general population who, if infected, may exhibit slower progression to AINS. Probes and primers (see AAW84127-36) are provided for use in diagnostic methods for detecting the presence of such variants. A method is provided for inhibiting HIV-1 infection of a cell expressing the CCR5 receptor. This involves introducing a nucleic acid encoding a CCR5 variant into the cell, thereby reference of such variants are considered by resent on the cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New CCR5 variant protein of the HIV-1 co-receptor - useful in developing resistance of CCR5-expressing cells to HIV-1 infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quillent C, Arenzana Siesdedos F, Braun J;
67. .87
/note= "transmembrane domain 2"
103. .124
/note= "transmembrane domain 3"
142. .167
/note= "transmembrane domain 4"
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                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-EP003437.
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                                                                                                                                                                                                                                                                          WO9854317-A1.
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        Domain
                                                                             Domain
                                                                                                                                                           Domain
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04-JUN-2001, 2001US-0295607P, 04-JUN-2001, 2001US-029661P, 06-JUN-2001, 2001US-029661P, 06-JUN-2001, 2001US-029661P, 06-JUN-2001, 2001US-0296418P, 12-JUN-2001, 2001US-0295573P, 12-JUN-2001, 2001US-0295573P, 12-JUN-2001, 2001US-0295573P, 13-JUN-2001, 2001US-0295573P, 13-JUN-2001, 2001US-0295573P, 13-JUN-2001, 2001US-0299573P, 13-JUN-2001, 2001US-029953P, 13-JUN-2001, 2001US-0399949P, 22-JUN-2001, 2001US-0399949P, 22-JUN-2001, 2001US-0399949P, 22-JUN-2001, 2001US-039999P, 22-JUN-2001, 2001US-039999P, 23-JUN-2001, 2001US-039999P, 23-JUN-2001, 2001US-039999P, 23-JUN-2001, 2001US-03999P, 23-JUN-2001, 2001US-0399P, 23-JUN-2001, 2001US-0399P, 23-JUN-2001, 2001US-0399P, 23-JUN-2001, 2001US-0399P, 23-JUN-2001, 2001US-0399P, 23-JUN-2001, 2001US-0399P, 23-JUN-2001US-0399P, 23-JUN-2001US-0399P,
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22-FBB-2002; 20020S-0359034P.
22-FBB-2002; 2002US-0359034P.
22-FBB-2002; 2002US-0359121P.
27-FBB-2002; 2002US-0359964P.
01-MAR-2002; 2002US-0359868P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAR-2002; 2002US-0363430P.
12-MAR-2002; 2002US-0363676P.
10-APR-2002; 2002US-0371346P.
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                                                                                                          04-JUN-2002; 2002WO-US017443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002US-0359122P
                     WO2003000842-A2
                                                                  03-JAN-2003
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(CURA-) CURAGEN CORP.

Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
Gerlach VL, Gorman L, Guo X, Herrmann VL, Hjalt T, Ji W, Kekuda R;
Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;
Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;
Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK;
Spyrek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
Burgess CE, Lepley DM;

WPI; 2003-210149/20. N-PSDB; ADC10141.

New isolated NOVX polypeptides and nucleic acid molecules useful for treating, preventing and diagnosing pathological conditions with NOVX-associated disorders, such as cancer, obesity, diabetes and inflammatory or CNS diseases.

Claim 1; SEQ ID NO 162; 772pp; English.

The invention relates to novel isolated polypeptides, mature form of the polypeptide, a sequence that is 95% identical to the polypeptide or the polypeptide comprising one or more conservative substitutions. The NOVX polypeptide is useful for treating or preventing a pathology associated with the polypeptide e.g. disorders associated with aberrant expression or activity of the polypeptide, such as cancer, diabetes, obesity, and endocrine, CNS and inflammatory disorders. They can also be used in various detection and screening assays, chromosome mapping, tissue typing

Homo sapiens

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04-JUN-2002; 2002US-00379444.
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAY-1998 (first entry)
                                                                                                                Burgess CE, Lepley DM;
                    (CURA-) CURAGEN CORP.
                                                                                                                                     WPI; 2003-210149/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 121
                                                                                                                                              N-PSDB; ADC10143.
                                                                                                                                                                                                                                                                                                                                                           Sequence 268 AA;
                                                                                                                                                                                                   or CNS diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW26766;
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                                                                                                                                                                                                                                                   cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective, antifilammatory; gene therapy; antisense therapy; thyrominetic; NOVX; pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder; inflammatory disorder; chromosome mapping; tissue typing;
                                                                        Gaps
and predictive medicine. This sequence corresponds to one of the polypeptides of the invention.
                                                                        .
0
                                                   100.0%; Score 126; DB 7; Length 268; 100.0%; Pred. No. 1.9e-11;
                                                                        0; Indels
                                                                        0; Mismatches
                                                                                                                                                                                                                                 Human NOVX polypeptide SEQ ID NO: 164.
                                                                                                                93 ÓWDFGNÍMCÓLLÍGLÝFIGFFS 114
                                                                                                                                                                   ADC10144 standard; protein; 268 AA.
                                                                                           1 OWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002US-0359035P.
2002US-0359121P.
2002US-0359964P.
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14-DEC-2001; 2001US-0341562P.
                                                                                                                                                                                                                                                                                                                                                                              04-JUN-2002; 2002WO-US017443
                                                                                                                                                                                                                                                                                                                                                                                                                                            2001US-0296575P
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                                                                                                                                                                                                          18-DEC-2003 (first entry)
                                                          Local Similarity 100.
                                                                                                                                                                                                                                                                                             predictive medicine.
                              Sequence 268 AA;
                                                                                                                                                                                                                                                                                                                                      WO2003000842-A2.
                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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10-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-FEB-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JUN-2001;
                                                                                                                                                                                      ADC10144;
                                                   Query Match
                                                                        Matches
                                                                                                                                             RESULT 6
                                                                                                                                                          ADC10144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalian mixed lymphocyte receptor; chemokine receptor; MMLR-CCR, human; monocyte; macrophage; chemotaxis; haematopoiesis; infection; inflammation; proliferative disease; cardiovascular disease; tumour; rheumatoid arthritis; alveolitis; atherosclerosis; chronic granulomatous disease; asthma; myasthenia gravis; diabetes; chronic granulomatous disease; asthma; myasthenia gravis; diabetes; inflammatory bowel disease; toxic shock syndrome; septic shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated NOVX polypeptides and nucleic acid molecules useful for treating, preventing and diagnosing pathological conditions with NOVX-associated disorders, such as cancer, obesity, diabetes and inflammatory
                                                                                                Kekuda R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "a claimed polypeptide has isoleucine at residue
121"
Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
Dipipo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
Gerlach VL, Gorman L, Guo X, Herrnann JL, Hjalt T, Ji W, Kekuda R
Khramtsov NV, Li Liu X, Malyankar UM, Miller CE, Millet I;
Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;
Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK;
Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 126; DB 7;
100.0%; Pred. No. 1.9e-11;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chediak-Higashi syndrome; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107. .128
/note= "conserved peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 164; 772pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QWDFGNTMCQLLTGLYFIGFFS 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human chemokine receptor MMLR-CCR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                        Polynucleotide encoding MMLR-CCR or MPHG-CCR chemokine receptor - useful to study, diagnose and treat, e.g. infection, inflammation, solid tumour and proliferative and cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention; inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma; idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer; atherosclerosis; autoimmune disorder.
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100.0%; Score 126; DB 2; Length 332;

Best Local Similarity 100.0%; Pred. No. 2.4e-11;

Matches 22; Conservative 0; Mismatches 0; Indels (
                                                                                                             Coleman R, Wilde CG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 QWDFGNTMCQLLTGLYFIGFFS 105
                                                                                                                                                                                                                             Claim 8; Page 37-38; 59pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 OWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW27407 standard; protein; 352 AA
                                   97WO-US006993
                                                            96US-00638081
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                                                                                     (INCY-) INCYTE PHARM INC
                                                                                                            Au-Young J, Bandman O,
                                                                                                                                      WPI; 1997-549729/50.
N-PSDB; AAT99542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 332 AA;
                                  25-APR-1997;
                                                             26-APR-1996;
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            06-NOV-1997
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Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour; asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy; diagnosis; leukocyte trafficking; G protein coupled receptor; ligand; modulator; antibody; human.
                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5), which is stimulated by MIP-1 alpha, MIP-1 beta or RAWIES chemokines, but not by monocyte chemoattractant protein 1 (MCP-1), MCP-2, MCP-3, interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha) chemokines, Active CGR-5 is also a receptor of human immundeficiency virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its CDNA can used to diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and absoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer, atherosclerosis and autoimmune disorders
                                                                                                                                                                                                                                                                  Active and inactive forms of human CC chemokine receptor CCR-5 - useful to diagnose, prevent and/or treat inflammatory disorders, autoimmune disease and viral infection.
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0
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                                                                                                                                        Vassart G, Libert F;
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| Jabel = Extracellular_domain
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/label= Intracellular_domain
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/label= Extracellular_domain
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|label= Intracellular_domain
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/label= Extracellular_domain
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/label= Intracellular_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Fig 1b-c; 94pp; English.
  96EP-00870021.
96EP-00870102.
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/label= Ert
?13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                     Samson M, Parmentier M,
                                                                                 (EURO-) EUROSCREEN SA
                                                                                                                                                                                       WPI; 1997-479829/44.
N-PSDB; AAT90117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 352 AA;
01-MAR-1996;
06-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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This polypeptide sequence comprises macaque chemokine receptor 88C, a G protein coupled receptor that is involved in laukcoyte trafficking. Its amno sequence from a 88C DNA (AAADS163) isolated by PCR amplification. It shows 97% identity to human 88C (AAM27123). 88C receptors and their polypeptide fragments can be produced in transformed host cells. The receptors of peptides comprising one or more of the extracellular or intracellular domains, and anti-receptor antibodies can be used to modulate receptor activities, particularly ligand and G protein binding, and are potentially potentially useful in the treatment of atheroslerosis, rheumatoid arthritis, tumours, asthma, viral infection, AIDS inflammatory conditions, pathological immune response, antibody that specifically binds to macaque 88C is claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G-protein chemokine receptor; HDGNR10; signal transduction; haematopoiesis; leukaemia; inflammation; rheumatoid arthritis; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human G-protein chemokine receptor, HDGNR10 - useful to identify (ant)agonists, for treatment of haematopoiesis, leukaemia, chronic and acute inflammation, rheumatoid arthritis, etc.
                                                                                                                                                     New nucleic acid encoding chemokine receptors 88-2B and 88C - used modulate leukocyte trafficking, e.g. for treatment of inflammation, tumours, viral infections, auto-immune diseases, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 126; DB 2; Length 352; 100.0%; Pred. No. 2.6e-11;
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                                               Raport CJ;
                                                                                                                                                                                                                                             Claim 36; Page 57-58; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QWDFGNTMCQLLTGLYFIGFFS 22
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                                             Gray PW, Schweickart VL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-FEB-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-043072/04.
                                                                                       WPI; 1997-341689/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
(ICOS-) ICOS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAT44042.
                                                                                                               N-PSDB; AAT85163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW07602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This polypeptide sequence comprises novel human chemokine receptor 88C, a givetein coupled receptor that is involved in leukocyte trafficking. Its amino sequence was deduced from a cDNA clone (AATB51G) isolated from a macrophage library. It shows 62% identity to CCCKR1. Chemokine receptor 89.2B (see AAW27124) has also been identified. 88C and 88-2B receptors and their polypeptide fragments can be produced in transformed host cells. The receptors, peptides comprising one or more of the extracellular or intracellular domains, and anti-receptor antibodies can be used to modulate receptor activities, particularly ligand and G protein binding, and are potentially potentially useful in the treatment of atheroslerosis rheumatoid arthritis, tumours, aschma, viral infection, AIDS, inflammatory conditions, pathological immune response, abnormal haematopoietic processes etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour; asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy; diagnosis; leukocyte trafficking; G protein coupled receptor; ligand; modulator; antibody.
                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding chemokine receptors 88-2B and 88C - used to modulate leukocyte trafficking, e.g. for treatment of inflammation, tumours, viral infections, auto-immune diseases, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 126; DB 2; Length 352; 100.0%; Pred. No. 2.6e-11; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                             Gray PW, Schweickart VL, Raport CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 16; Page 47-48; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93 QWDFGNTWCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 OWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW27125 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Macaque chemokine receptor 88C.
                                                                                       96WO-US020759
                                                                                                                                  95US-00S75967.
                                                                                                                                                        96US-00661393.
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96US-00661393
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Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                        WPI; 1997-341689/31.
                                                                                                                                                                                                  (ICOS-) ICOS CORP.
                                                                                                                                                                                                                                                                                                             N-PSDB; AAT85161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 352 AA;
  WO9722698-A2
                                                                                       20-DEC-1996;
                                                                                                                                                        07-JUN-1996;
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                                                                                                                                20-DEC-1995;
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07-JUN-1996;
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                                             26-JUN-1997.
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8

Gaps

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RESULT 13
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                 Novel human mature G-protein chemokine receptor HDGNRIO (AAW07602) is a 7-transmembrane protein involved in signal transduction. Its amino acid sequence was deduced from a cDNA clone (AAY44042) isolated from a human monocyte library. Isolation of the cDNA allows prodn. of recombinant HDGNRIO in host, e.g. E. coli, COS or Sf9, cells. The recombinant sceptor can be used to identify agonists or antagonists of the receptor; such cpds. can be used to treat conditions related to the under- and over-expression of G-protein chemokine receptors
                                                                                                                                                                                                                                                                                                                              CC chemokine receptor 5; CCR5; G-protein coupled receptor; human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.
                                                                                                                                                      0; Gaps
                                                                                                                                  Length 352;
                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "extracellular loop-3 (Claim 19)"
277. 300
[label= VII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197. .210
note= "extracellular loop-2 (Claim 19)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "extracellular loop-1 (Claim 19)"
                                                                                                                                 100.0%; Score 126; DB 2;
100.0%; Pred. No. 2.6e-11;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                               29. .55
/label= I
/note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "transmembrane domain"
109. .120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "transmembrane domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                            Human CC chemokine receptor 5 (CCR5).
                                                                                                                                                                                     OWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
Claim 1; Page 44-46; 61pp; English.
                                                                                                                                                                          1 OWDFGNIMCOLLIGLYFIGFFS 22
                                                                                                                                                                                                                                               AAW23835 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WO-US009586
                                                                                                                                                                                                                                                                                                                                                                                                                          104. .126
/label= III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238. .258
/label= VI
                                                                                                                           Query Match
Best Local Similarity 100.0
Marches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       label= IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194. .219
/label= V
                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .171
                                                                                                              Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-MAY-1997;
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                                                                                                                                                                                                                                                                    AAW23835,
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Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
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This protein sequence comprises of a novel human macrophage-selective CC chemoxime receptor that has been designated CCRS. The sequence was deduced from an isolated cDNA clone (see MAT76920). An Alal271eu variant (see W238340 of CCRS was also identified. The susceptibility of human macrophages to HTV infection depends on cell surface expression of CD4 and CCRS. CCRS is a member of the 7-transmembrane superfamily of G protein coupled cell surface molecules. It plays an essential role in the membrane tailon step of infection by some HIV isolates. The establishment of stable, non-human cell lines and transgenic mammals having cells that occapress human CD4 and CCRS provides valuable tools for research of HIV infection. Antibodies that bind to CCRS. CCRS variants, and CCRS-binding agents capable of blocking membrane fusion between HIV and target cells expresent potential anti-HIV therapeutics for macrophage tropic strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGT (Cys) in wild-type CCR5, TGA
                                                                                                              CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion between HIV and a target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 126; DB 2; Length 352; 100.0%; Pred. No. 2.6e-11; ive 0; Mismatches 0; Indels (
  Berger EA, Alkhatib G, Murphy PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7. .87
note= "transmembrane domain 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03. 7.124
note= "transmembrane domain 3"
42. .167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "transmembrane domain 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "transmembrane domain 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "transmembrane domain 6" 275. .301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "transmembrane domain 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "corresponds to
(Stop) in CCr5m303"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW88232 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 OWDFGNIMCOLLIGLYFIGFFS 22
                                                                                                                                                                     Claim 68; Fig 1C; 70pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .260
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/note= "
Combadiere C, Feng Y,
Broder CC, Kennedy PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy; human.
                                                     WPI; 1998-032650/03.
                                                                         N-PSDB; AAT76920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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WPI; 2001-602565/68.
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                                                                                                                                                                                                                                                                                                                                 detection of CCRS variants may be used to identify individuals at lower risk of infection relative to the general population who, if infected, may exhibit slower progression to AIDS. Probes and primers (see AAV84127-36) are provided for use in diagnostic methods for detecting the presence of such variants. A method is provided for inhibiting HIV-1 infection of a cell expressing the CCRS receptor. This involves introducing a nucleic acid encoding a CCRS receptor. This involves introducing a nucleic of functional CCRS molecules present on the cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, G-protein coupled receptor; G-protein chemokine receptor; HDGNR10; diagnosis; haematopoiesis; wound healing; coagulation; angiogenesis; tumour; infection; leukaemia; psoriaatis; allergy; T-cell mediated autoimmente disease; atherogenesis; anaphylaxis; inflammation; allergic reaction; silicosis; sarcoidosis; recein rheumatoid arthritis; hyper-eosinophilia syndrome.
                                                                                                                                                                 New CCR5 variant protein of the HIV-1 co-receptor - useful in developing resistance of CCR5-expressing cells to HIV-1 infection.
                                                                                                                                                                                                                             This is the amino acid sequence of wild-type human CCR5, which serves as a co-receptor for infection by macrophage-tropic (M-tropic) strains of HIV-1. The invention relates to the identification of a CCR5 variant (se AAW88231), designated CCR5, comprising the first two transmembrane domains of wild-type CCR5, but lacking transmembrane domains of wild-type CCR5, but lacking transmembrane domains 3-7. The posterive correlation with resistance to infection with M-tropic HIV-1 strains, and may indicate slower progression of the disease. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 126; DB 2; Length 352; 100.0%; Pred. No. 2.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                     Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human G-protein chemokine receptor HDGNR10 SEQ ID NO:2.
                                                                           (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                        Disclosure; Page 34-35; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY80128 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QWDFGNTMCQLLTGLYFIGFFS 22
                         98WO-EP003437.
                                                   97US-0048057P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                             WPI; 1999-059835/05.
                                                                                                                                           N-PSDB; AAV84126
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 352 AA;
                         29-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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 03-DEC-1998
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The present sequence represents a human G-protein chemokine receptor
designated HDGNR10. HDGNR10 polynucleotides are useful in methods of
screening for compounds which bind to and either: (1) activate the
HDGNR10 polypepides causing stimulation of haematopoiesis, wound
compound infections, leukaemia, T-cell mediated autoimmune diseases,
chronic infections, leukaemia, T-cell mediated autoimmune diseases,
parastici infections, psoriasis, and to stimulate growth factor activity,
or (2) inhibit activation of the HDGNR10 polypeptides which is useful for
preventing and/or treating allergy, atherogenesis, anaphylaxis,
malignancy, chronic and acute inflammation, histamine and immunoglobulin
E-mediated allergic reactions, prostaglandin-independent fever, bone
marrow failure, silicosis, sarcoidosis, rheumaciod arthritis shock and
hyper-eosinophila syndrome. The polypucleotides are also useful for
diagnostic assays for detecting diseases related to mutations in the
nucleic acid sequences encoding the polypeptides and for detecting an
altered level of the soluble form of the receptor polypeptides. The
polymucleotides are also useful for in vitro purposes related to
scientific research, synthesis of DNA and manufacture of DNA vectors
                                                                                                                                                                                                                                                                  Isolated nucleic acid encoding human G-protein chemokine receptor useful for diagnostic assays, scientific research and screening for compounds which bind to and activate or inhibit activation of the receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, receptor, DC-SIGN, dendritic cell, T lymphocyte, HIV, 9p120,
C-type lectin, ICAM3, HIV entry, T cell, macrophage, HIV infection, CCRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 126; DB 3; Length 352; 100.0%; Pred. No. 2.6e-11; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Van Kooyk Y, Geijtenbeek T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of human CCRS protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG79089 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 1; 22pp; English.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2001; 2001WO-US006322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAR-2000; 2000US-00517605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYNY ) UNIV NEW YORK STATE. (UYNI-) UNIV NIJMEGEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22; Conservative
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                                                                                                                                                    WPI; 2000-181807/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                              N-PSDB; AAZ91481
                                                                       Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200164752-A2.
                                                                                                                                                                                                                                                                                                                                                                                        polypeptides.
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42. .166 |label= Transmembrane_domain note= "Segment 4"

'label= Intracellular_loop_2

Domain Domain Domain

196. 223 /label= Transmembrane_domain /note= "Segment 5" 67. 195 |abel= Extracellular_loop_2

236. .260 /label= Transmembrane_domain

Domain

Domain

'note= "Segment 6"

label= Intracellular_loop_3

. 235

287. .305 /label= Transmembrane_domain /note= "Segment 7"

Extracellular_loop_3

/label= Ex

Domain Domain

The specification describes an antibody which is specific for an antiganic fragment of gapl20. This antiganic fragment binds to DC-SIGN or serviced upon gpl20 binding of DC-SIGN due to concontant conformational change. DC-SIGN is a receptor that is specifically expressed on dendritic cells and facilitates infection of T lymphocytes with HIV. DC-SIGN is identical to a HIV-1 gpl20-binding C-type lectin. DC-SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes with high affinity. The antibody of the invention inhibits the trans enhancement of HIV entry into a T cell or macrophage facilitated by infection. The present sequence represents a human CCRS protein, which is a translocation promoting agent that interacts with CD4. This receptor functions in HIV-1 entry into cells An antibody for the treatment or prevention of HIV-infection comprises a gpl20 portion which binds to DC-SIGN or is exposed upon gpl20 binding of DC-SIGN due to concomitant conformational change. Disclosure; Page 118-119; 131pp; English

Sequence 352 AA;

0; Gaps Query Match
Best Local Similarity 100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels (

1 OWDFGNIMCOLLIGLYFIGFFS 22 ŝ g

AAE07046 standard; protein; 352 AA.

AAE07046;

(first entry) 16-0CT-2001

Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.

Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; H1V; human immunodeficiency virus; antimicrobial; vascdilator; vulnerary; cytostatic; immunosuppressive; nootropic, neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrocintestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.

Homo sapiens

. .36 /label= Extracellular_domain /label= Transmembrane_domain 59. .67 /label= Intracellular_loop_1 Location/Qualifiers 'note= "Segment 1" Key Domain Domain Domain Domain THE LITERAL LITERAL SON THE STATE OF THE STA

58. .88 /label= Transmembrane_domain /note= "Segment 2" Jomain Domain

39. .102 /label= Extracellular_loop_1 103. 124 /label= Transmembrane_domain /hote= "Segment 3" 125. 141 Domain

Domain

306. .352 ⊂ /label= Intracellular_domain WO200158916-A2 Domain

16-AUG-2001,

09-FEB-2001; 2001WO-US004153

22-SEP-2000; 2000US-0234336P. 09-FEB-2000; 2000US-0181258P. 09-MAR-2000; 2000US-0187999P

(HUMA-) HUMAN GENOME SCI INC.

Li Y, Ruben SM; Rosen CA, Roschke V,

WPI; 2001-488966/53. N-PSDB; AAD13282. Isolated nucleic acid encoding a human G-protein chemokine receptor (CCRS) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.

Claim 102; Fig 1; 518pp; English.

The invention relates to human G-protein chemokine receptor (CCR5)

HDGNRIO polypeptides and polynucleotides. CCR5 HDGNRIO antibodies are
useful for treating, preventing or ameliorating a disease or disorder
associated with inflammation, defective or aberrant chemotaxis of immune
cells. HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's
sarcoma) or defective or aberrant T-cell antigen presenting cell
interaction. The disease or disorder may also be an infection a crapped san early stage HIV infection, a
cytomegalovirus infection such as an early stage HIV infection, a
cytomegalovirus infection or a poxvirus infection, an autoimmune
disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
disease or disorder may be associated with aberrant CCR5 expression, lack
of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand
function. CCR5 HDGNRIO protein is used as a food additive or preservative
continuous one identification and in gene therapy. CCR5 HDGNRIO DNA,
contromosome identification and in gene therapy. CCR5 HDGNRIO DNA,
contromosome identification and in gene therapy. CCR5 HDGNRIO DNA,
contromosome identification and in gene therapy. CCR5 HDGNRIO DNA,
controminate and prevention of cancer (breast, outpinmune
diagnosis, treatment and prevention of cancer (breast, outpinmune
diagnosis, treatment and prevention of cancer (breast, outpinmune
contents); immune disorders (Addison's disease, allergies, autoimmune
contents and wound healing. The
contents sequence is human CCR5 HDGNRIO protein

contents sequence is human CCR5 HDGNRIO protein

Sequence 352 AA;

Query Match

100.0%; Score 126; DB 4; Length 352;

ô Gaps ; ; Pred. No. 2.6e-11; 0; Mismatches 0; Indels 100.08; Best Local Similarity 100. Matches 22; Conservative

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RESULT 17 AAE07048

AAE07048 standard; protein; 352 AA.

AAE07048;

(first entry) 16-OCT-2001

Human G-protein chemokine receptor (CCRS) HDGNR10 protein #2.

Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation, HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostatic; immunosuppressive; nootropic; neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoms; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.

Homo sapiens.

WO200158916-A2.

16-AUG-2001.

09-FEB-2001; 2001WO-US004153.

09-FEB-2000; 2000US-0181258P. 09-MAR-2000; 2000US-0187999P. 22-SEP-2000; 2000US-0234336P.

HUMA- HUMAN GENOME SCI INC.

Li Y, Ruben SM; Rosen CA, Roschke V,

WPI; 2001-488966/53. N-PSDB; AAD13299.

Isolated nucleic acid encoding a human G-protein chemokine receptor (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.

Example 40; Page 504-505; 518pp; English.

The invention relates to human G-protein chemokine receptor (CCRS)

HDGNR10 polypeptides and polynucleotides. CCRS HDGNR10 antibodies are useful for treating, preventing or ameliorating a disease or disorder associated with inflammation, defective or aberrant chemotaxis of immune cells, HIV infection (such as Pheumovystis carinip pneumonia or Kaposi's arroma) or defective or aberrant T-cell antigen presenting cells interaction. The disease or disorder may also be an infectious disease interaction under as an early stage HIV infection, a cytomegalovirus infection, or a poxyriva infection, an autoimmune disorder may be associated with aberrant CCRS systession, lack of CCRS function, aberrant CCRS ingand expression, or lack of CCRS ligand function. CCRS HDGNR10 protein is used as a food additive or preservative for chromosome identification and in gene therapy. CCRS HDGNR10 DNA, protein antibodies, agoniates and antagonists are also useful in the disorder marrow, gastrointestinal tract, liver, lung, urogenital); immune disorders (Addison's disease, allergies, autoimmune

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     disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular disorders (myocardial ischaemias) and wound healing. The present sequence is human CCR5 HDGNR10 protein
autoimmune thyroiditis, diabetes mellitus, Crohn's
                                                               0; Gaps
                                                100.0%; Score 126; DB 4; Length 352; 100.0%; Pred. No. 2.6e-11; ive 0; Mismatches 0; Indels C
                                                                                           93 OWDFGNTMCOLLTGLYFIGFFS 114
                                                                                                                               AAG80111 standard; protein; 352 AA.
                                                                             1 OWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                          17-JAN-2002 (first entry)
                                                       Local Similarity 100.
 anaemia,
                                                                                                                                                                        Human CCR5 protein.
                                   Seguence 352 AA;
 haemolytic
                                                                                                                                            AAG80111;
                                                   Query Match
                                                                Matches
                                                                                                                 RESULT 18
8888888
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Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection; inflammation; autoimmune disease; metestasis; brondhal asthma; lupus; chronic bowel inflammation; rheumatoid arthritis; cytostatic; antiinflammatory; antiasthmatic; immunosuppressive; dermatological; Forssmann W, Adermann K, Heitland A, Spodsberg N; antirheumatic; antiarthritic. 31-MAR-2000; 2000DE-01016013. 02-APR-2001; 2001WO-EP003708. IPFP-) IPF PHARM GMBH. FORS/) FORSSMANN U. WPI; 2001-626256/72. WO200172830-A2 Homo sapiens.

Diagnostic agent containing two or more receptor-specific ligands, useful for detecting tumors, inflammation etc., also therapeutic use of ligand inhibitors.

Disclosure; Page 10; 26pp; German.

This invention describes a novel diagnostic agent (A) comprising at least two different ligands (I) for receptors (II) that are implicated in disease. (A) are used for the diagnosis of tumors (especially colorectal or prostatic), organ rejection, inflammation and autoimmune diseases. Also inflammation (particularly paroinst tumors (and their metastases), inflammation (particularly bronchial asthma or chronic bowel inflammation), or autoimmune diseases (theumatoid arthritis or lupus), where the (cardio) vascular, lymphatic, respiratory, nervous, digestive, andocrine, motor or urogenital systems or skin are affected, and bone marrow diseases. The products of the invention are chemokine derivatives immunosuppressive, dermatological, antitheumatic, antiarthritic. Chemokines act on specific tumor and inflammatory cells through a constablation of chemokine receptors (CR), which control migration and proliferation of these cells. Asd800128 represent human chemokine fragments used to illustrate the method of the invention

Sequence 352 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, transformed mammalian cell; CD4, reporter gene; translocation; human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy; chemokine receptor; CKR; cellular dysfunction; HIV infection; cofactor; CC-CKR-5; envelope glycoprotein; anti-HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transformed mammalian cell (I) that contains a CD4 gene, reporter gene and HIV LTR for identification of drugs and antibodies for treatment of
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Ouery Match
100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0
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100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human chemokine receptor (CKR), CC-CKR-5 related protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deng H, Ellmeier W, Landau NR, Liu R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Col 47-50; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AARO-) AARON DIAMOND AIDS RES CENT.
(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                              93 OWDFGNTMCOLLTGLYFIGFFS 114
                                                                                                                                                                1 OWDFGNIMCOLLIGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE04321 standard; protein; 352 AA.
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97US-00858660.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAY-1996;
19-JUN-1996;
19-MAY-1997;
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1 QWDFGNTMCQLLTGLYFIGFFS 22

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Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostatic; immunosuppressive, notropic; neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crobin's disease; wound healing; cardiovascular disorder; myocardial ischaemia.
                                                                                                                           Human G-protein chemokine receptor (CCRS) HDGNR10 protein #1.
                                                                                                                                                                                                                                                                                                     . .36
label= Extracellular_domain
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/label= Transmembrane_domain
/note= "Segment 6"
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/label= Transmembrane_domain
/note= "Segment 7"
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/label= Transmembrane_domain
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label= Transmembrane_domain
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label= Intracellular_loop_2
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| Jabel = Transmembrane_domain
| Inote = "Segment 4"
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/label= Transmembrane_domain
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| Jabel = Extracellular_loop_3
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|Tabel= Intracellular_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     label= Extracellular loop 1
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93 OWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                       AAE07037 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "Segment 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                note= "Segment 2"
                                                                                                                                                                                                                                                                                                                                                                       "Segment 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "Segment 5"
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36.
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                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                     16-OCT-2001
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                                                                              AAE07037;
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                                   RESULT 20
                                               AAE0703.
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HDGNR10; human; G-protein chemokine receptor; antiinflammatory;
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                                                                                                                                                                                                                                                                                                                                          2001-488965/53.
                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAD13198.
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                                           WO200158915-A2.
    Homo sapiens.
                                                                                     16-AUG-2001.
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AAB46858
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10 protein. CCR5 HDGNR10 cDNA is included in ATCC Deposit No: 97183. CCR5 HDGNR10 antibodies are useful for treating, preventing or ameliorating a disease or disorder associated with inflammation, defective or aberrant chemotaxis of immune cells, HIV infection (such as Pheumocystis carinii presenting cell interaction. The disease or disorder may also be an infections disease (e.g. a viral infection such as an early stage HIV infections disease (e.g. a viral infection, or a poxyirus infection, autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The disease or disorder may be associated with aberrant CCR5 ingand expression, or a contoinmune disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The disease or disorder may be associated with aberrant CCR5 ingand function. CCR5 HDGNR10 protein is used as a food additive or preservative to increase or decrease storage capabilities. CCR5 HDGNR10 by the dispense the control of the contr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapy. Crss HDGNR10 DNA, protein, antibodies, agonists and antagonists are also useful in the diagnosis, treatment and prevention of cancer (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract, liver, lung, urogenital); immune disorders (Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular disorders (myocardial ischaemias) and wound
                                                                                                                                                                                                                                  Isolated nucleic acid encoding a human G-protein chemokine receptor (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostatic; immunosuppressive; noctropic, neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; hosemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.
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                                                                                                                               Li Y, Ruben SM;
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                                                                                                                                                                                                                                                                                                                                             Claim 102; Fig 1; 495pp; English.
09-FEB-2000; 2000US-0181258P.
09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
                                                                                     (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                   neurodegenerative disorders.
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1es 22; Conservative
                                                                                                                               Rosen CA, Roschke V,
                                                                                                                                                                      WPI; 2001-488965/53.
N-PSDB; AAD13181.
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The present sequence is human G-protein chemokine receptor (CCRS) HDGNR10 protein. CCRS HDGNR10 antibodies are useful for treating, preventing or ameliorating a disease or disorder associated with inflammation, defective or aberrant chemotaxis of immune cells, HIV infection (such as perman) and the coll of interaction. The disease or disorder may also be an infectiona or Kappsal's sarcoma) or defective or aberrant T-cell antigen presenting cell interaction. The disease or disorder may also be an infection, a cytomegalovirus infection such sorvirus infection), an autoimmune disease (e.g. with aberrant CCRS expression, lack of CCRS function, aberrant CRS expression, and of CCRS incider, aberrant CRS expression, or lack of CCRS incider, aberrant CRS incider, aberrant CRS expression, or lack of CRS ingand function. CRS HDGNR10 protein is used as a food additive or preservative to increase or decrease identification and in gene therapy. CCRS HDGNR10 DNA, protein, antibodies, agonists and antagonists are also useful in the diagnosis, creatment and prevention of cancer (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract, liver, lung, urogenital); immune disorders (Addison's disease, allergies, autoimmune thempolytic anaemia, autoimmune thyroiditis, diabetes mellitus, crohu's disease, multiple sclerosis, rheumatoid arrhritts and ulcerative colitis); cardiovascular disorders (myocardial ischaemias) and wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid encoding a human G-protein chemokine receptor (CCRS) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 40; Page 486-487; 495pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA, Roschke V, Li Y, Ruben SM;
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                                                                                                  09-FEB-2000; 2000US-0181258P.
09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
09-FEB-2001; 2001WO-US004152.
                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurodegenerative disorders.
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This invention describes a novel receptor polypeptide (I) selected from (i) a fully defined 329 amino acid sequence (II) fully disclosed in the specification, and (ii) a polypeptide encoded by the CDNA concained in a plasmid, and fragments, analogs and derivatives of the polypeptide. The products of the invention have antiinflammatory, immunomodulatory, antiparastic, antiparatic, antiparatic, antialtergic, immunosuppressive, vulnerary, cytostatic, antiparastic, antiparatic, infertion chemokine activity and can be used for gene therapy. The groducts of the invention can also be used for stimulating anematopolesis, wound healing, coagulation, also be used for stimulating neomatopolesis, parastic infections, psoriasis, and sute inflammation, histenmine and immunoglobulin E (ISE) -mediated allergic reactions, prostaglandin-independent fever, bone marrow failure, estimulating syndrome. (N.B. This record was resubmitted to correct errors in the keyword formatting)
immunomodulatory; anticoagulant; antiallergic; immunosuppressive; cytostatic; antiparasitic; antiparotic; antirheumatic; antiarthritic; vasctropic; gene therapy; haematopolesis; wound healing; coagulation; vasctropic; gene therapy; haematopolesis; wound prowth factor activity; T-cell mediated autoimmune disease, psoriasis; allergy; atteroor activity; anapingates; malignancy; inflammation; histamine; IGE; silicosis; shock; immunosiboluin E-mediated allergic reaction; rheumatoid arthritis; prostaglandin-independent fever; bone marrow failure; sarcoidosis; hyper-eosinophilic syndrome; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human G-protein chemokine receptor polypeptides and polynucleotides, useful for identifying (ant)agonists to the G-protein chemokine receptor.
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100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                                                        98US-00195662.
99US-00339912.
                                                                                                                                                                                                                                                                                                                                                        29-NOV-2000; 2000US-00725285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-226317/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Li Y, Ruben SM;
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                                                                                                                                                                                                                                                                   US2001000241-A1.
                                                                                                                                                                                                                            Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                   06-JUN-1995;
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Identifying agonists of G protein-coupled receptors (GPCRs) for use in disease treatment, comprises contacting candidate compounds with versions
                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to G protein-coupled receptors (GPCRs) for which the endogenous ligand has been identified. Non-endogenous constitutively activated versions of known GPCRs are used in the invention for the direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists. Such agonists are useful as therapeutic agents for diseases or disorders associated with GPCRs. The present sequence is a non-endogenous version of a known human GPCRs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5; human immunodeficiency virus; anti-inflammatory disease; human.
                                                       Human; G protein-coupled receptor; GPCR; non-endogenous; mutant; constitutively activated GPCR; agonist; disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 126; DB 4; Length 352; 100.0%; Pred. No. 2.6e-11; tive 0; Mismatches 0; Indels C
                             Non-endogenous human GPCR protein, SEQ ID NO: 477
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 277-278; 394pp; English.
                                                                                                                                                                                                                                                                                            Lehmann-Bruinsma K, Liaw CW, Lin I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 QWDFGNTMCQLLTGLYFIGFFS 114
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                                                                                                                                                                                                      05-APR-2001; 2001WO-US011098.
                                                                                                                                                                                                                                 07-APR-2000; 2000US-0195747P.
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12-JAN-2000; 2000GB-0000661.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human CCR5 protein sequence.
(first entry)
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1es 22; Conservative
                                                                                                                                                                                                                                                              (AREN-) ARENA PHARM INC.
                                                                                                                                                                                                                                                                                                                      WPI; 2001-648759/74.
N-PSDB; ABI97978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 352 AA;
                                                                                                                                              WO200177172-A2.
                                                                                                   Homo sapiens.
Synthetic.
18-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                             of GPCRs.
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(AARO-) AARON DIAMOND AIDS RES CENT.
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(LIYY/)
(RUBE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the human CCR5 protein sequence. The invention relates to a method for determining whether an agent is capable of modulating the interaction of chemother receptor 5 (CCR5) with gp120, comprising incubating the agent with GCR5 and gp120 and determining whether the agent modulates the interaction, where gp120 is associated with CDR, and where the interaction is a low affinity binding. The method is used to identify an agent capable of modulating the method is used to identify an agent capable of modulating the interaction of CCR5 with gp120. An agent identified by the method is used to prepare a pharmaceutical composition for the treatment of a disease or condition associated with CCR5 and gp120 interaction, to treat a subject with a disease or condition associated with CCR5 and gp120 interaction, and for preparing a pharmaceutical for treating human immunodeficiency virus (HIV). It can also be treat anti-inflammatory diseases. The method is commercially useful, amenable to high throughput screening, and is commercially useful, amenable to high throughput screening, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCR5; chemokine; co-receptor; human immunodeficiency virus type 1; HIV-1; infection; therapy; vaccine; anti-HIV-1.
                                                                                                                      Determining if an agent can modulate CCRS-gp120 interaction, comprises incubating the agent with CCR5 and gp120 and determining if the agent
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 126; DB 4; Length 352; 100.0%; Pred. No. 2.6e-11; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2. .18 /note= "binds to HIV-1 gp120"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB82948 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 OWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                      Claim 1, Page 110; 113pp; English.
                                                            Rickett GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-FEB-2000; 2000US-0165667P.
19-MAY-2000; 2000US-0205839P.
07-FEB-2001; 2001US-0267231P.
12-JAN-2000; 2000GB-00000663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human HIV-1 co-receptor CCR5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PROG-) PROGENICS PHARM INC.
                                                                                                                                              modulates the interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 22; Conservative
                                                            Perros M,
                                                                                  WPI; 2001-477088/52.
N-PSDB; AAF87099.
                     (PFIZ ) PFIZER LTD.
(PFIZ ) PFIZER INC.
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200164710-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-SEP-2001.
                                                            Dobbs S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB82948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 25
AAB82948
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The present sequence is that of human HIV-1 co-receptor CCR5. Amino acids 2-18 in the N-terminal region of CCR5 comprise an HIV-1 gpl20-binding 2-18 in the N-terminal region of CCR5 comprise an HIV-1 gpl20-binding CR5 and HIV-1 gpl20. Post-translational sulfation of the tyrosine residues in the TW-1 gpl20. Post-translational sulfation of the tyrosine residues in the CCR5 N-terminals is required for gpl20 binding and may critically modulate the susceptibility of target cells to HIV-1 infection in vivo. The invention provides claimed sulfated peptides (see AAB82947) that are based on the CCR5 N-terminal region and which are effective for inhibiting HIV-1 binding to CCR5. These peptides are used in claimed methods of inhibiting HIV infection of CD4+ cells, of preventing CD4+ cells are infected with HIV, and of identifying an agent which inhibits binding of a CCR5 ligand to a CCR5 receptor. The methods may be carried out in a subject, sepscially a human, infected (therapeutic method), not infected with HIV (prophylactic method), or in a subject who is not infected with, but has been exposed to, HIV
                                                                                                                                                                                                Novel compounds comprising specific amino acids within CCR5 (HIV 1 coreceptor) amino terminal domain including negatively charged and two sulfated tyrosine residues is useful for treating HIV infection in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immune cell chemotaxis, autoimmune disease, rheumatoid arthritis, neurodegeneration, viral infection, Kaposi sarcoma, cancer, hyperproliferative disease, neurological disease, receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; G-protein chemokine receptor; CCRS; HDGNR10; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 126; DB 4; Length 352; 100.0%; Pred. No. 2.6e-11; vative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human G-protein chemokine receptor (CCR5) HDGNR10 #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU97150 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 30; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-FEB-2000; 2000US-0181258P.
09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-FEB-2001; 2001US-00779879.
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Dragic T, Olson WC;
                                                                                WPI; 2001-611273/70.
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                                                                                                                    N-PSDB; AAH26903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2002048786-A1.
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The present invention relates to the isolation of a novel human G-protein chemokine receptor (CCR5) designated HDGNR10, and polynucleotide sequences encoding it. The invention also describes antibodies that bind human G-protein chemokine receptor (CCR5) HDGNR10 and polynucleotide that bind human G-protein chemokine receptor (CCR5) HDGNR10 and polynucleotide sequences encoding the antibodies. The antibodies are useful for treating or preventing inflammation, defective or aberrant chemotaxis of immune cells and T-cell/antigen-presenting cell interactions, infections and autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral infections for segociated with aberrant or deficient expression of the CCR5 receptor or its ligands. The antibodies are also useful to determine CCR5 expression, e.g. for diagnosis, prognosis and monitoring of cancer and other hyperproliferative diseases. The polynucleotide sequences encoding human G-protein chemokine receptor, (CCR5) HDGNR10 can be used to produce the recombinant receptor, and in the treatment of a wide range of diseases such as infectious diseases (e.g. influenza), neurological diseases (e.g. Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The present sequence represents human G-protein chemokine receptor (CCR5) HDGNR10 #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 126; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps
                                                                                                     New nucleic acid encoding an antibody specific for the G-protein chemokine receptor CCR5, useful for treatment and diagnosis of e.g. inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, G-prötein chemokine receptor; CCR5; HDGNR10; inflammation; immune cell chematoid arthritis; insurodegeneration; viral infection; Kaposi sarcoma; cancer; hyperproliferative disease; neurological disease; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human G-protein chemokine receptor (CCRS) HDGNR10 #2.
                 Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 QWDFGNTWCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 OWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU97152 standard; protein; 352 AA
                                                                                                                                                                                               Claim 61; Fig 1; 180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-FEB-2000; 2000US-0181258P.
09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-FEB-2001; 2001US-00779879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                 Rosen CA, Roschke V,
                                                        WPI; 2002-434754/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROSEN C A.
                                                                           N-PSDB; ABK51853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2002048786-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU97152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ROSE/)
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The present invention relates to the isolation of a novel human G-protein chemokine receptor (CCRS) designated HDGMR10, and polynucleotide chemokine receptor (CCRS) HDGMR10, and polynucleotide that bind human G-protein chemokine receptor (CCRS) HDGMR10 and polynucleotide bind human G-protein chemokine receptor (CCRS) HDGMR10 and polynucleotide for treating cardinaces encoding the antibodies. The antibodies are useful for treating or preventing inflammation, defective or aberrant chemotaxis of immune cells and T-cell/antigen-presenting cell interactions, infections and autofendmune diseases, rheumathoid arthritis, meurodegeneration, viral infections (especially early-stage human immune deficiency virus (HIV), cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions associated with aberrant or deficient expression of the CCRS receptor or its ligands. The antibodies are also useful to determine CCRS expression, e.g. for diagnosis, prognosis and monitoring of cancer and other chyprotein chemokine receptor (CCRS) HDGMR10 can be used to produce the recombinant receptor (CCRS) HDGMR10 can be used to produce the recombinant receptor (CCRS) HDGMR10 can be used to greduese such as infectious diseases (e.g. influenza), neurological diseases (e.g. present sequence represents human G-protein chemokine receptor (CCRS) present sequence represents human G-protein chemokine receptor (CCRS) presents equence represents human G-protein chemokine receptor (CCRS) presents equence represents human G-protein chemokine receptor (CCRS) presents equence represents human G-protein chemokine receptor (CCRS) are presents equence represents human G-protein chemokine receptor (CCRS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCRS; CC chemokine receptor 5; human; HIV infection; human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome; drug screening; identification; variant.
                                                                                                                                                                         New nucleic acid encoding an antibody specific for the G-protein chemokine receptor CCR5, useful for treatment and diagnosis of e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Glu replaces wild-type Leu; encoded by CTG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 126; DB 5; Length 352; 100.0%; Pred. No. 2.6e-11; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                            Disclosure, Page 165-166; 180pp; English.
                                                                Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Encoded by AGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 OWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM52829 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 OWDFGNIMCQLLIGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2001; 2001WO-US009155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human CCR5 Gln 55 variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22; Conservative
                                                                Rosen CA, Roschke V,
                                                                                                        WPI; 2002-434754/46.
N-PSDB; ABK51870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 58
(LIYY/) LI Y.
(RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200171346-A2
                                                                                                                                                                                                                      inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 28
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  셤
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Sequence 352 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG70597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 30
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method for identifying a binding compound for CC Chemokine receptor 5 (CCR5). The method involves screening a library of test molecules (particularly peptides) with immobilised CCR5, and then identifying those molecules which bind. The invention also relates to CCR5-binding molecules identified using the method of the invention, methods for identifying consensus motifs for CCR5-binding peptides, a transfer vector encoding tagged CCR5, a computer-aided methods for determining the relative binding affinity of a test molecule to CCR5 and a computer aided frug screening assay that utilises the three-dimensional structure of CCR5. Compounds identified using the methods of the invention are useful for treating or preventing HIV (human immunodeficiency virus) infection or AIDS (acquired immunodeficiency syndrome) in a patient. The methods of the invention may also be used to identify agonists or antagonists of the interaction of CCR5. The present squence represents a naturally courting variant of human CCR5 in which there is a glutamine, rather than a leucine, at position 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCR5; CC chemokine receptor 5; human; HIV infection;
human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
drug screening; identification.
                                                                                                                                                                                                                                                                    Identifying CC chemokine receptor 5 binding compound for treating AIDS, comprises binding a molecule from library to a molecule having binding property corresponding to CCR5 and identifying bound molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 126; DB 5; Length 352;
100.0%; Pred. No. 2.6e-11;
tive 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                 Tan Hehir CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human CC chemokine receptor 5 (CCR5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 ÓWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM52828 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                 Example 3; Fig 4B; 50pp; English.
                                                                                                                                                                                 See RH,
             21-MAR-2000; 2000US-0190946P.
21-MAR-2000; 2000US-0191299P.
21-MAR-2001; 200US-001348.
20-MAR-2001; 2001US-00813448.
20-MAR-2001; 2001US-00813651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2000; 2000US-0190946P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2001; 2001WO-US009155
                                                                                                                                           (CONS-) CONSENSUS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
1es 22; Conservative
                                                                                                                                                                                 Nestor JJ, Wilson CJ,
                                                                                                                                                                                                                  WPI; 2002-010610/01.
                                                                                                                                                                                                                                    N-PSDB; ABA02318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200171346-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM52828;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 29
AAM52828
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The invention relates to a method for identifying a binding compound for CC chemokine receptor 5 (CCR5). The method involves screening a library of CC chemokine receptor 5 (CCR5). The method involves screening a library of test molecules (particularly peptides) with immobilised CCR5, and then clantifying those molecules which bind. The invention also relates to CRS-binding molecules which binds the method of the invention, consensus motifs for CCR-binding peptides, a crampisfer vector encoding tagged CCR3, a computer-aided methods for determining the relative binding assay that utilises the three-dimensional computer aided drug screening assay that utilises the three-dimensional convention are useful for treating or preventing HIV (human invention are useful for treating or preventing HIV (human convention) infection or AIDS (acquired immunodeficiency syndrome) in a patient. The methods of the invention may also be used to sidentify agonists or antagonists of the interaction of CCR5 with its natural ligand, and to determine a binding motif for CCR5. The present sequence represents human CCR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; G-protein chemokine receptor; HDGNR10; CCRS receptor; haematopoiesis; solid tumour; chromic infection; leukaemia; T-cell mediated autoimmune disease; parasitic infection; leukaemia; T-cell mediated autoimmune disease; parasitic infection; psoriasis; growth factor activity; allergy; attherogenesis; anaphylaxis; mallignancy; inflammation; histamine; immunoglobulin E; IgE-mediated allergic reaction; sarcoidosis; prostaglandin-independent fever; bone marrow failure; shock; rheumatoid arthritis; hyper-cosinophilic syndrome; cycostatic; antiparasitic; antiparasitic; antiparasitic; antiparasitic; antiparasitic; antiateriosclerotic; antiinflammatory; antirheumatic; antiathritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying CC chemokine receptor 5 binding compound for treating AIDS, comprises binding a molecule from library to a molecule having binding property corresponding to CCR5 and identifying bound molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 126; DB 5; 100.0%; Pred. No. 2.6e-11;
                                                                                                                                                                                                                                                                                                                                                    Tan Hehir CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human G-protein chemokine receptor, HDGNR10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QWDFGNTMCQLLTGLYFIGFFS 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Fig 4A; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                    See RH,
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21-WAR-2000; 2000US-0190996P.
21-WAR-2001; 2000US-0191299P.
20-MAR-2001; 2001US-00813448.
20-MAR-2001; 2001US-00813651.
20-WAR-2001; 2001US-00813653.
                                                                                                                                                                                                                                                                     (CONS-) CONSENSUS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-DEC-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                    Nestor JJ, Wilson CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antipyretic; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-010610/01.
N-PSDB; ABA02317.
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WO200264612-A2

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The present invention relates to the isolation of human G-protein chemokine receptor, HDGNR10 (CCRS receptor), and the polynucleotide sequences according it. HDGNR10 polypeptide and polynucleotide sequences are or useful for diagnosine of HDGNR10. They are useful for identifying related to underexpression of HDGNR10. They are useful for identifying modulators for stimulating haematopoiesis, wound healing, coagulation, angiogenesis, to treat solid tumours, chronic infections, psoriasis, or for stimulating growth factor activity. The sequences are also useful for preventing and/or treating allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histamine and immunoglobulin E (IgE)-mediated allergic reactions, prostaglandin-independent fever, bone marrow failure, sarcoidosis, theumatoid arthitis, shock and hypersoening and the therapy to treat conditions related to underexpression of HDGNR10. The present sequence represents human G-protein chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 126; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human G-protein chemokine receptor polypeptide useful for identifying modulators for stimulating hematopoiesis, wound healing, leukemia, for treating allergy, rheumatoid arthritis, shock and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Fig 1; 22pp; English.
                                                                                                                                                          95US-00466343,
                                                                             99US-00339912
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-690494/74.
N-PSDB; ABS54272.
                                                                                                                                                                                                                           (LIYY/) LI Y.
(RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor, HDGNR10
                                                                                                                                                                                                                                                                                                                                                        Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      research agents.
                                                                         25-JUN-1999;
                                                                                                                                                      06-JUN-1995;
25-JUL-2002
                                                                                                                                                                                                                                                                                                                                           Li Y,
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Immunoglobulin; variable heavy chain; variable light chain; human; G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation; immunologic deficiency syndrome; blood protein disorder; nephritis; ataxia telangiectasia; endocaxin lethality; inflammatory bowel disease; histiocytosis; chemotaxis; infectious disease; autoimmune disease; Addison's disease; dermatitis; rheumatoid arthritis; allergy; neurodegenerative disorder; viral infection; proxvirus infection; HIV; human immunodeficiency virus; cytomegalovirus; kaposi's sarcoma; pneumocystis carnii infection; cardiovascular disorder; atherosclerosis;
                                                                                                                                                                                                                                                             Human immunoglobulin variable heavy domain #1.
                     93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                      ABG92883 standard; protein; 352 AA.
1 OWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                    19-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lymphocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                               ABG92883;
                                                                                                 RESULT 31
                                                                                                                     ABG92883
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The invention describes an isolated polymucleotide encoding a first antibody at least 95-100% identical to a second antibody consisting of an antibody at least 95-100% identical to a second antibody consisting of a wariable heavy (WH) or variable light (NL) domain of the antibody conversable by a hybridoma cell line consisting of XF3.5F1, XF11.1F8, XF27.281.8B5, XF27/28.18B5, X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human G-protein Chemokine Receptor gene (HDGNR10) useful for treating, preventing, ameliorating or monitoring diseases or disorders associated with aberrant expression of HDGNR10 e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 126; DB 5; Length 352;
100.0%; Pred. No. 2.6e-11;
tive 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunoglobulin; variable heavy chain; variable light chain; human; G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human G-protein chemokine receptor (CCR5) HDGNR10 #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 OWDFGNIMCOLLIGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG92880 standard; protein; 352 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 55; Fig 4; 562pp; English.
                                                                                                                                                                                                                                                                                                                                                                                   Roschke V, Rosen CA, Ruben SM;
                                                                                                                                                                                               12-JUN-2001; 2001US-0297257P.
08-AUG-2001; 2001US-0310488P.
12-OCT-2001; 2001US-0326447P.
21-DEC-2001; 2001US-0341725P.
                                                                                                08-FEB-2002; 2002WO-US003634.
                                                                                                                                                                           2001WO-US004153
                                                                                                                                                                                                                                                                                                                              HUMA-) HUMAN GENOME SCI INC.
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Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-643455/69.
N-PSDB; ABS68606.
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                                               22-AUG-2002.
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The invention describes an isolated polynuclectide encoding a first antibody at least 95-100% identical to a second antibody consisting of antibody at least 95-100% identical to a second antibody consisting of an anino acid sequence comprising at least one, two or three CDR regions of a variable heavy (VH) or variable light (VL) domain of the antibody consisting of XE3-512, XE71.1E%, XE7-728.1819. XE77.28.1819. XE77.28
                                                                                                                                                                                                                                     neurodegenerative disorder; viral infection; poxvirus infection; HIV;
human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;
Pneumocystis carnii infection; cardiovascular disorder; atherosclerosis;
immunologic deficiency syndrome, blood protein disorder; nephritis; ataxia telanquectalar, endotoxin lethality; inflammatory bowel disease; histicoytosis; chemotaxis; infectious disease, autoximune disease; Addison's disease; dermatitis; rheumatoid arthritis; allergy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roschke V, Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-FEB-2001; 2001WO-US004153.
12-UUN-2001; 2001US-0297257P.
08-AUG-2001; 2001US-0310458P.
12-OCT-2001; 2001US-032447P.
21-DEC-2001; 2001US-0341725P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 22; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-643455/69.
                                                                                                                                                                                                                                                                                                                                                                                                                         lymphocytopenia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-AUG-2002.
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The invention relates to human G-protein chemokine receptor (CCR5), HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5 antibodies are used for the treatment or prevention of inflammation, defective or aberrant chemotaxis of immune cells or T cell antigenpresenting cell interaction, viral infections (specifically human immune deficiency (including its early stages), cytomegalo or pox viruses), autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis carinii infection, kaposi's sarcoma or any condition associated with aberrant expression of CCR5 or their ligands. They are also used for the detection, diagnosis, prognosis and monitoring of cancers or other hyperproliferative diseases. The present sequence is human G-protein chemokine receptor (CCR5), HDGNR10 DNA
                                                                                                                    Human, G-protein chemokine receptor, CCR5, HDGNR10 protein, cancer, inflammation, viral infection, autoimmune disease, neurodegeneration, rheumatoid arthritis, Pneumocystis carinii infection, Kaposi's sarcoma, hyperproliferative disease, receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding antibodies to the human CCRS receptor HDGNR10, useful for treatment, prevention and diagnosis of e.g. cancer, also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                              Human G-protein chemokine receptor (CCR5), HDGNR10 #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 61; Page 163-164; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 OWDFGNTMCOLLTGLYFIGFFS 114
AAE25808 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE25811 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 OWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                        09-FEB-2001; 2001US-00779880.
                                                                                                                                                                                                                                                                                                                                  09-FEB-2000; 2000US-0181258P.
09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li Y,
                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA, Roschke V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-499674/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 related antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                     (ROSE/) ROSEN C A. (ROSC/) ROSCHKE V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAD42409.
                                                                                                                                                                                                                                         US2002061834-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 352 AA;
                                                                                                                                                                                                            Homo sapiens.
                                                              24-FEB-2003
                                                                                                                                                                                                                                                                          23-MAY-2002.
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Gaps . 0

0; Indels

Mismatches

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Conservative

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QWDFGNTWCQLLTGLYFIGFFS 114 1 QWDFGNTMCQLLTGLYFIGFFS 22

> RESULT 33 AAE25808

98US-00195662.

18-NOV-1998;

20-JUN-2002.

US2002076745-A1.

Homo sapiens.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human G-protein chemokine receptor (CCRS), which is and nucleic acid molecules encoding such proteins. CCRS antibodies are used for the treatment or prevention of inflammation, defective or aberrant chemotaxis of immune cells or T cell antigenpresenting cell interaction, viral infections (specifically human immune deficiency (including its early stages), cytomegalo or pox viruses), autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis carinii infection, Kaposi's sarcoma or any condition associated with detection, diagnosis, prognosis and monitoring of cancers or other hyperproliferative diseases. The present sequence is human G-protein chemokine receptor (CCRS), HDGNR10 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7-transmembrane receptor; G-protein coupled receptor; GFCR; HDGNR10; G-protein chemokine receptor; haematopoietic; immunosuppressant; antiparasitic; antipsoriatic; antiallergic; antiinflammatory; cytostatic; antirheumatic; antiarthritic; gene therapy; human; receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding antibodies to the human CCRS receptor HDGNR10, useful for treatment, prevention and diagnosis of e.g. cancer, also
                                                         Human; G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer; inflammation; viral infection; autoimmune disease; neurodegeneration; rheumatiod arthritis; Pheumocystis carinii infection; Kaposi's sarcoma; hyperproliferative disease; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 126; DB 5; Length 352; 100.0%; Pred. No. 2.6e-11; cive 0; Mismatches 0; Indels (
Human G-protein chemokine receptor (CCR5), HDGNR10 #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G-protein chemokine receptor, HDGNR10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 170; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 OWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB81054 standard; protein; 352 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-FEB-2000; 2000US-0181258P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
                                                                                                                                                                                                                                                                                                                                                                                                                               09-FEB-2001; 2001US-00779880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen CA, Roschke V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-499674/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    related antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ROSE/) ROSEN C A. (ROSC/) ROSCHKE V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAD42426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 352 AA;
                                                                                                                                                                                                                                                                                         US2002061834-A1
                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (RUBE/)
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                                                                                                                                                                                                                                                                                      New polynucleotide encoding a human G protein chemokine receptor HDGNR10, useful e.g. for treating tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human chemokine C-C motif receptor 5, CCR5, haplotype pair; isogene; single nuclectide polymorphism; SNP; human immunodeficiency virus 1; HIV-1 infection; acquired immunodeficiency syndrome; AIDS; antiviral; genotype; polymorphic variant; transgenic; drug screening; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human chemokine (C-C motif) receptor 5 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB08343 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 OWDFGNIMCOLLIGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           label= Leu, Gln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Phe, Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 223
/label= Arg, Gln
                                                                                                                                                                                                                                                                                                                                   Claim 7; Fig 1; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22; Conservative
                                                                                                                                                                                                                                            WPI; 2002-598724/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 182
                                                                                                                                                               (LIYY/) LI Y.
(RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 55
                                                                                                                                                                                                                                                         N-PSDB; ABN86542
                                                                                                                                                                                                              Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome 3p21
                                                                                                                                    36-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB08343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New haplotypes of the human chemokine (C-C motif) receptor 5 gene, useful to diagnose and treat diseases associated with its abnormal expression or function, including human immunodeficiency virus-1 infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 126; DB 5; Length 352; 100.0%; Pred. No. 2.6e-11; tive 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human G-protein chemokine receptor, HDGNR10, protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG75540 standard; protein; 352 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 29; Fig 3; 61pp; English.
                                                                                                                                                                                                                                                                                                                      (GENA-) GENAISSANCE PHARM INC.
                                                                                                                                                           04-APR-2001; 2001WO-US010708.
                                                                                                                                                                                                                                           05-APR-2000; 2000US-0194361P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABA97318, ABA97319.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                      Kliem SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 352 AA;
WO200177125-A2.
                                                                           18-OCT-2001,
                                                                                                                                                                                                                                                                                                                                                                                                           Choi JY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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The invention discloses a G-protein chemokine receptor (sometimes referred to as a 7-transmembrane receptor) polypeptide, HDGNR10, and the polynucleotide encoding it. G-protein chemokine receptors are involved in signal transduction pathways. The polynucleotide and polypeptide can be used to identify compounds which activate or inhibit activation of the protein and those compounds which encivate or inhibit activation of the protein and providing to the patient DNA encoding the agonist or antagonist and expressing them in vivo (gene therapy). The polynucleotides and polypeptide are also useful for for diagnosing a polynucleotides and polypeptide are also useful for for diagnosing a fisease or susceptibility to a disease related to an under-expression of the protein, for chromosome identification or as immunogens for producing and intipodies. Agonists are useful in stimulating hematopolesis, wound
                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human G-protein chemokine receptor polypeptide useful for diagnostic purposes and for identifying modulators of the polypeptide useful for treating leukemia, autoimmune diseases, psoriasis and allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              healing, coagulation, anglogenesis, to treat solid tumours, chronic infections, leukaemia, T-cell mediated auto-immune diseases, parasitic infections, postiasis and to stimulate growth factor activity. Antagonists are useful in the prevention and treatment of allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histamine and Igs-mediated allergic reactions, prostaglandin-independent fever, bone marrow failure, silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-eosinophilic syndrome. The sequence presented is the
sarcoidosis; rheumatoid arthritis; shock; hyper-eosinophilic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, cancer; diagnosis; screening; modulator; leukaemía; ischaemía; heart disease; atherosclerosis; endometriosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 126; DB 6; Length 352; 100.0%; Pred. No. 2.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cancer related protein SEQ ID NO:259.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 ÓWDFGNÍWCÓLLÍGLÝFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABR58602 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Fig 1; 22pp; English.
                                                                                                                                                                              11-FEB-2000; 2000US-00502783.
                                                                                                                                                                                                                            95US-00466343.
                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JUL-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human HDGNR10 protein
                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-208944/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABX10635.
                                                                                        US2002132269-A1.
                                                                                                                                                                                                                                                                                                                  Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 352 AA;
                                                                                                                                                                                                                          06-JUN-1995;
                                            Homo sapiens.
                                                                                                                                  19-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABR58602;
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ABU61654;
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                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down-regulated in specific cancers (e.g. about 1031 genes up-regulated in a require lukemia). ACC72641 to ACC72860 represent cancer related gene nucleotide sequences which encode the proteins given in ARR58709. Also described: (1) determining the presence or absence of a pathological cell in a patient; (2) an expression vector comprising a nucleic acid molecule described above; (3) a host cell comprising the vector; (4) an isolated polypeptide, which is encoded by the nucleic acid; (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a patient by administering to the patient the antibody above; and (7) a patient by administering to the patient the antibody above; and (7) a drug screening assay. The nucleic acid is useful for therapeutic targets. In particular, the nucleic acid is useful for charpeutic targets. In particular, the nucleic acid is useful for bancheds, prostate, skin and uterus, wounds, ischaemia, heart diseases, atherosclerosis and endometriosis. The nucleic acid is also useful in a bathology, earticularly for identifying agents for treating these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, urological disorder, stress urinary incontinence, prostate cancer, benign prostatic hyperplasia; overactive bladder,
                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                               New genes that are up-regulated or down-regulated in cancers, useful a markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 126; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human C-C chemokine receptor type 5 (333) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                     Claim 12; Page 745; 767pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 OWDFGNIMCOLLIGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA029514 standard; protein; 352 AA.
                                                                                                     17-SEP-2001, 2001US-0323469P.
20-SEP-2001, 2001US-0323887P.
13-NOV-2001, 2001US-0350666P.
08-FEB-2002; 2002US-0355145P.
08-FEB-2002; 2002US-0355257P.
12-APR-2002; 2002US-0372246P.
                                                                                                                                                                                                     (EOSB-) EOS BIOTECHNOLOGY INC
                                                                               17-SEP-2002; 2002WO-US029560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                         WPI; 2003-354600/33.
                                                                                                                                                                                                                                                                                   N-PSDB; ACC72740.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 352 AA;
                          WO2003025138-A2.
 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-AUG-2003
                                                     27-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pathologies
                                                                                                                                                                                                                                             Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA029514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 39
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SXXXXX
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The invention relates to a method for treating an urological disorder which comprises assaying the ability of the compound to modulate 313, 333, 5464, 188717 or 33524 nucleic acid expression or polypeptide activity. The method is useful for identifying a compound for treating an urological disorder comprising urinary incontinence e.g., overactive/oversensitive bladder, overflow urinary incontinence, stress urinary incontinence caused by dysfunction of the bladder, urethra or central/protableral nervous system, prostatitis, benign prostatic hyperplasia, prostate cancer or kiney disorders. It is also used in gene therapy. The prostate cancer or kiney disorders. It is also used in gene therapy. The protein. This sequence is used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying a compound, capable of treating urological disorder e.g., benign prostatic hyperplasia, by assaying the ability of the compound to modulate 313, 333, 5464, 188717 or 33524 nucleic acid expression or polypeptide activity.
overflow urinary incontinence; gene therapy; nephrotropic; prostatitis; kidney disorder; C-C chemokine receptor type 5; CCR5; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human G-protein chemokine receptor (HDGNR10) polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; G-protein chemokine receptor; receptor; HDGNR10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 81; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU61654 standard; protein; 352 AA.
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                                                                                                                                                                                                                                                                                                        07-NOV-2002; 2002WO-US035824.
                                                                                                                                                                                                                                                                                                                                                                          07-NOV-2001; 2001US-0344552P.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-00195662,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-SEP-2002; 2002US-00232686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-00466343,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-449396/42.
N-PSDB; AALS9912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Silos-Santiago I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 352 AA;
                                                                                                                                                                    WO2003039475-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2003023044-A1.
                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-AUG-2003
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Page 22

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Producing an antibody, involves immunizing an animal with a polypeptide or with a polypeptide encoded by the human G-protein chemokine receptor clone in ATCC 97183, and recovering the antibody.
                                                                                                                              Claim 1; Fig 1; 23pp; English.
25-JUN-1999; 99US-00339912.
                  (HUMA-) HUMAN GENOME SCI INC.
                                                        WPI; 2003-456307/43.
N-PSDB; ACA61721.
                                      Li Y, Ruben SM;
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The invention relates to a method of producing an antibody, involving immunishing an animal with a human G-protein chemokine receptor (HDGNR10) polypeptide (also referred to as a human 7-transmembrane receptor) and recovering an antibody which binds the polypeptide. The method is useful for producing an antibody which binds specifically to the human G-protein chemokine receptor polypeptide. This sequence represents the HDGNR10 polypeptide of the invention Sequence 352 AA;

93 QWDFGNTMCQLLTGLYFIGFFS 114 1 OWDFGNIMCOLLIGLYFIGFFS 22 Query Match Best Local Similarity 100.0 Matches 22, Conservative ò

0; Gaps

100.0%; Score 126; DB 6; Length 352; 100.0%; Pred. No. 2.6e-11; tive 0; Mismatches 0; Indels (

Search completed: September 28, 2004, 09:03:37 Job time : 56.525 secs

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September 28, 2004, 09:00:23; Search time 19.8 Seconds (without alignments) 57.362 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                             389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                126
1 QMDFGNTMCQLLTGLYFIGFFS 22
                                                                                              OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                          Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 4, Appli Sequence 1, Appli Sequence 2, Appli Sequence 13, Appli Sequence 13, Appli Sequence 2, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 52, Appli Sequence 5, Appli Sequence 1, Appli Sequence 9, Appli Sequence 9, Appli Sequence 4, Appli Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli Description Sequence Sequence Sequence Sequence Sequence Sequence Seguence Sequence Sequence US-08-833-752-4 US-09-08-33-752-6 US-08-466-343D-2 US-08-61-105-14 US-08-575-96-7-14 US-08-575-96-7-14 US-09-534-185-52 US-09-534-185-52 US-09-534-185-52 US-09-534-185-52 US-09-534-185-52 US-09-534-185-52 US-09-534-185-52 US-09-54-18-244-3 US-09-646-343D-9 US-08-466-343D-9 US-08-466-343D-9 US-08-466-343D-9 US-08-466-343D-9 US-08-466-343D-9 US-08-466-343D-9 US-08-466-383-50 US-09-645-583-50 US-09-645-583-50 US-09-645-583-50 US-08-643-752-7 US-09-131-827A-2 US-09-131-827A-20 PCT-US95-00476-4 PCT-US95-00476-2 US-08-307-499-30 US-08-446-669-2 SUMMARIES Query Match Length DB Score Result No.

83 65.9 269 3 US-08-269-268-30 82 65.1 355 1 US-08-461-244-2 82 65.1 355 3 US-09-045-581-56 81 64.3 360 4 US-09-544-185-56 81 64.3 360 4 US-09-544-185-51 80 63.5 354 4 US-09-544-185-51 80 63.5 354 4 US-09-544-185-51 81 64.3 360 4 US-09-86-31-51 82 63.3 355 1 US-08-012-988A-2 83 71 56.3 355 1 US-08-46-669-5 84 08-09-045-583-53 85 3 US-08-446-669-5 86 3 355 4 US-09-045-583-53 86 3 355 4 US-09-284-185-53 86 3 355 4 US-09-886-319A-14 86 3 355 4 US-09-886-319A-14	Sequence 30, Appl Sequence 2. Appli	56,	56	51,	51,	7	Sequence 13, Appl	equence 9,	~		'n	53	ť		Sequence 14, Appl	Sequence 5, Appli	Sequence 9, Appli	
6 6 7 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	-09-299-268- -08-461-244-	-09-045-583-5	-09-534-185-5	-09-045-583-5	-09-534-185-5	-08-724-984A-	-09-886-319A	-09-502-783A-	-08-012-988A-	J8-450-393A-	18-446-669-	09-045-583-5	09-239-938	-09-534-185-5	-09-886-319A-1	-00476-	-08-833-752-	ALIGNMENTS
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				64.	64.	63.	.09	58	26.	56.	56.	56.	26	26	.96	56	54.	

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APPLICANT: SAMSON, MICHEL
APPLICANT: SAMSON, MICHEL
APPLICANT: VASSART GILEER
APPLICANT: VASSART GILEER
APPLICANT: VASSART, GILEER
APPLICANT: LIBERY, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEWOKINES RECEPTOR
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEWOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 1
CORRESPONDENCE LORDES: Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STREET: CA
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

MAPLICATION NUMBER: 9-APF-1997

FLING DATE: 9-APF-1997

CLASSIFICATION: 5.56

ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E

NEGISTRATION NUMBER: 34,115

REFERENCE/DOCKET NUMBER:

INFORMATION POR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 184 amino acids

TYPE: amino acid

TOPOLLOGY: linear

MOLECULE TYPE: protein

US-08-833-752-4

INFORMATION PROSED:

100.0%; Score 126; DB 4; Length

US-08-833-752-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 184;
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100.0%; Score 126; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 OWDFGNTMCQLLTGLYFIGFFS 22
                                               Sequence 4, Application US/08833752
Patent No. 6448375
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22; Conservative
RESULT 1
US-08-833-752-4
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RESULT

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: 352 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                           22; Conservative
                                                                                                                                                                                                                                                                                                                                      / MOLECULE TYPE: protein US-08-833-752-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein US-08-466-343D-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: DC
COUNTRY: USA
20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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US-08-466-343D-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                 APPLICANT: Quillent et al.
TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE BAKET & Botts, L.L.P. attn. Lisa Kole
STREET: 30 ROCKefeller Plaza
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: SAMSON, MICHEL
APPLICANT: PARABUTIER, MARC
APPLICANT: PARABUTIER, MARC
APPLICANT: PARABUTIER, MARC
APPLICANT: UASSART, GIBBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 126; DB 3; Length 215; Best Local Similarity 100.0%; Pred. No. 1.5e-11; Matches 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/087,232A
FILING DATE: 28 MAY 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 28 MAY 1998
CLASAFIRICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/048,057
FILING DATE: 30 MAY 1997
ATTORNEY AGENT INFORMATION:
NAME: KOLE, LISA B., 225
REFERENCE/DOCKET NUMBER: 35,225
REFERENCE/DOCKET NUMBER: 35,225
REFERENCE/DOCKET NUMBER: 36,225
FELEPHONE: (212) 408-2628
TELEPHONE: (212) 765-2519
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 ÓWDFGNÍMCQLLÍGLÝFIGFFS 114
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
              Sequence 17, Application US/09087232A Patent No. 6153431 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08833752
Patent No. 6448375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
GY: linear
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                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 10112
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US-09-087-232A-17
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08466343D
Patent No. 6025154
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: CHEMOKINE RECEPTOR HIGHRIO (AS AMENDED)
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 126; DB 4; Length 215; Best Local Similarity 100.0%; Pred. No. 1.5e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 126; DB 3; Length 352; Best Local Similarity 100.0%; Pred. No. 2.5e-11; Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,343D FILING DATE: 06-UUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                 APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 QWDFGNTMCQLLTGLYFIGFFS 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                       JOLECULE 215 amino acids
TOPOLOGY: 111
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Matches
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KENOLIS 1.

Sequence 13. Application US/09087232A

Sequence 13. Application US/09087232A

PARENT NO. 6153431

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Quillent et al.

TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR

TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESSE:

ADDRESSEE: 30 Rockefeller Plaza

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-861-105-14

US-08-861-105-14

Sequence 14, Application US/08861105

Sequence 14, Application US/08861105

Patent No. 6258627

APPLICANT: LITTMAN, DAN R.
APPLICANT: DENG, HONGKUI
APPLICANT: LANDAU, NATHANIEL R.
APPLICANT: LANDAU, NATHANIEL R.
APPLICANT: LANDAU, NATHANIEL R.
APPLICANT: LIU, RONG
ITILE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
ITILE OF INVENTION: USES THEREOF
INVENTION: USES THEREOF
INVENTION: USES THEREOF
INVENTION: USES THEREOF
INVENTION: ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
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Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New YOFK
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUNT TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA: US/09/087,232A
PPLICATION NUMBER: US/09/087,232A
FILING DATE: 28 MAY 1998
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 60/048,057
FILING DATE: 30 MAY 1997
ATTONIEV-AGENT INFORMATION:
NAME: KOULE, LISA B.
REGISTRATION NUMBER: 35,225
REFERENCE/DOCKET NUMBER: AP 31115
TELECHONE: (212) 408-2628
TELECHONE: (212) 408-2638
TELECHONE: (212) 408-2638
TELECHONE CHARACTERISTICS:
LENGTH: antho acid
TYPE: antho acid
TYPE: antho acid
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STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 QWDFGNTMCQLLTGLYFIGFFS 114
93 QWDFGNTMCQLLTGLYFIGFFS 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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Sequence 2, Application US/08575967A

Patent No. 6265184
GENEMATION:
APPLICANT: Gray et al.
TITLE OF INVENTION: Chemokine Receptor Materials and Methods
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS: ADDRESSEE: Marchall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 126; DB 3; Length 352; Best Local Similarity 100.0%; Pred. No. 2.5e-11; Matches 22; Conservative 0; Mismatches 0; Indels C
                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentur Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,105
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARS: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/575,967A
                                                                                                                                                                                                                                                                                                    TILING DATE:

CLASSIFICATION: 436

PILING APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PILING DATE: 19-JUN-1996

CLIASSIFICATION: 436

PRIOR APPLICATION: 436

PRIOR APPLICATION: 436

PRIOR APPLICATION UMBER: US 08/227,319

FILING DATE: 13-APR-1994

ATTORNEY AGENT INFORMATION:

NAME: Jackson Esq., David A.

REFERENCE/DOCKET NUMBER: 1049-1-004 NI

TELEPHONE: 201-487-5800

TELEPHONE: 201-487-5800

TELEPHONE: 201-487-5800

TELEPHONE: 201-487-5801

TELEPHONE: 201-243-1684

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE: CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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                           New Jersey
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 6300 Sear
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                07601
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US-09-517-605-5
Sequence 5, Application US/09517605
PACENT NO. 6391567
GENERAL INFORMATION:
APPLICANT: Littman, Dan R.
APPLICANT: Kwon, Douglas S.
APPLICANT: van Kooyk, Yvette
APPLICANT: van Edijtenbeck, Theo
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 52, Application US/09534185
Patent No. 6403767
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 126; DB 4; Length 352; 100.0%; Pred. No. 2.5e-11; tive 0; Mismatches 0; Indels 0
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COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24 Mar-2000
CLASSIFICATION NUMBER: US/09/534,185
PRIOR APPLICATION NUMBER: 09/045,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: <Unknown>
ATTORNEY/ABCATU INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/POCKER NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 1049-1-017
CURRENT APPLICATION NUMBER: US/09/517,605
CURRENT FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
                                                   93 OWDFGNTMCOLLTGLYFIGFFS 114
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       1 OWDFGNTMCQLLTGLYFIGFFS 22
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INFORMATION FOR SEQ ID NO: 52:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.0
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSGANISM: Homo sapiens US-09-517-605-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-09-534-185-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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          à
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APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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100.0%; Score 126; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature; OTHER INFORMATION: /= "88C amino acid sequence" US-08-575-967A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 126; DB 3; Best Local Similarity 100.0%; Pred. No. 2.5e-11; Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATE:
FILLING DATE:
ATTORNEY, FAGENT INFORMATION:
NAME: MANDEAGORIAS, AMY E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMUNICATION INFORMATION:
TELECOMUNICATION:
(617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-WAR-98
FILING APPLICATION: 435
PLIASSIFICATION DATA:
APPLICATION NUMBER:
NAME: NO. 6265184and, Greta E.
REGISTRATION NUMBER: 35.302
REFERENCE/DOCKET NUMBER: 32918
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-485-1900
TELEPAX: 206-485-1900
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 QWDFGNTWCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 OWDFGNIMCOLLIGLYFIGFFS 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (617)227-7400
TELEPAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 28 State Streer CITY: Boston STATE: Massachusetts COUNTRY: USA
                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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RESULT 14
US-08-466-343D-9
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US-09-796-202-1
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                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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Fatent No. 6448375

GENERAL INCRMATION:

APPLICANT: SANGON, MICHEL

APPLICANT: PARMENTIER, WARC

APPLICANT: LIBERT, GILDERT

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR

TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

CORRESPONDENCE: 10 Martens, Olson & Bear

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                           .
                                                                                                                                                                                                                                             Query Match

100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 126; DB 4; Length 352; Best Local Similarity 100.0%; Pred. No. 2.5e-11; Matches 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NAMBER: US/08/833,752
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-534-185-52
                                                                                                                                                                                                                                                                                                                                                                                                93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 OWDFGNTMCQLLTGLYFIGFFS 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 9-APR-1997
CLASSIFCATION: 536
ATTORNEY/AGENT INPORMATION:
NAME: Altman, Daniel E
REGISTATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 352 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-833-752-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Li, Yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-502-783A-2
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APPLICANT: Ruben, Steven M.

TITLE OF INVENTION: Polymuclectides Encoding Human G-Protein Chemokine Receptor (CCR5)
FILE OF INVENTION: PLOSMING
FILE OF INVENTION: HDGNIO
FILE OF INVENTION: 1488.1150006
CURRENT APPLICATION NUMBER: US/09/502,783A
CURRENT FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SEQ ID NOS: 9
SEQ ID NO SEQ ID NOS: 9
LENGTH: 352
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Patent No. 6025154
Patent No. 6025154
Patent No. 6025154
TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGNRIO (AS AMENDED)
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09796202
| Patent No. 6548636
| GENERAL INFORMATION:
| APPLICANT: Dragic, Tatjana |
| APPLICANT: Olson, William |
| TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION |
| TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION |
| FILE REFERENCE: 2048/64010/JPW/SHS |
| CURRENT APPLICATION NUMBER: US/09/796,202 |
| CURRENT PILING DATE: 2001-02-28 |
| NUMBER OF SEQ ID NOS: 17 |
| SOFTWARE: Patentin version 3.0 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 126; DB 4; Length 352; Best Local Similarity 100.0%; Pred. No. 2.5e-11; Matches 22; Conservative 0; Mismatches 0; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 QWDFGNTWCQLLTGLYFIGFFS 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 OWDFGNTMCOLLIGLYFIGFFS 22
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-502-783A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1100 NEW CITY: WASHINGTON STATE: DC
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TYPE: PRT
ORGANISM: human
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                       Query Match 69.0%; Score 87; DB 1; Length 347; Best Local Similarity 66.7%; Pred. No. 2e-05; Matches 14; Conservative 3; Mismatches 4; Indels
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Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
IIILE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTEACTANT
IIILE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 17
US-08446-669-4
US-08446-669-4
Sequence 4, Application US/08446669
Sequence 10. 6132987
GENERAL INFORMATION:
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: PROMEMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROMEMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/450,393A
FILING DATE: May 25, 1995
CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-237/02US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                          92 EWVFGNAMCKLFTGLYHIGYF 112
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                                                                                                                                                                                                                                              RESULT 16
US-08-450-393A-4
US-08-450-393A-5
Sequence 4, Application US/08450393A
Patent No. 5707915
GENERAL INFORMATION:
                                                                                                                             1 OWDFGNTMCQLLTGLYFIGFF 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 OWDFGNIMCQLLTGLYFIGFF 21
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TELEPAX: 415-885-0663
TELEX: 380816001eyPA
INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 360 amino acids
amino acid
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-450-393A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Palo Alto
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Soppet, Daniel R.
APPLICANT: Yi, Li
APPLICANT: Ruben, Steven M.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARRLLA, BYRNE, BAIN, GILFILLAN, CECCHI, ADDRESSEE: STUART & OLSTEIN
STREET: 6 Becker Farm Road
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,343D
FILING DATE: 0-JUN 1995
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
TELEORWUNICATION INFORMATION:
TELEPRAK: (202) 371-2600
INFORMATION EN REQ ID NO: 9:
SRQUENCE CRARACTERISTICS:
LENGTH: 344 animo acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWATING SYSTEM: Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 69.0%; Score 87; DB 3; I Local Similarity 66.7%; Pred. No. 1.9e-05; Ne 14; Conservative 3; Mismatches 4;
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NAME: Perrarc, Gregory D.
REGISTATION NUMBER: 36,134
REFERENCE/DOCKET WUMBER: 325800-445
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPHONE: 201-994-1700
TELEPHONE: SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/461,244
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
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Patent No. 5776729
GENERAL INFORMATION:
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TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                  LENGTH: 344 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-244-3
                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Roseland
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-466-343D-9
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US-08-461-244-3
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US-055-583-50

Sequence 50, Application US/09045583

Patent No. 6287805

GENERALI INFORMATION:

TITLE OF INVENTION: No. 6287805e1 Molecules of the G Protein-Coupled

TITLE OF INVENTION: No. 6287805e1 Molecules of the G Protein-Coupled

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 69.0%; Score 87; DB 3; Length 360; Best Local Similarity 66.7%; Pred. No. 2e-05; Matches 14; Conservative 3; Mismatches 4; Indels
                                         CUNTRY: VAIO

CUNTRY: USA

ZIPATE: CALIfornia

COUNTRY: USA

ZIP : 94306-215

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: LIBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/446,669

FILING DATE: MAY 25, 1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Neel-Sy, Richard

REFERENCE/DOCKET NUMBER: 30,092

REFERENCE/DOCKET NUMBER: UCAL-237/01US

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION TOR SEQ ID NO: 4:

SEQUIRENE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONTINUE READABLE FORM:

MEDIUM TYER READABLE FORM:

MEDIUM TYER: Floppy disk
COMPUTER: IEM PC COMPACIBLE
OPERATING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FLING DATE: O-MAR-98
CLASSIFICATION 1435
FRIGHT APPLICATION ATA:
APPLICATION NUMBER: 35,207
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: MNI-044
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 OWDFGNIMCOLLIGLYFIGFF 21
5 Palo Alto Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 360 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-669-4
                             Palo Alto
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
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PREDIT 19 PROMITON POR SEQ IN NO. 50;

LENGTH: 350 amino acids

TORIGONAL CRANCTRESTICS:

LENGTH: 350 amino acids

TORIGONAL CRANCTRESTICS:

TORIGONAL CRANCTRESTICS:

LENGTH: 350 amino acids

TORIGONAL CRANCTRESTICS:

COMPANY Tree: Infernal

US-0-0-464-583-50

COMPANY TREE: Infernal

US-0-1-464-583-50

LIGHT 19

LOWER TREE: INFERNAL CRANCTRESTICS:

REBUIL 19

LOWER THE CRANCTRESTICS:

COMPANY CRANCTRESTICS:

LOWER TREE TORIGONAL CRANCTRESTICS:

REBUIL 19

COMPANY CRANCTRESTICS:

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1 QWDFGNTMCQLLTGLYFIGFF 21
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Best Local Similarity 66...
Cohes 14; Conservative
Query Match
Best Local Similarity 66.74
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , ORGANISM: Homo sapiens
US-09-131-827A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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LENGTH: 360
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                                                                                 APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: PASSART, GILBERT
APPLICANT: USSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: ACTIVE AND INCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.0%; Score 87; DB 4; Length 360; 66.7%; Pred. No. 2e-05; tive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CCOMPATIBLE
COMPUTER: IBM CCOMPATIBLE
COMPUTER: BY
COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
RILING DATE: 9-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: O'Brian, Michael
APPLICANT: O'Brian, Stephen J.
APPLICANT: O'Brian, Stephen J.
APPLICANT: Carrington, Mary
ITILE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
ITILE OF INVENTION: DELAYED PROGRESSION TO THE CR2
FILE REFERENCE: 14014 0333
CURRENT APPLICATION NUMBER: US/09/131,827A
CURRENT FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PASTERQ for Windows Version 4.0
SEQ ID NO 2
ENGTH: 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 EWVFGNAMCKLFTGLYHIGYF 125
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Patent No. 6600030
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFRENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 anino acids
TYPE: amino acid
STRANDEDNESS: single
                      Sequence 7, Application US/08833752
Patent No. 6448375
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: No. 6448375e
US-08-833-752-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 9-APR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Conservative
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CRGANISM: Homo sapiens
US-09-131-827A-2
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Best Local Similarity
Matches 14; Conserva
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  US-08-833-752-7
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69.0%; Score 87; DB 4; Length 360; 66.7%; Pred. No. 2e-05; tive 3; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application PC/TUS9500476
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
ADDRESSEE: RObbins, Berliner & Carson
STREET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: O'BTIEN, Michael
APPLICANT: O'BTIEN, Stephen J.
APPLICANT: O'BTIEN, Stephen J.
APPLICANT: Carrington, Mary
TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
TITLE OF INVENTION: DELAYED PROGRESSION TO GENE
FILE REFERENCE: 14014.0333
CURRENY PRILING DATE: 1990-08-10
PRIOR APPLICATION NUMBER: 60/055,659
PRIOR APPLICATION NUMBER: 60/055,659
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIF: 90012-2628
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00476
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NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-291
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-977-1001
                                                                                                                                                                                                                                                         US-09-131-827A-20
; Sequence 20, Application US/09131827A
Patent No. 6600030
; GENERAL INFORMATION:
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; Patent No. 6132987
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Sequence 2, Application US/08450393A

Patent No. 5707815

GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Couglin, Shaun
ITILE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
ITILE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto
COUNTRY: 105A

COUNTRY: 105A

COUNTRY: 05A

COUNTRY: 05A

COUNTRY: 105A

COUNTRY: 105A
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69.0%; Score 87; DB 1; Length 374;
Best Local Similarity 66.7%; Pred. No. 2.1e-05;
Matches 14; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                Query Match 69.0%; Score 87; DB 5; Length 360; Best Local Similarity 66.7%; Pred. No. 2e-05; Matches 14; Conservative 3; Mismatches 4; Indels
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                                                              INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: ALENGUENTE: protein
PCT-US95-00476-4
TELEFAX: 310-977-1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
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Gaps
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GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooley Godward Castro Huddleson & Tatum
STREET: Palo Alto Square
CITY: Palo Alto
STREET: Palo Alto
STREET: Palo Alto
COMPUTER: Palo Alto
COMPUTER: Palo Alto
COMPUTER: PRABABLE FORM:
MEDIUM TYBE: Righty disk
COMPUTER: IBM PC Compatible
OOFERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,669
FILING DATE: MAY 25, 1995
CLASSIFICATION INDRESS: 30,092
REGISTRATION NUMBER: 30,092
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET UNFORMATION:
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 26
PCT-USSS-00476-2
Sequence 2, Application PC/TUSSS00476
GENERAL INFORMATION:
TABLE APPLICANT: The Regents of the University of California TITLE OF INVENTION: MAMMALIAN MONOCYBE CHEMOATTRACTANT: TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Robbins, Berliner & Carson STREET: 201 N. Figueroa Street, 5th Floor CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
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ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRATI APPLICATION DARA:
APPLICATION NUMBER: PCT/US95/00476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.0%; Score 87; DB 3; 166.7%; Pred. No. 2.1e-05; tive 3; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: THOUSEN: 374 amin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 i LENGTH: 374 amino acids
i TYPE: amino acid
i TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-446-669-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.7%
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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Tue Sep 28 15:49:55 2004

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Query Match 65.9%; Score 83; DB 1; Length 269; Best Local Similarity 54.5%; Pred. No. 6e-05; Matches 12; Conservative 7; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                US-09-299-268-30

| Sequence 30, Application US/09299268
| Patent No. 6217804
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Moyer, Richard W. APPLICANT: Vi uela, Eladio
| APPLICANT: OF INVENTION: Use of Recombinant Swine Poxvirus as ITILE OF INVENTION: Live Vaccine Vector
| NUMBER OF SEQUENCES: 60
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/ACENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRAHION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF35.1.FWCC1
TELECOMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEPHONE: 904-375-800
TELEPHONE: 904-375-800
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
APPLICATION NUMBER: US 07/908,241
FILING DATE: 1-UTL-1992
APPLICATION DATA:
APPLICATION NUMBER: US 07/908,630
FILING DATE: 29-JUN-1992
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/342,212
FILING DATE: 21-APR-1992
CLASSIFICATION:
                                                                                                                                                                                                    1 OWDFGNIMCOLLIGLYFIGFFS 22
                                                                                                                                                                                                                                 20 QWIFGNILCKIMSVLYYVGFFS 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/901,127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 269 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 54.5
Matches 12; Conservative
  ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-307-499-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-268-30
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Florida COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                             Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,499
                                                                                                                                                                                                                                                                                                                                                                69.0%; Score 87; DB 5; I
66.7%; Pred. No. 2.1e-05;
tive 3; Mismatches 4,
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/908,241
FILING DATE: 1-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,630
PILING DATE: 29-JUN-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION: 435
PRIOR APPLICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: SALIWANCHILK, DAVIG R.
REGISTRATION NUMBER: 31,794
REGISTRATION NUMBER: 31,794
REGISTRATION NUMBER: 31,794
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF35.1.FWCC1
TELECHOME: 904-375-8100
                                                     5555-291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 EWVFGNAMCKLFTGLYHIGYF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QWDFGNTMCQLLTGLYFIGFF 21
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFRENCE/DOCKET NUMBER: 5555
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-977-1001
TELEPAX: 310-977-1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                 TELEX:
| INFORMATION FOR SEQ ID NO: 2:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 374 amino acids:
| TYPE: amino acid
| TOPOLOGY: linear |
| MOLECULE TYPE: protein |
| PCT-US95-00476-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 269 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                              14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 14; Conserva
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STATE: Florida
COUNTRY: U.S.A.
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COMPUTER:
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Sequence 56, Application US/09045583
Patent No. 6287805
GENERAL INPORATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805e1 Molecules of the G Protein-Coupled NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESSE:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 54.5%; Pred. No. 0.00011;
Matches 12; Conservative 6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sopper, Daniel R.
APPLICANT: Yi, Li
APPLICANT: Yi, Li
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32
NUMBER OF SEQUENCES:
ADDRESSE: START & OLSTEIN
ADDRESSE: STURY & OLSTEIN
ADDRESSE: STURY & OLSTEIN
ATTERT: 6 Becker Farm Road
CITY: Roseland
STRET: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: ISM PC compacible

COMPUTER: ISM PC compacible

COMPUTER: ISM PC compacible

COMPUTER: Deventin Release #1.0, Version #1.30

SOFTWARE: Percentin Release #1.0, Version #1.30

CURRENT APPLICATION WURBER: US/08/461,244

FILING DATE: O5-UN-1995

CLASSIFICATION: 36

ATTORNEY/AGENT INFORMATION:

NAME: PERTER-O, GT-GGOTY D.

REGISTRATION NUMBER: 36,134

REGISTRATION NUMBER: 36,134

REJECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICAT
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20 QWIFGNILCKIMSVLYYVGFFS 41
                                                                                                                                                                                                                                             Sequence 2, Application US/08461244
Patent No. 5776729
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-045-583-56
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Sequence 56, Application US/09534185
Patent No. 6403767
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
ITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled TITLE OF INVENTION: Heptahelical Receptor Superfamily and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA

COUNTRY: USA

ZIP: 02109

COUNTRY: USA

ZIP: 02109

COMPUTER: ENDABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Paterin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/534,185

FILING DATE: 24 Mar-2000

CLASSIFICATION NUMBER: 09/045,583

FILING DATE: 4 Mar-2000

CLASSIFICATION NUMBER: 09/045,583

FILING DATE: 4 UNKNOWN-

PRICATION NUMBER: 36,207

RADE: Mandradoutes, Amy E.

REFERNACA DOCKER: MUMBER: MNI-044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 65.1%; Score 82; DB 3; Length 355; Best Local Similarity 54.5%; Pred. No. 0.00011; Matches 12; Conservative 6; Mismatches 4; Indels
                 OCHIALTIA STATEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MAIGHAGOURAE, AMW E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMUNICATION INFORMATION:
TELEPHONE: (617)727-7400
TELEPAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 QWVFGTVMCKVVSGFYYIGFYS 119
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TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Therefor
IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
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US-09-534-185-56
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GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
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Patent No. 6388055

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: CKS Receptor
ITILE OF INVENTION: CKS Receptor
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SMITHKIINE Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION: UNKNOWN>
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 09/045,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 64.3%; Score 81; DB 4; Length 360; Best Local Similarity 65.0%; Pred. No. 0.00016; Matches 13; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: PA
COUNTRY: USA
COUNTRY: USA
COUNTRY: BADABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MD STORAGE
MEDIUM TYPE: DISKETTE, 9.5 INCH, 1.44 MD STORAGE
MEDIUM TYPE: DISKETTE, 9.5 INCH, 1.44 MD STORAGE
                                                                                                                                                                         ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGNENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-534-185-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 EWVPGNAMCKLFTGLYHIGY 124
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QWDFGNTMCQLLTGLYFIGF 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                        CITY: Boston
STATE: Massachusetts
                                                                                                                                   NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 34
US-08-724-984A-2
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IITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                 / Match 65.1%; Score 82; DB 4; Length 355; Local Similarity 54.5%; Pred. No. 0.00011; nes 12; Conservative 6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.3%; Score 81; DB 3; Length 360;
65.0%; Pred. No. 0.00016;
iive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 20-MAR-98
CLASSIFICATION: 435
                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
                                                                                                                                                                                                                                                                                                                      98 QWVFGTVMCKVVSGFYYIGFYS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                           1 QWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 51, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 33
US-09-534-185-51
; Sequence 51, Application US/09534185
; Patent No. 6403767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 EWVFGNAMCKLFTGLYHIGY 124
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                   LENGTH: 355 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 51.
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 65.0%
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                              Matches
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APPLICANT: Ruben, Steven M.

IITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCR5)
TITLE OF INVENTION: HDGNR10
FILE REPERENCE: 1488 1150006
CURRENT APPLICATION NUMBER: US/09/502,783A
PRIOR PILING DATE: 2001-08-23
PRIOR FILING DATE: 1995-06
NUMBER OF SEQ ID NOS: 9
SEQ ID NOS: 9
SEQ ID NO 9
LENGTH: 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Sequence 2, Application US/08012988A

Patent No. 5652133

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

MACROPHAGE INFORMATION:

MACROPHAGE INFORMATION:

MUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew

STREET:

STR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/012,988A
FILING DATE: 19930128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 OWDFGNIMCOLLIGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 WVFGDAMCKILSGFYYTGLYS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 WDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 15.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31,677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 19930128
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 355 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 54.5'
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: One Market Pl.
CITY: San Francisco
STATE: California
COUNTRY: USA
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 37
US-08-012-988A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-502-783A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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APPLICANT: Wolf, Eckard
APPLICANT: Wolf, Eckard
APPLICANT: Wolf, Eckard
APPLICANT: Halle, Join-Peter
APPLICANT: Halle, Join-Peter
APPLICANT: Regembogen, Johannes
APPLICANTON: Healing and for the Identification of Pharmacologically
TITLE OF INVENTION: Active Substances
TITLE OF STATION NUMBER: US/09/886,319A
CURRENT APPLICATION NUMBER: US 60/222,081
PRIOR FILING DATE: 2000-08-01
PRIOR FILING DATE: 2000-08-01
PRIOR FILING DATE: 2000-06-01
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 84
SOFTWARE FRASERE FRASERE for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 63.5%; Score 80; DB 4; Length 354; Best Local Similarity 57.1%; Pred. No. 0.00023; Matches 12; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 60.3%; Score 76; DB 4; Length 355; Best Local Similarity 52.4%; Pred. No. 0.00093; Matches 11; Conservative 6; Mismatches 4; Indels
   APPLICATION NUMBER: US/08/724,984A
                                                                                                                                                                                                                                                                                                                                 ATG50023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/09886319A Patent No. 6586185 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99 WIFGDAMCKLLSGFYYLGLYS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 WDFGNTMCQLLTGLYFIGFFS 22
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GENERAL HYPRMATION:
APPLICANT: Li, Yi
                              FILING DATE: OCCOBE 3, 1996
CLASSIPICATION: 800
PRIOR APPLICATION B00
PRIOR APPLICATION DATE:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: William T. Han
REGISTRATION UNUMBER: 34, 344
REFRENCE/DOCKET NUMBER: ATGS:
TELEPHONE: 610 270 5024
TELEPHONE: 610 270 5024
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                      October 3, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LENGTH: 354
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-724-984A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -09-886-319A-13
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LENGTH: 355
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US-08-446-669-5
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                   Secretary Application US/08450393A

Patent No. 5707815

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 5 Palo Alto Square
STREET: 61 Palo Alto
COUNTRY: 015A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.3%; Score 71; DB 1; Length 355; 47.6%; Pred. No. 0.0053; tive 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: PROTEIN RECEPTORS
INTER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UCAL-237/02US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/450, FILING DATE: MAY 25, 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CBETT. LUANN
REGISTRATION NUMBER: 31,822
REFRENCY/DOCKET NUMBER: UCAL-
TELECHONE: 415-843-5165
TELECHONE: 415-843-5165
TELEX: 38.0916COOL9YPA
INFORMATION FOR SEQ ID NO: 5: SEQUENCE GHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08446669 Patent No. 6132987
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Best Local Similarity 47.69
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94306-2155
COMPUTER READABLE FORM:
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CITY: Palo Alto
STATE: Californía
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                        94306-2155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                      US-08-450-393A-5
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US-08-446-669-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
RESULT 38
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COMPUTER, TENPE P. COMPARING
COMPUTER, TENPE C. COMPARING
COMPUTER, TENPE C. COMPARING
COMPUTER, TENPE C. COMPARING
COMPARING
COMPUTER, TENPE C. COMPARING
COMPUTER, TENPE C. COMPARING
COMPARIN
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                                                                                                            Query Match

56.3%; Score 71; DB 3; Length 355;
Best Local Similarity 47.6%; Pred. No. 0.0053;
Matches 10; Conservative 6; Mismatches 5; Indels
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-53
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Search completed: September 28, 2004, 09:21:31 Job time : 20.8 secs

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September 28, 2004, 09:06:23; Search time 72.875 Seconds (without alignments) 97.074 Million cell updates/sec
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"GGNZ 6/ptodata1/pubpaa/DGNZ NEW PUB.pep:*

"GGNZ 6/ptodata1/pubpaa/USO6 NEW PUB.pep:*

"GGNZ 6/ptodata1/pubpaa/USO6 PUBCOMB.pep:*

"GGNZ 6/ptodata1/pubpaa/USO6 PUBCOMB.pep:*

"GGNZ 6/ptodata1/pubpaa/USO8 PUBCOMB.pep:*

"GGNZ 6/ptodata1/pubpaa/USIO8 PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1349238
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1349238 seqs, 321558718 residues
                                                                                                                          OM protein - protein search, using sw model
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Maximum Match 1008
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                      US-10-084-813-12
126
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                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 12, Appl Sequence 4, Appli Sequence 4, Appli	Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 6, Appli	Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 18, Appli	188. 7 188. 7 189. 7
SUMMARIES	US-10-084-813-12 US-09-938-719-4 US-09-939-226-4	US-09-938-703-4 US-10-661-798-4 US-10-612-791-4 US-09-938-719-6	US-09-939-226-6 US-09-938-703-6 US-10-661-798-6 US-10-661-798-18	US-10-612-791-6 US-10-612-791-18 US-10-095-876A-2 US-09-725-285-2
DB	400	6446	00011	9116 946
% Query Match Length DB	22 184 184	184 184 184 215	215 215 215 215	215 215 332 352
% Query Match	100.0	1000.0	1000.0	100.0 100.0 100.0
Score	126 126 126	126 126 126 126	126 126 126 126	126 126 126 126
Result No.	3 2 1	4 R O L	8 6 11 110 11	1111 144 154

Seguence 2, Appli	equence 2.	,	emience 2.	equence 22	equence 15	equence 17	equence 1.	Sequence 2. Appli	equence 2.	equence 5.	'n	equence 5.	equence 2.	a	4	equence 5	equence 2	equence 2	equence 2	equence 1	equence 2	echence 2	equence 6	equence 3	٦.	1 -	r annaima) d	ednence
0	-09-779-8	779-87	8-62-50-	-09-779-88	3-653-1	-09-813-653-1	-09-796-20	-09-195-66	-09-339-9	09-938-719-	939-22	-09-938-703-	9-502-78	09-734-2	19-826-5	10-151-274-	10-106-6	-10-106-623	10-232-6	-10-086-8	-10-067-8	7-800-	-10	ι	-10-323-3	-10-072-301-	-10-164-6	-10-071-866-1	- (
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352	352	352	352	352	352	352	352	352	352	352	352	352	352	352	352	352	352	352	352	352	352	352	352	352	352	352	352	352	352
ö	100.0	。	0	8	0	0	8	100.0	8	8	8	100.0	100.0	100.0	00		100.0	100.0	100.0	100.0	-	-			100.0		٠.	100.0	100.0
126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126
16	17	18	19	20	21	22	23	. 24	25	56	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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US-10-084-813-12

Sequence 12, Application US/10084813

Publication No. US20030066615A1

GENERAL INFORMATION:

JEDELICANT: SAXINGER,

TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC

TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE

FILE REFERENCE: 216875

CURRENT APPLICATION NUMBER: US/10/084,813

CURRENT FILING DATE: 2000-08-25

PRIOR PILING DATE: 2000-08-25

PRIOR PILING DATE: 1999-08-27

PRIOR FILING DATE: 1999-08-27

WUMBER OF SEQ ID NOS: 1242

SOFTWARE: PATCHILL VERSION 3.1

SEQ ID NO 12

LENGTHARE: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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100.0%; Score 126; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 4e-11;
Matches 22; Conservative 0; Mismatches 0; Indels
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RESULT 2 US-09-938-719-4 ; Sequence 4, Application US/09938719 ; Patent No. US20020106742A1

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COUNTRY: U.S.A.
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US-09-938-703-4
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Fatent No. US20020110805A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                    TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gabs
                                                                                                                                                                                                                                                                                                                               COMPUTER: U.S.A.

ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,719
FILING DATE: 24-Aug-2001
CLASSIFICATION: «URKNOWN»
PRIOR APPLICATION: «URKNOWN»
APPLICATION NUMBER: 09/626,939
FILING DATE: 27-UULY-2000
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 100.0%; Score 126; DB 9; Length 184; 1 Similarity 100.0%; Pred. No. 3.3e-10; 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
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ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Altman, Daniel B
REGIGTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: «Unknown»
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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MEDIUM TYPE: Floppy disk
GENBRAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
                                                                                                                                                                                                                                                                                           Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Newport Beach
                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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Best Local Similarity
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US-09-939-226-4
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Sequence 4, Application US/09938703

Patent No. US20020110870A1

GENERAL INFORMATION:

APPLICANT: SAMON, MICHEL

PARMENTIER, MARC

VASSART, GILBERT

LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOXINES RECEPTOR

AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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PRIOR APPLICATION NUMBER: 09/626,939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 126; DB 9; Length 184; Best Local Similarity 100.0%; Pred. No. 3.3e-10; Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel B
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <UNKNOWN>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: <university control of the control of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; IENGTH: 184 amino acids
; TYPE: amino acid
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-939-226-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 QWDFGNTMCQLLTGLYFIGFFS 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 184 amino acids TYPE: amino acid
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CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
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APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER: US/09/938,719
FILING DATE: 24-Aug-2001
CLASSIFFCATION: cUnknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 126; DB 16;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 126; DB 9; Best Local Similarity 100.0%; Pred. No. 3.9e-10; Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Altman, Daniel B
REGISTRATION NUMBER: 34,115
REGISTRATION NUMBER: «Unknown>
INFORWATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
PRIOR APPLICATION UNDBER: 09/626,939
FILING DATE: 27-ULLY-2000
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECTLE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-09-938-719-6
                                                        96870102.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 QWDFGNTMCQLLTGLYFIGFFS 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09938719
Patent No. US20020106742A1
GENERAL INFORMATION:
              PRIOR FILING DATE: 1996-03-01
PRIOR APPLICATION NUMBER: EP 968
PRIOR FILING DATE: 1996-08-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-10-612-791-4
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US-09-938-719-6
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is Sequence 4, Application US/10661798

sequence 4, Application US/10661798

sequence 4, Application NO. US20040110127A1

sequence 4, Application NO. US20040110127A1

septicant: Parmentier, Marc

septicant: Vassart, Gilbert

APPLICANT: Parmentier, Marc

SCURRENT APPLICATION NUMBER: 09/938,703

PRIOR APPLICATION NUMBER: 09/626,939

PRIOR APPLICATION NUMBER: 08/833,752

PRIOR APPLICATION NUMBER: 08/833,752

PRIOR APPLICATION NUMBER: 08/810,028

PRIOR APPLICATION NUMBER: EP 96870012.1

PRIOR APPLICATION NUMBER: EP 96870102.9

PRIOR APPLICATION NUMBER: EP 96870102.9

PRIOR APPLICATION NUMBER: EP 96870102.9

PRIOR FILING DATE: 1996-03-03

PRIOR APPLICATION NUMBER: EP 96870102.9

PRIOR PILING DATE: 1996-03-03

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          Length 184;
                                                                          Indels
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Query Match
100.0%; Score 126; DB 9; I
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 126; DB 16;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
Matches 22; Conservative 0; Mismatches 0;
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SQUENCE 2/31-4

Publication No. US20040161739A1

GENERAL INFORMATION:

APPLICANT: Sameon, Michael

APPLICANT: Sameon, Michael

APPLICANT: Sameon, Michael

APPLICANT: Vassart, Gilbert

FILE OF INVENTION: HIV Diagnostic Methods.

FILE REFERENCE: 9409/2023E

CURRENT APPLICATION NUMBER: US/10/612,791

CURRENT APPLICATION NUMBER: 09/938,703

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2000-07-27

PRIOR FILING DATE: 2000-07-27

PRIOR FILING DATE: 1997-04-09

PRIOR FILING DATE: 1997-04-09

PRIOR FILING DATE: 1997-04-09

PRIOR PLING DATE: 1997-04-09

PRIOR PLING DATE: 1997-04-09

PRIOR PLING DATE: 1997-04-03

PRIOR APPLICATION NUMBER: 08/810,028

PRIOR PAPLICATION NUMBER: EP 96870021.1
                                                                                                                                                                                     93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                   1 OWDFGNTMCQLLTGLYFIGFFS 22
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CORGANISM: Homo sapiens
US-10-661-798-4
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Sequence 6, Application US/09938703
Sequence 6, Application US/09938703
Setent No. US20020110870A1
GENERAL INFORMATION, MICHEL
GENERAL INFORMATIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                               APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDENICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: CURKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 215;
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STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 126; DB 9;
100.0%; Pred. No. 3.9e-10;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:

**APPLICATION WUMBER: 09/626,939

**FILING DATE: 2000-07-27

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-939-226-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 QWDFGNTMCQLLTGLYFIGFFS 114
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                                          Sequence 6, Application US/09939226 Patent No. US20020110805A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 215 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                     Newport Beach
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
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Best Local Similarity 100.(
Matches 22; Conservative
                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 92660
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US-09-938-703-6
RESULT 8
US-09-939-226-6
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US-10-661-798-6

Sequence 6, Application US/10661798

Publication No. US20040110127A1

GENERAL INFORMATION:

APPLICANT: Samson, Michael

APPLICANT: Variable of the control of the control
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                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 126; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
Matches 22; Conservative 0; Mismatches 0; Indels C
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100.0%; Pred. No. 3.9e-10;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Altman, Daniel B
REGIGTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                             APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-Aug-2001
CLASSIFICATION: vUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QWDFGNTMCQLLTGLYFIGFFS 22
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 215 amino acids TYPE: amino acid
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Best Local Similarity 100.0%;
Matches 22; Conservative C
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US-10-661-798-6
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1 OWDFGNTMCQLLTGLYFIGFFS 22

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Sequence 2, Application US/10095876A;
Publication No. US20030148294A1;
GENERAL INFORMATION:
APPLICANT: AU-Young, Janice; Bandman, Olga;
APPLICANT: Coleman, Roger; Wilde, Craig G.
TITLE OF INVENTION: DNA ENCODING NOVEL CHEMOKINE RECEPTORS;
FILE REFERENCE: PF-0060-1 CON
CURRENT APPLICATION NUMBER: US/10/095,876A;
CURRENT FILING DATE: 2002-03-11;
PRIOR APPLICATION NUMBER: US 08/638,081;
PRIOR FILING DATE: 1996-04-26;
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INCUGANTICAN

GENERAL INCUGANTICAN

APPLICANT: Parmentier, Marc

APPLICANT: Galbert

GILDER

TILE ARBERTOR: 9409/2023E

CURRENT APPLICATION NUMBER: 08/910/612,791

CURRENT FILING DATE: 2003-07-02

PRIOR PILING DATE: 2001-08-24

PRIOR FILING DATE: 2000-07-27

PRIOR FILING DATE: 1997-04-09

PRIOR FILING DATE: 1997-04-09

PRIOR FILING DATE: 1997-04-09

PRIOR FILING DATE: 1997-03-01

PRIOR FILING DATE: 1997-04-09

PRIOR FILING DATE: 1997-04-09

PRIOR FILING DATE: 1997-04-09

PRIOR FILING DATE: 1996-09-06

NUMBER OF SEQ ID NOS: 18

SEQ ID NO 18

LENGTHER PATCHTION NUMBER: EP 96870102-9

PRIOR FILING DATE: 1996-09-06

NUMBER OF SEQ ID NOS: 18

SEQ ID NO 18

LENGTHER PATCHTION NUMBER: EP 96870102-9

PRIOR FILING DATE: 1996-09-06

NUMBER: PATCHTION NUMBER: EP 96870102-9

PRIOR FILING DATE: 1996-09-06

NUMBER: PATCHTION NUMBER: EP 96870102-9

PRIOR FILING DATE: 1996-09-06

NUMBER: PATCHTION NUMBER: EP 96870102-9

PRIOR FILING DATE: 1996-09-06

NUMBER: PATCHTION NUMBER: EP 96870102-9

PRIOR FILING DATE: 1996-09-06

NUMBER: PATCHTION NUMBER: EP 96870102-9

PRIOR FILING DATE: 1996-09-06

NUMBER: PATCHTION NUMBER: EP 96870102-9

PRIOR FILING DATE: 1996-09-06

NUMBER: PATCHTION NUMBER: EP 96870102-9

PRIOR FILING DATE: 1996-09-06

NUMBER: PATCHTION NUMBER: EP 96870102-9

PRIOR FILING DATE: 1996-09-06

NUMBER: PATCHTION NUMBER: EP 96870102-9
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                                                                                                                                                                                                                                                                                                                                                     1 QWDFGNTMCQLLTGLYFIGFFS 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
US-10-612-791-18
US-10-612-791-18
Sequence 18, Application US/10612791
Publication No. US20040161739A1
GENERAL INFORMATION
                                  TYPE: PRT
CORGANISM: Homo sapiens
US-10-612-791-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRGANISM: Homo sapiens JS-10-612-791-18
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US-10-095-876A-2
LENGTH: 215
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LENGTH: 332
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                                                                                                                                                                                                                                                                                     APPLICANT: Parmentic. Marcally APPLICANT: Vassart, Gilbert APPLICANT: Vassart, Gilbert APPLICANT: Vassart, Gilbert TITLE OF INVENTION: Screening Methods for Identifying Compounds which Decrease HIV Entitle OF INVENTION: a Cell TITLE OF INVENTION: a Cell CURRENT APPLICATION NUMBER: US/10/661,798

CURRENT APPLICATION NUMBER: 08/938,703

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-09-27

PRIOR FILING DATE: 1997-04-09

PRIOR FILING DATE: 1997-04-09

PRIOR FILING DATE: 1997-03-03

PRIOR FILING DATE: 1997-03-03

PRIOR FILING DATE: 1997-03-01

PRIOR FILING DATE: 1996-03-01

PRIOR FILING DATE: 1996-03-01
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Best Local Similarity 100.0%; Pred. No. 3.9e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0;
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TITLE COF INVENTION: HIV Diagnostic Methods
FITLE REFERENCE: 9409/2021B
CURRENT APPLICATION NUMBER: US/10/612,791
CURRENT FILING DATE: 2003-07-02
PRIOR APPLICATION NUMBER: 09/626,939
PRIOR FILING DATE: 2000-07-27
PRIOR FILING DATE: 1997-04-09
PRIOR FILING DATE: 1997-04-09
PRIOR FILING DATE: 1997-04-03
PRIOR FILING DATE: 1997-04-03
PRIOR FILING DATE: 1997-04-03
PRIOR FILING DATE: 1997-04-03
PRIOR FILING DATE: 1996-03-01
PRIOR PRILING DATE: 1996-03-01
PRIOR PRILING DATE: 1996-03-01
PRIOR PLING DATE: 1996-03-01
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                                                                                                                                            US-10-661-798-18
. Sequence 18, Application US/10661798
; Publication No. US20040110127A1
; GENERAL INFORMATION:
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Publication No. US20040161739A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Homo sapiens
US-10-661-798-18
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US-10-612-791-6
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APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Li, Yi
TILLE OF INVENTION: Huben, Steven, M.
TILLE OF INVENTION: Huben, G-protein Chemokine Receptor (CCRS) HDGNR10
FILLE REFERENCE: 1488 115000A
CURRENT APPLICATION NUMBER: US/09/779,879A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,258
PRIOR APPLICATION NUMBER: US 60/187,999
PRIOR PILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 60/187,999
PRIOR FILING DATE: 2000-02-09
PRIOR PILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 58

NUMBER OF SEQ ID NOS: 58
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APPLICANT: Rosen, Craig A.

APPLICANT: Rosen, Craig A.

APPLICANT: Rosen, Steven, M.

TILLS OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNRIO

FILE REPERENCE: 1480.1150004.

CURRENT APPLICATION NUMBER: US (09/779, 879A

CURRENT APPLICATION NUMBER: US 60/181, 258

PRIOR APPLICATION NUMBER: US 60/181, 258

PRIOR PILING DATE: 2000-02-09

PRIOR PILING DATE: 2000-03-09

PRIOR FILING DATE: 2000-03-09

PRIOR FILING DATE: 2000-03-09

PRIOR FILING DATE: 2000-03-09

PRIOR PILING DATE: 2000-03-09
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                                                                                                                                                       100.0%; Score 126; DB 9; Length 352; 100.0%; Pred. No. 6.3e-10; ative 0; Mismatches 0; Indels 0
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Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 OWDFGNTMCOLLIGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09779879A, Patent No. US20020048786A1, GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.0
                                                                                                                           APPLICANT: Rosen, Craig A. APPLICANT: Roschke, Viktor
                                     TYPE: PRT
CRGANISM: Homo sapiens
US-09-759-841-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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US-09-779-879A-22
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US-09-779-879A-2
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LENGTH: 352
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         LENGTH: 352
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APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven, M.
Antibodies to Human G-Protein Chemokine Receptor HDGNR10
TITLE OF INVENTION: (CCR5 Receptor)
FILE REPERENCE: 1488.1150003
FULNS REPERENCE: 1488.1150003
FULNS REPERENCE: 1488.1150003
FULNS REPERENCE: 1989.11-29
PRIOR APPLICATION NUMBER: 09/339,912
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1998-11-18
PRIOR PELLOR TON NUMBER: 08/466,343
PRIOR FILING DATE: 1996-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATCHIN VERSION 3.0
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                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 6e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0;
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                                                               ; NAME/KEY: misc feature
? OTHER INFORMATION: Incyte ID No. US20030148294A1 478861
US-10-095-876A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION: Deduced Amino Acid Sequence US-09-725-285-2
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Petent No. US20010039026A1

GENERAL INFORMATION:

APPLICANT: Rickett, Graham A

APPLICANT: Dobbs, Susan

APPLICANT: Dobbs, Manoussos

ITILE OF INVENTION: Assay Method

FILE REFERENCE: PC10348APME

CURRENT APPLICATION NUMBER: US/09/759,841

CURRENT FILING DATE: 2001-01-12

PRIOR PLICATION NUMBER: GB 0000661.9

PRIOR FILING DATE: 2000-01-12

PRIOR PLILING DATE: 2000-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence: Genomic
                                                                                                                                                                                                                                                                                                                                     84 QWDFGNTMCQLLTGLYFIGFFS 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 QWDFGNTMCQLLTGLYFIGFFS 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09725285; Patent No. US20010000241A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.0
Matches 22; Conservative
ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-725-285-2
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Gaps

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Query Match
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels C
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                                                                                                                                                                                                                                                                   1 OWDFGNTMCQLLTGLYFIGFFS 22
       , ORGANISM: Homo sapiens
US-09-779-880A-22
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US-09-813-653-15
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Sequence 2, Application US/09779880A

Patent No. US20020061834A1

GENERAL INFORMATION:

APPLICANT: Rosen, Craig A.

APPLICANT: Rosen, Viktor.

APPLICANT: Li, Yi

APPLICANT: NUMBER: US/09/779,880A

FILE REFERENCE: 1488.11500C

CURRENT APPLICATION NUMBER: US 60/181,258

FRIOR FILING DATE: 2000-02-09

FRIOR PILING DATE: 2000-03-09

FRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 352
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Sequence 22, Application US/09779880A

Sequence 22, Application US/09779880A

Patent No. US2020061834A1

GENERAL INFORMATION:
APPLICANT: Roschke, Viktor
APPLICANT: Roschke, Viktor
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGNR10

TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGNR10

TITLE OF INVENTY BAPLICATION NUMBER: US/09/779,880A

CURRENT PAPLICATION NUMBER: US 60/181,258

PRIOR PAPLICATION NUMBER: US 60/181,258

PRIOR PAPLICATION NUMBER: US 60/187,999

PRIOR PAPLICATION NUMBER: US 60/187,999

PRIOR PLING DATE: 2000-03-09

PRIOR FILING DATE: 2000-03-09
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100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                   Query Match 100.0%; Score 126; DB 9; Length 352; Best Local Similarity 100.0%; Pred. No. 6.3e-10; Matches 22; Conservative 0; Mismatches 0; Indels
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-879A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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US-09-779-880A-2
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LENGTH: 352
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## APPLICANT: Nestor, John
## APPLICANT: Nestor, John
## APPLICANT: Nestor, John
## APPLICANT: Wilson, Carol
## APPLICANT: Wilson, Carol
## APPLICANT: Wilson, Carol
## APPLICANT: Tan Hehir, Christina
## APPLICANT: Tan Hehir, Christina
## TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
## TITLE OF INVENTION: Binding Compounds
## TITLE OF INVENTION: Binding Compounds
## TITLE OF INVENTION: UNMBER: US 60/190,946
## PRIOR APPLICATION NUMBER: US 60/190,946
## PRIOR FILING DATE: 2000-03-21
## 
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Sequence 17, Application US/09813653

Sequence 17, Application US/09813653

GENERAL INFORMATION:

APPLICANT: Nestor, John

APPLICANT: Wilson, Carol

APPLICANT: See, Raymond

APPLICANT: See, Raymond

APPLICANT: Tan Hehlr: Christina

APPLICANT: Tan Hehlr: Christina

APPLICANT: Tan Hehlr: Christina

TILE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds

TILE REPRENCE: CNS-005

CURRENT FILING DATE: 2001-03-20

PRIOR APPLICATION NUMBER: US 60/190,996

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21
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Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0
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Sequence 15, Application US/09813653; Patent No. US20020064770A1; GENERAL INFORMATION:
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APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Li, Yi
TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNRIO
TITLE OF INVENTION: (CCR5 Receptor)
FILE REPERENCE: 1488-115-001
CURRENT APPLICATION NUMBER: US/09/339,912A
CURRENT FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 352
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Patent No. US20020106742A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSERT, GILBERT
LIBERT, FEEDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOXINES RECEPTOR
AND NUCLEIC ACID-MOLECULES ENCODING SAID RECEPTOR
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COMPUTER: IBM PC compatible
COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 126; DB 9; Length 352; Best Local Similarity 100.0%; Pred. No. 6.3e-10; Matches 22; Conservative 0; Mismatches 0; Indels 0
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STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Deduced Amino Acid Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Altman, Daniel B
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: «Unknown»
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,719
FILING DATE: 24-Aug-2001
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 09/626,939
FILING DATE: 27-JULY-2000
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence: Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 QWDFGNTMCQLLTGLYFIGFFS 114
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Sequence 2, Application US/09339912A Patent No. US20020099176A1 GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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APPLICANT: Li, Yi
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGNRIO (CGRS Receptor)
FILE REPERENCE: 1488 1150002
CURRENT APPLICATION NUMBER: US/09/195,662A
CURRENT FILING DATE: 1998-11-18
PRIOR PILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
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                                               Query Match
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010/JPW/SHS
CURRENT APPLICATION NUMBER: US/09/796,202
CURRENT FILING DATE: 2010-02-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 126; DB 9; Length 352; Best Local Similarity 100.0%; Pred. No. 6.3e-10; Matches 22; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence: Genomic
                                                                                                                                                                                      93 QWDFGNTMCQLLTGLYFIGFFS 114
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Patent No. US20020068813A1
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Matches 22; Conservative
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APPLICANT: Li, Yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-195-662A-2
  US-09-813-653-17
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LENGTH: 352
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LENGTH: 352
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US-09-339-912A-2
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TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: ISOPPY disk
COMPUTER: PAIDPY disk
SOFTWARE: PAIDPY DATA:
APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-Aug-20.01
PRIOR APPLICATION: CURKNOWN-
PRIOR APPLICATION: CURKNOWN-
PRIOR APPLICATION: COMPUTER: 09/626,939
FILING DATE: 2000-07-27
ATTORBY/AGENT INFORMATION:
NAME: Altern. Daniel E
REGISTRATION NUMBER: 34,115
REFREENCE/DOCKET UNMBER: CURKNOWN-
                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSES: KNobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 126; DB 9;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 5: US-09-938-703-5
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                       RESULT 27
US-09-939-226-5
i Sequence 5, Application US/09939226
j Sequence 5, Application US/09939226
j Patent No. USZ0020110805A1
j GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: SAMSON, MICHEL
ILBERT, FREDERICK
i LIBERT, FREDERICK
i TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AD NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Version #1.25 (EPO)
                                                                                                           Length 352;
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                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSES: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
                                                                                             Query Match
100.0%; Score 126; DB 9;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 126; DB 9; 100.0%; Pred. No. 6.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE PORM:
MUDDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
SOFTWARE: PatentIn Release #1.0, Vers
FILING DATE: 24-Aug-2001
CLASSIFICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION NUMBER: 09/626,939
APPLICATION NUMBER: 09/626,939
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: 4UKNOWN>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: maino acids
MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 5: US-09-938-719-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) MOLECULE TYPE: protein
) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-939-226-5
                                                                                                                                                                                                                                             93 OWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                 1 OWDFGNIMCOLLIGLYFIGFFS 22
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Best Local Similarity 100.
Matches 22, Conservative
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Sequence 2, Application US/09502783A

Patent No. US20020132269A1

GENERAL INFORMATION:

APPLICANT: Li, Yi

APPLICANT: Li, Yi

APPLICANT: Ruben, Steven M.

TITLE OF INVENTION: POlynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS)

TITLE OF INVENTION: HABS.1150006

CURRENT APPLICATION NUMBER: US/09/502,783A

CURRENT APPLICATION NUMBER: 08/466,343

PRIOR FILING DATE: 1995-06-06

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.0

SEQ ID NO 2

LENGTH: 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-502-783A-2
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0; Indels

Mismatches

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Sequence 5, Application US/09938703
Sequence 5, Application US/09938703
Sequence 100 US20020110870A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC

RESULT 28 US-09-938-703-5

Gaps

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Length 352; Indels

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us-10-084-813-12.rapb

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APPLICANT: Lehmann-Bruinsma, Karin
APPLICANT: Liaw, Chen W.
APPLICANTON: No. US20030204073A1-Endogenous, Constitutively Activated Known G.
TITLE OF INVENTION: Precein-Coupled Receptors
TITLE OF INVENTION: Precein-Coupled Receptors
CURRENT APPLICATION NUMBER: US/09/826,509
CURRENT APPLICATION NUMBER: 2001-04-05
PRIOR PILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: Patentin Version 2.1
ENGTH: 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Littman, Dan R.
APPLICANT: Littman, Douglas S.
APPLICANT: Kwon, Douglas S.
APPLICANT: Wan Kooyk, Yvette
APPLICANT: Waltenbeck, Theo
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY
TITLE OF INVENTION: CELLS
FILE REFERENCE: 1049-1-017
CURRENT APPLICATION NUMBER: US/10/151,274
CURRENT PILING DATE: 2002-05-20
PRIOR FILING DATE: 2002-03-02
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 100.0%; Score 126; DB 11; Local Similarity 100.0%; Pred. No. 6.3e-10; les 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 OWDFGNTMCOLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 OWDFGNIMCOLLIGENES 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 OWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/10151274; Publication No. US20030064071A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 22, Conservative
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LENGTH: 352
TYPE: PRT
COCGANICA: Homo sapiens
US-10-151-274-5
                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-826-509-477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 32
US-10-151-274-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                    MACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                             DENG, HONGKUI
ELLMEIBR, WILFRIED
LANDAU, NATHANIEL R.
LIU, RONG
TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE DAVIG 3. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTEN: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/734,221A
FILING DATE: 11-Dec-2000
CLASSIFICATION NATA:
APPLICATION NATA:
APPLICATION NUMBER: US 08/666,020
FILING APALICATION NUMBER: US 08/666,020
FILING DATE: 19-UN-1996
APPLICATION NUMBER: US 08/671319
FILING DATE: 13-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-004 N2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPHONE: 201-487-5801
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; SEQUENCE ORGANISM: Home sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
08-09-734-221.h-14
93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 OWDFGNTMCOLLTGLYFIGFFS 114
                                                                                                                                                 Sequence 14, Application US/09734221A
Publication No. US20030096221A1
GENERAL INFORMATION:
APPLICANT: LITTMAN, DAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 OWDFGNIMCOLLIGLYFIGFFS 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 352 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 22; Conservative
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                                                                                                 RESULT 30
US-09-734-221A-14
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Query Match

RESULT 31

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Sequence 2, Application US/10232686;
Publication No. US20030023044A1
GENERAL INFORMATION:
APPLICANT: Li, Yi,
APPLICANT: Li, Yi,
TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNRIO
FILE REFERENCE: 1488.11500N
CURRENT APPLICATION NUMBER: US/10/232,686
CURRENT FILING DATE: 2002-09-03
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1998-11-18
PRIOR FILING DATE: 1998-11-18
PRIOR FILING DATE: 1998-11-18
PRIOR FILING DATE: 1998-10-66
SOFTWARE: PALCATION NUMBER: 09/466,343
PRIOR FILING DATE: 1998-11-18
SOFTWARE: PALCATION NUMBER: 09/466,343
PRIOR FILING DATE: 1998-11-18
SOFTWARE: PALCATION NUMBER: 1998-11-18
SOFTWARE OF SEQ ID NOS: 9
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                    CLASSIFICATION TATA:

**PRIOR APPLICATION DATA:

**APPLICATION NUMBER:

**ATTORNEY/AGENT INFORMATION:

**INTORNEY/AGENT INFORMATION:

**REGISTRATION NUMBER: 35,302

**REGISTRATION NUMBER: 27866/33670

**TELEPHONE: 312-474-6330

**INFORMATION FOR SEQ ID NO: 20:

**SEQUENCE CHARACTERISTICS:

**INFORMATION FOR SEQ ID NO: 20:

**INFORMATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 126; DB 13;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 QWDFGNTWCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 OWDFGNTMCQLLTGLYFIGFFS 22
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NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) NAME/KEY: misc_feature
; OTHER INFORMATION: /= "88C amino acid sequence"
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-106-623-2
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/10/106,623

FILING DATE: 26-Mar-2002

CLASSIFICATION: UNKnown-
PRIOR APPLICATION NUMBER: US/711,276

FILING DATE: 40hAnown-
APPLICATION NUMBER: 08/771,276

FILING DATE: 40hAnown-
ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 35,302

REGISTRATION NUMBER: 35,302

REGISTRATION NUMBER: 35,302

TELEPHONE: 312-474-63300

TELEPHONE: 312-474-6448

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 352 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein FEATURE:
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Gaps
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         Length 352;
                                                                                                                                                                                                         RESULT 36
US-10-086-814-1
S-quence 1, Application US/10086814
Publication No. US20030092632A1
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William C.
TITLE OF INVENTION SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 61010-AB-1
CURRENT APPLICATION NUMBER: US/10/086,814
                                                      Indels
Query Match 100.0%; Score 126; DB 14; Best Local Similarity 100.0%; Pred. No. 6.3e-10; Matches 22; Conservative 0; Mismatches 0;
                                                                                                                         93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                              1 OWDFGNTMCQLLTGLYFIGFFS 22
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TYPE: PRT ORGANISM: Homo sapiens

JULIANS SEQUENCE 20, Application US/10106623

Fublication No. US20020150888A1

GENERAL INFORMATION:

SCHWEIGHT OF SCHWEIGH

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/106,623
FILING DATE: 26-Mar-2002

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Query Match
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0

à g RESULT 34 US-10-106-623-20

.. 0

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Sequence 352, Application US/1022567A

Publication No. US20030113798A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
Brown, Joseph P.
APPLICANT:
Brown, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REPERENCE: 1920-44
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
FRIOR PEPLING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Publication No. US20030104455A1

Publication No. US20030104455A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Urological Disorders Using 313, 333, 5464, 18817 or 33524

TITLE OF INVENTION: Urological Disorders Using 313, 333, 5464, 18817 or 33524

TITLE OF INVENTION: Urological Disorders Using 313, 333, 5464, 18817 or 33524

TITLE OF INVENTION: UNMBER: W310/290,058A

CURRENT FILING DATE: 2002-11-07

PRIOR PRILING DATE: 2001-11-07

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 126; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0
PRIOR APPLICATION NUMBER: 09/779,880
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-06-12
PRIOR FILING DATE: 2001-06-12
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/310,458
PRIOR FILING DATE: 2001-08-08
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PATCHTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 ÓWDFGNTMCOLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 OWDFGNTMCQLLTGLYFIGFFS 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 OWDFGNIMCOLLIGLYFIGFFS 22
                                                                                                                                                                                                                                                                    LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 40
US-10-225-567A-352
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                                                                                                                                                                                                                                                                                                                                 US-10-067-800-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 6
LENGTH: 352
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                                                                                                                                                                                                                           SOFTWARE: PESEQ ID NO 22
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                                                                                                                                                                                                                                                                                                                                                                                    RESULT 38
US-10-067-800-22
US-10-067-800-22
Sequence 22, Application US/10067800
Publication No. US20030100058A1
GENERALI NROPATION:
APPLICANT: Rosenke, Viktor
APPLICANT: Rosenke, Viktor
TITLE OF INVENTION: Human Gprotein Chemokine Receptor (CCR5) HDGNR10
FILE REFERENCE: 1488.115001
CURRENT APPLICATION UNMERE: US/10/067,800
CURRENT FILING DATE: 2002-02-08
PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 126; DB 14; Length 352; 100.0%; Pred. No. 6.3e-10; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                     100.0%; Score 126; DB 14; Length 352; 100.0%; Pred. No. 6.3e-10;
                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                               0; Mismatches
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CURRENT FILING DATE: 2002-02-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 352
                                                                                                                                                                                                         Best Local Similarity 100. Matches 22; Conservative
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                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-10-067-800-2
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Matches 22; Conserva
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Query Match
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0;
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 35.2
; LENCHH: 35.2
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-35.2
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0; Gaps

Search completed: September 28, 2004, 09:44:41 Job time: 74.875 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

- protein search, using sw model OM protein

September 28, 2004, 08:57:36; Search time 11.825 Seconds (without alignments) 178.961 Million cell updates/sec Run on:

US-10-084-813-12 126 1 QWDFGNTMCQLLTGLYFIGFFS 22

Title: Perfect score:

Seguence:

Scoring table:

283366 seqs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

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length: 0 length: 2000000000 Minimum DB Maximum DB

summaries Minimum Match 0% Maximum Match 100% Listing first 45 st Post-processing:

Database :

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Result No.	Н	Ŋ	m	4	Ŋ	9	7	∞	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	125	26	27	28	59

mu opioid receptor thrombin receptor	arpha-uniombin rec hypothetical prote probable TonB-depe	fusin (LESTRA) - c - neuropeotide Y/pep	probable transport	probable transport thrombin receptor	G protein-coupled	protein B0212.5 [i	neprameticai F215- bradykinin Bl rece
A57510 A37912 S17148	AG1086 A81848	G00048 A45747	F65067 F91091	A85937 IS1667	S65766 T37241	D88651	JC4681
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30 31 32		3 3 3 3	38	6 4 0 0	4 4 1 2	4 4 6 4	45

ALIGNMENTS

Addilla
Clobete: 12-U11-1995 #feequence revision 12-U11-1996 #fext change 20-Jun-2000
C.Species: Homo aspiens (man)
C.Species: Homo aspiens (man)
C.Species: Homo aspiens (man)
C.Accession: Addilla; ST1809; E58934; A58935; A58535; A58535
R.Samson, M.; Labbe, O.; Mollareau, C.; Vassatt, G.; Parmentier, M.
Biochemistry 35, 3562-3367, 1996
A.Accession: Addilla
A.Accession: S71808
A.Attle: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of A.Accession: S71808
A.Accession: S71808
A.Accession: S71808
A.Accession: ASSANA
A.Accession: ASSANA
A.Accession: Addilla
A.Accession: Assana
A

R;Combadiere, C. submitted to the EMBL Data Library, May 1996 submitted to the EMBL Data Library, May 1996 A;Reference number: H01541 A;Accession: G02653

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Chemckine (C-C) receptor 2, splice form A - human

Chamckine (C-C) receptor 2, splice form A - human

Chamckine (C-C) receptor 2, splice form A - human

Chacesesion aspiens (man)

Chacesesion: 138450

R; Charc 1.5: Myezr, S.J; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.

Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994

A; Title: Molecular cloning and functional expression of two monocyte chemoattractant pro

A; Reference number: A53477; MUID:94195821; PMID:8146186

A; Accession: 138450

A; Reference number: A53477; MUID:94195821; PMID:8146186

A; Reference number: A53477; MUID:94195821; PMID:8146186

A; Residues: 1-374 < RES.

A; Residues: 1-374 < RES.

A; Residues: 1-374 < RES.

A; Cross-references: EMBL:U03882; NID:9472555; PIDN:AAN19119.1; PID:9472556

C; Gentics: CDB:CMKBR2

A; Cross-references: GDB:337364; CMIM:601267

A; Map position: 372-3721

C; Superfamily: vartebrate rhodopsin

C; Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane #status predicted < TML>

F; 178-97 Domain: transmembrane #status predicted < TMS>
F; 178-97 Domain: transmembrane #status predicted < TMS>
F; 208-225 Domain: transmembrane #status predicted < TMS>
F; 224-255 Domain: transmembrane #status predicted < TMS>
F; 224-255 Domain: transmembran
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O protein-coupled receptor CKR-L1 - human

NiAlternate names: chemokine receptor-like protein TER1; GPR-CY6

C;Species: Al-Jan-1997 #sequence revision 31-Jan-1997 #text_change 21-Jul-2000

C;Accession: JC5067; G0276; G02387

R;Zaballos, A.; Varona, R; Guterrez, J; Lind, P; Marquez, G.

Biochem. Biophys. Res. Commun. 227, 846-853, 1996

A;Title: Molecular cloning and RNA expression of two new human chemokine receptor-like g

A;Accession: JC5067; MUID:97040707; PMID:8886020

A;Accession: JC5067

A;Molecule type: DNA

A;Rolecule type: DNA

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(covalent) #status predicted
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                                                                                                                                                             69.0%; Score 87; DB 2; I
66.7%; Pred. No. 1.4e-05;
Live 3; Mismatches 4;
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Pred. No. 1.5e-05;
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      F;14/Binding site: carbohydrate (Asn) (covale
F;113-190/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 EWVFGNAMCKLFTGLYHIGYF 125
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Local Similarity 66.7%;
es 14; Conservative
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les 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C, Function:
A, Description: G protein-coupled receptor for chemokines MIP-lalpha, MIP-lbeta and RANTE
A, Description: G protein-coupled receptor for chemokines MIP-lalpha, MIP-lbeta and RANTE
A, Mote: probably acts to control granulocyte proliferation and differentiation
C, Superfamily: vertebrate rhodopsin
C, Keywords: AlDS, G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane
F; 32-56/Domain: transmembrane #status predicted <TM1>
F; 67-87/Domain: transmembrane #status predicted <TM2>
F; 142-166/Domain: transmembrane #status predicted <TM5>
F; 25-57/Domain: transmembrane #status predicted <TM5>
F; 256-257/Domain: transmembrane #status predicted <TM5>
F; 256-250/Domain: transmembrane #status predicted <TM5>
F; 258-30/Domain: transmembrane #status predicted <TM5>
F; 258-250/Domain: transmembrane #status predicted <TM5>
F; 258-250/Domain: transmembrane (Sen) (covalent) #status predicted
F; 336, 337, 342/Binding site: phosphate (Sen) (covalent) #status predicted
F; 340, 343/Binding site: phosphate (Thr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chemokine (C-C) receptor 2, splice form B - human chemokine (C-C) receptor 2, splice form B - human chemokine (C-C) receptor 2, splice form B - human C;Species: Homo sapiens (man) (Species: Homo sapiens) (Homo sapiens) (H
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S.Superfamily: Vertebrate rhodopsin
C;Superfamily: Vertebrate rhodopsin
C;Superfamily: Vertebrate rhodopsin
C;Superfamily: Vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane #status predicted <TM1>
F;181-10/Domain: transmembrane #status predicted <TM3>
F;181-115-136/Domain: transmembrane #status predicted <TM4>
F;184-268/Domain: transmembrane #status predicted <TM4>
F;244-268/Domain: transmembrane #status predicted <TM5>
F;244-268/Domain: transmembrane #status predicted <TM6>
F;244-268/Domain: transmembrane #status predicted <TM7>
                                                  A;Molecule type: mRNA
A;Residues: 1-352 «RAP»
A;Cross-references: GB:U54994; NID:g1457945; PIDN:AAC50598.1; PID:g1457946
C;Comment: This is a receptor for chemokines MIP-lalpha (see PIR.A30574), MIP-lbeta (see
C;Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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A,Status: preliminary
A,Molecule type: mgNA
A,Residues: 1-360 <RES>
A,Cross-references: EMBL:U03905; NID:g472557; PIDN:AAA19120.1; PID:g472558
G,Genetics: GDB:CMKER2
A,Cross-references: GDB:337364; OMIM:601267
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                                                                                                                                                                                                                                                                                    C; Comment: Macrophage- and dual-tropic strains of HIV-1 1 C; Genetics:
A; Gene: GDB: CKRBR5; CCR5; CKR-5; CC-CKR-5; CKR5; ChemR13
A; Cross-references: GDB: L230510; OMIM: 601373
A; Map position: 3p21-3p21
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Best Local Similarity 100.0
Them 22; Conservative
      A; Accession: A58833
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Cyreywords: disulfiede bond; G protein-coupled receptor; glycoprotein; phosphoprotein; tx [Sfeywords: disulfiede bond; G protein-coupled receptor; glycoprotein; phosphoprotein; tx [Sfe 60/Domain: transmembrane #status predicted <TM1>
Fig 1-91/Domain: transmembrane #status predicted <TM3>
Fig 1-91/Domain: transmembrane #status predicted <TM4>
Fig 106-229/Domain: transmembrane #status predicted <TM4>
Fig 106-229/Domain: transmembrane #status predicted <TM6>
Fig 106-264/Domain: transmembrane #status predicted <TM6>
Fig 106-264/Domain: transmembrane #status predicted <TM7>
Fig 106-264/Domain: transmembrane #status predicted <TM7>
Fig 106-108/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cinate: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999 C; Accession: A45177; I55671 R; Neote, K; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J. (2011 72, 415-425, 1993 A; Title: Molecular cloning, functional expression, and signaling characteristics of a C-A; Reference number: A45177; MUID:93161416; PMID:7679328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Exp. Med. 177, 1421-1427, 1993
A;Title: Structure and functional expression of the human macrophage inflammatory 1 alp. A;Reference number: I55671; MUID:93240122; PMID:7683036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chemokine (C-C) receptor 1 - human
NyAlternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1998
C;Accession: 149341
       A; Residues: 1356 - RES>
A; Cross-references: EMBL:U28405; NID:g881549; PIDN:AAA89154.1; PID:g881550
C; Superfamily: vertebrate rhodopsin
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A)Molecule type: mRNA
A)Residues: 1-355 <NBO>
A)Residues: 1-355 <NBO>
A)Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
A)Experimental source: HL60 cells
A)Rote: sequence extracted from NCSI backbone (NCBIP:124876)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
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                                                                                                                                                            Query Match 58.7%; Score 74; DB 2; Length 356; Best Local Similarity 47.6%; Pred. No. 0.0013; Matches 10; Conservative 6; Mismatches 5; Indels
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47.6%; Pred. No. 0.0038;
ive 6; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: GDB:CMKBR1; CMKR-1
A;Cross-references: GDB:138446; OMIM:601159
A;Map position: 3p21-3p21
G;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                        100 WIFGNAMCKFVSGFYYLGLYS 120
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MIP-1 alpha receptor like-2 - mouse
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Matches 10; Conservative
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A; Residues: 1-355 <RES>
A; Molecule type: DNA
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C;Species: Wus musculus (house mouse)
C;Date: 02-Jul-1996 #touse mouse)
C;Date: 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: I49940
E;Gao. J.L.; Murphy, P.M.
J; Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemoki A;Reference number: I49339; MUID:95340546; PMID:7542241
A;Accession: 149340
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Molecule type: DNA
A;Residues: 1-35 < RES.
A;Cross-references: EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g881548
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                          A)Residues: 1-355 <BON>
A)Cross-references: EMBL:U45983; NID:g1245056; PID:g1245057
C;Comment: This protein belongs to the family of beta chemokine receptors.
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A,Gene: GDB:CMSPRB; CDS3733; OMIM:601834
A,Map position: 3921-3921
C,Superfamily: vertebrate rhodopsin
C,Superfamily: vertebrate rhodopsin
C,Keywords: G protein-coupled receptor; transmembrane protein
F)36-631/Domain: transmembrane #status predicted <TML>
F)73-94/Domain: transmembrane #status predicted <TM2>
F)108-129/Domain: transmembrane #status predicted <TM3>
F)108-129/Domain: transmembrane #status predicted <TM3>
F)23-260/Domain: transmembrane #status predicted <TM5>
F)23-260/Domain: transmembrane #status predicted <TM6>
F)23-260/Domain: transmembrane #status predicted <TM6>
F)281-304/Domain: transmembrane #status predicted <TM6>
                   A;Reaidues: 1-355 <NAP>
A;Reaidues: 1-355 <NAP>
A;Cross-references: EMBL:U62556; NID:g1468978; PID:g1468979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 65.1%; Score 82; DB 2; I Local Similarity 54.5%; Pred. No. 7.9e-05; nes 12; Conservative 6; Mismatches 4;
                                                                                           R,Bonner, T.I.
submitted to the EMBL Data Library, January 1996
A,Reference number: H01154
A,Accession: G02387
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA.
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Matches
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N;Alternate names: C-C CKR-4
C;Gspecies: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A57160
R;Species: Can, Meyer, A.; Nameth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; W
J; Biol. Chem. 270, 19455-19500, 1995
A;Title: Molecular Cioning and functional expression of a novel CC chemokine receptor CD
A;Residues: 1-360 e-FOW>
A;Residues: GD:CKRER4
A;Rocss-references: GB:R85740; NID:g1370103; PIDN:CAA59743.1; PID:g971452
A;Noce: source clone KS-5
C;Genetics: GD:CKRER4
A;Genetics: GD:CKRER4
A;Genetics: GD:CKRER4
A;Genetics: GD:CKRER4
A;Genetics: GD:CKRER4
A;Genetics: GD:CKRER4
A;Genetics: Gpochain: transmembrane #status predicted cTM2>
F;40-65;Domain: transmembrane #status predicted cTM3>
F;12-133/Domain: transmembrane #status predicted cTM3>
F;12-135/Domain: transmembrane #status predicted cTM3>
F;12-135/Domain: transmembrane #status predicted cTM3>
F;21-175/Domain: transmembrane #status predicted cTM3>
F;21-176-187/Distlifide bonds: #status predicted cT
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C.Species: Mus musculus (house mouse)
C.Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
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les 9; Conservative
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nes 10; Conservative
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A.Map position: 3p21-3p21
C.Superfamily: vertebrate rhodopsin
C.Superfamily: vertebrate rhodopsin
C.Superfamily: vertebrate rhodopsin
C.Superfamily: vertebrate rhodopsin
C.Superfamily: vertebrate produced receptor; glycoprotein; phosphoprotein; transmembrane #status predicted <TM1>
F.71-91/Domain: transmembrane #status predicted <TM2>
F.71-91/Domain: transmembrane #status predicted <TM3>
F.147-171/Domain: transmembrane #status predicted <TM4>
F.205-223/Domain: transmembrane #status predicted <TM6>
F.240-261/Domain: transmembrane #status predicted <TM6>
F.240-261/Domain: transmembrane #status predicted <TM6>
F.288-105/Domain: transmembrane #status predicted <TM7>
F.288-105/Domain: transmembrane #status predicted <TM7>
F.240-261/Domain: transmembrane #status predicted <TM7>
F.288-105/Domain: transmembrane (Ser) (covalent) (by casein kinase II) #status predicted
                             R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Coning and differential tissue-specific expression of three mouse beta chemoki
A;Reference number: 149339; MUID:9S340546; PMID:7542241
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R;Combadiere, C.; Ahuja, S.K.; Murphy, P.M.
J. Biol. Chem. 270, 16491-16494, 1995
A;Title: Cloning and functional expression of a human eosinophil CC chemokine receptor. A,Reference number: A57237, MUID:95348056; PMID:7622448
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A;Residues: 1-166,'N',108-275,'S',277-280,'R',282-355 <COM>
A;Coss-references: GB:U28694; NID:g1199579; PIDN:AACS0469.1; FID:g1199580
A;Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AACS0469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N;Alternate names: C-C CKR-3
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change·04-Mar-2000
C;Accession: G02436; AS7237
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53.2%; Score 67; DB 2; Length 355;
Best Local Similarity 52.4%; Pred. No. 0.015;
Matches 11; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:U28406; NID:9881551; PID:9881552 C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                A,Accession: I49341
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-359 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, February 1996 A;Reference number: H01272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 EWGFGHYMCKMLSGFYYLALYS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 OWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 WVFGHGMCKLLSGFYHTGLYS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-355 <PON>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chemokine (C-C) receptor 3 - human
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 40...
Best Local Similarity 60...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: G02436
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Gaps

chemokine (C-C) receptor 4 - human

RESULT 10

Gaps

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C;Accession: JC4304
R;Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Gene 163, 295-299, 1995-299, 1995
A;Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to g
A;Reference number: JC4304; MUID:96011651; PMID:7590284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1.355 < RAP>
A; Residues: 1.355 < RAP>
A; Residues: 1.355 < RAP>
A; Cross-references: GB: U20350; NID: 9655580; PIDN: AAA91783.1; PID: 9665581
A; Experimental source: peripheral blood mononuclear cell
C; Comment: This protein is a cell-surface receptor which recognizes extracellular signal
C; Comment: This protein is a key regulator of many immune and homeostatic responses, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Homo sapiens (man)
Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: equine herpesvirus 2
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
C;Accession: S5559
B;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: S55594; MUID:95302501; PMID:7783207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                             transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
A,Map position: 6q27-6q27
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane pr
F;42-68/Domain: transmembrane #status predicted <TM1>
F;79-99/Domain: transmembrane #status predicted <TM2>
F;10-180/Domain: transmembrane #status predicted <TM3>
F;10-180/Domain: transmembrane #status predicted <TM3>
F;212-233/Domain: transmembrane #status predicted <TM5>
F;250-271/Domain: transmembrane #status predicted <TM5>
F;292-315/Domain: transmembrane #status predicted <TM5>
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F:66-88/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G protein-coupled receptor El - equine herpesvirus 2
C;Species: equine herpesvirus 2
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C, Keywords: G protein-coupled receptor; lymphokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 59; DB 2; Pred. No. 0.26; 2; Mismatches
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Best Local Similarity 52.6%;
Matches 10; Conservative
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N;Alternate names: V28 protein
C;Species: Homo sapiens (man)
C;Date: 16-Nov-1995 #sequence_rer
C;Accession: JC4304
R;Raport, C.J.; Schweickart, V.L.
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les 9; Conserv
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Matches
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C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate ratio receptor; thymus
C;24,703,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;2,103,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pred
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
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R.Harrison, J.K.; Barber, C.M.; Lynch, K.R.
Neurosci. Lett. 169, 85-89, 1994
A.Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and A.Reference number: ISBNB6; MUID:94323113; PMID:8047298
A.Accession: ISBNB6
A.Acce
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C; Accession: UCS068
S; A; Varona, UCS068
B; Cabhys. Res. Commun. 227, 846-853, 196
A; Title: Molecular Cloning and RNA expression of two new human chemokine receptor-like g A; Reference number: UCS067; MUID:97040707; PMID:8886020
A; Reference number: UCS067
A; Residues: 1-369 < 2AB>
A; Residues: 1-369 < 2AB>
A; Residues: 1-369 < 2AB>
A; Cross-references: EMBL:Z79784; NID:g1668737; PIDN:CAB02144.1; PID:g1668738
C; Comment: This protein belongs to the family of alpha chemokine receptors.
A; Gene: GDB:CMKBR6; STRL22; GPR29; CCR6; CKR; CXR4
A; Cross-references: GDB:S370659; OMMM:601838
                           R;Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A. Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines A;Reference number: JC4587; MUID:96136324; PMID:8573157
A;Molecule type: mRNA
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A;Cross-references: EMBL:X90862; NID:gl167851; PIDN:CAA62372.1; PID:gl167852
A;Experimental source: thymus
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Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: mRNA
A,Residues: 1-354 «RES»
A;Cross-references: BMBL: U04808; MID:g2558635; PIDN:AAB87093.1; PID:g439861
C;Superfamily: vertebrate rhodopsin
C;Reywords: G protein-coupled receptor
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Pred. No. 0.18;
2; Mismatches
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QWVFGLGLCKIVSWMYLVGFYS 123
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ilarity 62.5%;
Conservative
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Best Local Similarity
'' 9; Conserv?
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les 10; Conserv
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RESULT 13

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melanin-concentrating hormone receptor [validated] - human
NyAlternate names: MCHR; orphan somatostatin-like receptor 1 (SLC-1)
(Species: Homo sapiens (man)
(Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G protein-coupled peptide receptor EBI 1 - human (5.9bcdess: Homo sapiens (man) (5.7bcdession: A45680 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999 (5.7bcdession: A45680 #revision K:; Yalamanchili, R.; Lenoir, G.; Kieff, E. J. 2.20-2220, 1993 A; Pitle: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled p. Aritle: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled p. Aritle: preliminary A45680 A; Residues: preliminary A; Residues: 1-378 carrs and A45680 A; Residues: 1-378 carrs and A456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nyabhocyte-specific G protein-coupled receptor EBI1 - human
NyAlternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
CySpecies: Homo sapiens (man)
CyDate: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
CyAccession: B55735; SS2443
Ryaccession: B55735; SS2443
Ryaccession: B55735; SS2443
Ayhitle: Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled receptor AyReference number: A55735; MUID:95154835; PMID:7851893
AyAccession: B55735
AyAccession: B55735
AyAccession: B5735
AyAc
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A;Note: sequence extracted from NGBI backbone (NCBIN:127094, NCBIP:127095)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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41.3%; Score 52; DB 2; Length 378;
Best Local Similarity 42.9%; Pred. No. 3.1;
Matches 9; Conservative 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.1%; Score 53; DB 2; Length 422; 57.1%; Pred. No. 2.5; 4; Indels ive 2; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 WHFGETMCTLITAM 191
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Matches 8; Conservative
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: A-May-1996 #sequence_revision 24-May-1996 #text_change 21-Jul-2000
C;Accession: 138973
R;O'Dowd, B.F.; Scheideler, M.A.; Nguyen, T.; Cheng, R.; Rasmussen, J.S.; Zastawny, R.;
R;O'Dowd, B.F.; Scheideler, M.A.; Nguyen, T.; Cheng, R.; Rasmussen, J.S.; Zastawny, R.;
Genomics 28, 84-91, 1995
A;Title: The cloning and chromosomal mapping of two novel human opioid-somatostatin-like
A;Title: The cloning and chromosomal mapping of two novel human opioid-somatostatin-like
A;Title: The cloning and chromosomal mapping of two novel human opioid-somatostatin-like
A;Title: The cloning and chromosomal mapping of two novel human opioid-somatostatin-like
A;Accession: 18973
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: EMBL:U22491; NID:g953232; PIDN:AAC50197.1; PID:g953233
C;Genetics:
A;Gene: GDB:GRR7
A;Cross-references: GDB:371714; OMIM:600730
A;Map position: 10q11.2-10q21.1
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A55735
G protein-coupled receptor EBII - mouse
C protein-coupled receptor EBII - mouse
C protein-coupled receptor EBII - mouse
C protein-coupled receptor EBII - mouse
C; Species: Mus musculus (house mouse)
C; Accession: A55735
E; Schweickart, V.U.; Raport, C.U.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
Genomics 23, 643-650, 1994
A; Title: Cloning of human and mouse EBII, a lymphoid-specific G-protein-coupled receptor A; Reference number: A55735; MUID:95154835; PMID:7851893
A; Reterence number: A55735
A; Reterence in Preliminary
A; Rossiques: 1-378 < SCH>
A; Rossiques: 1-378 < SCH>
A; Rossiques: GB:L31580; NID:9468340; FIDN:AAA74232.1; FID:9468341
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
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                                          A;Cross-references: GB:U20824; NID:9695172; PIDN:AAC13788.1; PID:9695173 C;Superfamily: vertebrate rhodopsin C;Keywords: G protein-coupled receptor
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                                                                                                                                                                                                                                                                                                       43.7%; Score 55; DB 2; Length 383; 38.1%; Pred. No. 1.1; tive 7; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 38.1%
Matches 8; Conservative
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Matches 9; Conservative
A; Residues: 1-383 <TEL>
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C, Accession: JN0621

*Martsucka, I; Mori, T.; Aoki, U.; Sato, T.; Kurihara, K.

Biochem. Biophys. Res. Commun. 194, 504-511, 1993

A, Title: Identification of novel members of G-protein coupled receptor superfamily expr
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y.Rosidues: 1-359 cCER>
y.Cross-references: GB:L23637; NID:g435093; PIDN:AAA39305.1; PID:g435094
y.Suzuki, H.; Prado, G.N.; Wilkinson, N.; Navarro, J.
Estol. Chem. 269, 18263-18266, 1994
Title: The N terminus of interleukin-8 (IL-8) receptor confers high affinity binding the procession: A53677; MuID:94308043; PMID:7518426
                                                                                                                                                                                                                                                                                                              A/ACCESLEULU: NUOLELA

A/ACCESLEULU: NUOLELA

A/ROCCESLEULU: NUOLELA

A/ROCCESLE 1-350 «MAT»

A/ROCCEST - references: G856348; NID:9399710; PIDN:AAB27547.1; PID:9399711

A/CTOSE-references: G856348; NID:9399710; PIDN:AAB27547.1; PID:9399711

A/EXPERIMENTAL SOURCE: tongue taste papillae

C/COMMENT: This protein is involved in modulating taste sensitivity or regeneration of t

C/Superfamily: vertebrate rhodopsin

C/SUPERFAMILY: vertebrate rhodopsin

C/SUPERFAMILY: vertebrate rhodopsin

C/SUPERFAMILY: vertebrate #status predicted <TM1>

F/14-155/Domain: transmembrane #status predicted <TM2>

F/14-175/Domain: transmembrane #status predicted <TM4>

F/200-222/Domain: transmembrane #status predicted <TM6>

F/242-265/Domain: transmembrane #status predicted <TM6>

F/244-265/Domain: transmembrane #status predicted <TM6>

F/244-265/Domain: transmembrane #status predicted <TM7>

F/244-306/Domain: transmembrane #status predicted <TM7>

F/244-306/Domain: transmembrane #status predicted <TM7>

F/244-306/Domain: transmembrane #status predicted <TM7>
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K;Bozic, C.R.; Gerard, N.P.; von Uexkull-Guldenband, C.; Kolakowski, L.F.
J. Biol. Chem. 269, 29355-29358, 1994
A;Title: The murine interleukin 8 type B receptor homologue and its ligands. Expression A;Reference number: 155421; MUID:95050766; PMID:7961909
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C,Specias: Mus musculus (house)
C,Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text change 05-Nov-1999
C;Accession: A48921; A58677; I49348; I55421; H48909; I53774
R;Cerretti, D.P.; Nelson, N.; Kozlosky, C.J.; Morrissey, P.J.; Copeland, N.G.; Gilbert, Genomics 18, 410-413, 1993
A;Title: The murine homologue of the human interleukin-8 receptor type B maps near the A;Reference number: A48921; MUID:94117014; PMID:8288247
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A;Cross-references: GB:L26549
A;Cross-references: GB:L26549
A;Note: sequence extracted from NCBI backbone (NCBIP:149812)
B;Note: J.; Cacalano, G.; Camerato, T.; Toy, K.; Moore, M.W.; Wood, W.I.
J. Immunol. 155, 2158-2164, 1995
A;Title: Chemokine binding and activities mediated by the mouse IL-8 receptor.
A;Reference number: 149348; MUID:95363183; PMID:7636264
                                    24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 19-May-2000
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Pred. No. 5.8;
4; Mismatches
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38.1%;
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Best Local Similarity 38.1
Matches 8; Conservative
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C; Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; inflammation; F;1-38 Domain: extracellular #status predicted eX1-38 Domain: extracellular #status predicted eX1-39 G_Domain: transmembrane #status predicted eX1-39 G_Domain: intracellular #status predicted eX1-39 G_Domain: transmembrane #status predicted eX1-30 G_Domain: transmembrane #status pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complement C5a anaphylatoxin receptor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S27357
R;Perret, J.J.; Raspe, E.; Vassart, G.; Parmentier, M.
Biochem. J. 288, 911-917, 1992
A;Title: Cloning and functional expression of the canine anaphylatoxin C5a receptor. Evi
                  the chemokine receptor BLR2/EBI1 is specifically transa
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A,Status: preliminary
A,Nolecule type: mRNA
A,Residues: 1-352 <PER-
A,Cross-references: EMBL:X65860; NID:g878; PIDN:CAA46690.1; PID:g879
C,Function:
A,Description: mediates the inflammatory and chemotactic responses of
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40.5%; Score 51; DB 1
Best Local Similarity 33.3%; Pred. No. 4.1;
Matches 7; Conservative 5; Mismatches
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A, Description: The expression of the chemokine A, Reference number: $52443
A, Reference number: $52443
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 21-378 EBUR>
A, Genetics:
C, Superfamily: vertebrate rhodopsin
C, Superfamily: vertebrate rhodopsin
C, Keywords: G protein-coupled receptor
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41.3%; Score 52;
Best Local Similarity 42.9%; Pred. No.
Matches 9; Conservative 4; Mismatc
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A,Status: preliminary, translated from GB/EMBL/DDBJ A,Molecule type: DNA

G protein-coupled receptor type B - bovine C; Species: Bos primigenius taurus (cattle)

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Gaps

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Length 350; 9; Indels

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A; Residues: 1-359 < RE2>

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Glasses in II receptor - turkey
C'Species: Meleagits gallopavo (common turkey)
C'Species: Meleagits gallopavo (common turkey)
C'Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 24-Nov-1999
C'Accession: 151372; Nov049
R'HWUDDY, T.J.; Nakamura, Y.; Takeuchi, K.; Alexander, R.W.
Nol. Planacol. 44 kl.7 1984
A'TILE: A Clond angiotensin receptor isoform from the turkey adrenal gland is pharmaco.
A,Recession: 151372; MUDD:9341466; PMD:8141266
A,Recession: 151372
A,Status: Preliminary; translated from GB/EMBL/DDBJ
A,Rocession: 151372
A,Status: Preliminary; translated from GB/EMBL/DDBJ
A,Rocession: BSI (120)
A,Recession: BSI (120)
A,Reference unmber: PN0449; MUDD:9321469; PMD:7916599
A,Title: Isolation of turkey adrenocortical call angiotensin II (AII) receptor partial carcial carcial carcial call angiotensin II (AII) receptor partial carcial predicted carcial c
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Riw, X.
Submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F35C8.
A;Description: The sequence of C. elegans cosmid F35C8.
A;Reference number: 218486
A;Reference number: 218486
A;Retaus: preliminary; translated from GB/EMBL/DDBJ
A;Rotaus: preliminary; translated from GB/EMBL/DDBJ
A;Rotaus: preliminary; translated from GB/EMBL/DDBJ
A;Rotaus: DNA
A;Rotaus: DNA
A;Rotaus: DNA
A;Rotaus: DNA
A;Rotaus: T148 < WUX>
A;Coss-references: EMBL:U40941; NID:g1072184; PID:g1072189; PIDN:AAAB1711.1; CESP:F35C8
CGenetics:
A;Genetics:
A;Genetics: Cipacetics: A;Genetics: 
                                                                                                                                                                                           hypothetical protein F35CB.3 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Jan-2000
C.Accession: T16256
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320 WSLGITVYQLVTGLY 334
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Best Local Similarity 60.0
Matches 9; Conservative
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R, Kawasaki, M.; Hisamoto, N.; Iino, Y.; Yamamoto, M.; Ninomiya-Tsuji, J.; Matsumoto, K.
E, Rawasaki, M.; Hisamoto, N.; Iino, Y.; Yamamoto, M.; Ninomiya-Tsuji, J.; Matsumoto, K.
E, M.; A acarorhabditis elegans JNK signal transduction pathway regurates coordinated
A, Reference number: Z21688; MUID:99321749; PMID:10393177
A, Rocession: T37324
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Status: preliminary;
A, Molecule type: MRNA
A, Residues: 1-435 KRNA>
A, Rocesidues: 1-435 KRNA
A, Rocesidues: 1-435 KRNA>
A, Rocesidues: 1-435 KRNA>
A, Rocesidues: 1-435 KRNA>
A, Rocesidues: 1-435 KRNA>
A, Rocesidues: 1-435
A; Cross-references GB:L13239; NID:g293665; PIDN:AAA62109.1; PID:g293666
B; Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G Genomics 19, 175-184, 1993
A; Title: Identification, chromosomal location, and genome organization of mammalian G-px A; Title: Identification, chromosomal location, and genome organization of mammalian G-px A; Title: Identification, chromosomal location, and genome organization of mammalian G-px A; Title: Identification, chromosomal location, and genome organization of mammalian G-px A; Title: preliminary; nucleic acid sequence not shown
A; Molecule type: MRNA
A; Molecule type: Markami, S.; Matsushima, K.
Gene 142, 297-300, 1994
A; Title: Cloning of a cDNA encoding a mouse homolog of the interleukin-8 receptor.
A; Molecule type: MJND:94252584; PMID:8194768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.7%; Score 50;
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-359 <RE3>
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J. Biol. Chem. 270, 15877-15883, 1995

A.Title: Characterization of the murine mu opioid receptor gene.
A.Fitle: Characterization of the murine mu opioid receptor gene.
A.Facession: A57510
A.Status: nucleic acid sequence not shown
A.Status: nucleic acid sequence not shown
A.Status: nucleic acid sequence not shown
A.Status: 1-398 «KAU»
A.Residues: 1-398 «KAU»
A.Residues: 1-398 «KAU»
A.Title: Genomic structure analysis of promoter sequence of a mouse mu opioid receptor y Proc. Natl. Acad. Sci. U.S.A. 91, 9081-9085, 1994
A.Title: Genomic structure analysis of promoter sequence of a mouse mu opioid receptor A.Reference number: 148665, MUID:94377496; PMID:8090773
A.Reference number: 148665
A.Status: translated from GB/EMBL/DDBJ
A.Residues: 1-398 «RES
A.Residues: 1-398 «RES
A.Residues: 1-398 «RES
A.Coss-references: EMBL:U10561; NID:9555696; PIDN:AAB60673.1; PID:9555699
A.Coss-references: EMBL:U10561; NID:9555696; PIDN:AAB60673.1; PID:9555699
A.Title: Antisense mapping the MOR-1 opioid receptor: evidence for alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Introns: 95/2; 213/1; 386/3
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteolytic
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A,Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
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AjGene GDB:P2R
AjGene GDB:127737; OMIN:187930
A;Rap position: 5913-5613
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F;1-26/Domain: signal sequence #status predicted <81G>
F;27-425/Product: thrombin receptor #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-Nov-1999
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A;Residues: 1-425 <VUA>
A;Cross_references: GB:M62424; NID:g339676; PIDN:AAA36743.1; PID:g339677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo saptens (man)
C;Species: Homo saptens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change (C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change (S;Accession: A37912, Wheaton, V.I.; Coughlin, S.R.
Cell 64, 1057-1068, 1991
A;Title: Molecular cloning of a functional thrombin receptor revision with the following of A;Accession: A37912; MuID:91168254; PMID:1672265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 398;
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Pred. No. 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 49; DB 2;
Pred. No. 9.5;
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 WPFGNILCKIVISIDYYNMFT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 WQFGSELCRFVTAAFYCNMYA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 WDFGNTMCQLLTGLYFIGFFS 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.9%;
ilarity 23.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 28.6
les 6; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interferon-inducible protein 10 (IP-10) receptor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 05-Reb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
C;Accession: JE0349
Biochem. Biophys. Res. Commun. 251, 41-48, 1998
Biochem. Biophys. Res. Commun. 251, 41-48, 1998
A;Itile: Cloning of the murine interferon-inducible protein 10 (IP-10) receptor and its A;Reference number: JE0349
A;Accession: JE0349
A;Accession: JE0349
A;Residues: 1-367 < TAM>
A;Residues: 1-367 < TAM>
A;Residues: 1-367 < TAM>
A;Comment: This protein is important for lymphocyte trafficking to lymphoid organs.
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                  G protein-coupled receptor GPR2 - human (fragment)
C;Species: Home sapiens (man)
C;Species: Home sapiens (man)
C;Accession: B55733
R;Marchese, A.; Docherty, J.M.; Nguyen, T.; Heiber, M.; Cheng, R.; Heng, H.H.Q.; Tsui, Genomics 23, 609-618, 1994
A;Title: Cloning of human genes encoding novel G protein-coupled receptors.
A;Reference number: A55733; MUID:95154831; PMID:7851889
A;Accession: B55733
A;Accession: B55733
A;Accession: Apel;DNA
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A57510
mu opioid receptor - mouse
C;Species: Mus musculus (house mouse)
C;Species: O8-Dec-1995 #sequence revision O8-Dec-1995 #text_change 24-Nov-1999
C;Accession: A57510; I48665; $\overline{S}_66513; I49300
C;Accession: A57510; I48665; Anton, B.; Tian, J.; Magendzo, K.; Newman, D.;
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                                                                     Gaps
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                                                                     Indels
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        Score 49.5; DB 2;
Pred. No. 7.1;
i; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.9%; Score 49; DB 36.8%; Pred. No. 8.4; iive 4; Mismatches
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38.9%; Score 49; DB
Best Local Similarity 36.4%; Pred. No. 8.7;
Matches 8; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GDB:371708; OMIM:600240
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C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | |: |: ::||| |
WSLGSATCRTISGLYSASF 116
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QWPFGNCLCKLASAGISF 110
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                                                                                                                 OWDFGNIMCOLLT-GLYF 17
        39.3%;
Query Match 39.38
Best Local Similarity 50.08
Matches 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 36.8'
Matches 7; Conservative
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A;Cross-references: GB:U13667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: GDB: GPR2
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A;Cross-references: GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CAB84785.1; PID:g738019
A;Experimental source: serogroup A, strain 22491
C;Genetics:
A;Gene: NWA1558
                                                                                                                                                                                                                                                                                                                                                                             2 WDFG---NTMCQLLTGLYFIGF 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 WOFGGESNT----LTGLYFRGY 58
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                                                                                                                                                                                                              Query Match
Best Local Similarity 54.5'
Matches 12; Conservative
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A; Residues: 1-352 < HER>
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A; Residues: 1-352 < FED>
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A;Molecule type: mRNA
A;Residues: 1-352 <LOE>
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                                                                                      alpha-thrombin receptor - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S1748
R;Rasmussen, U.B.; Vouret-Craviari, V.; Jallat, S.; Schlesinger, Y.; Pages, G.; Pavirani A;Tile: cDNA cloning and expression of a hamster alpha-thrombin receptor coupled to Ca(A;Reference number: S1748
A;Accession: S1
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A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mack, C.; Schluerer, T.; Simose, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Ritile: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein lmo0094 [imported] - Listeria monocytogenes (strain EGD-e) (Species: Listeria monocytogenes (C;Decies: Listeria monocytogenes C;Decies: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 (;Accession: AG1086
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A;Cross-references: GB:NC_003210; PIDN:CAC98309.1; PID:g16409453; GSPDB:GN00177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X61958; NID:9940495; PIDN:CAA43957.1; PID:g49538 C;Keywords: G protein-coupled receptor; transmembrane protein
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Pred. No. 10;
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A;Gene: 1mo0094
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Best Local Similarity 28.67
Matches 6; Conservative
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Matches 10; Conservative
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A;Molecule type: DNA
A;Residues: 1-706 <PAR>
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A;Status: preliminary
A;Molecule type: DNA
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neuropeptide Y/peptide YY receptor Y3 - human N;Alternate names: fusin; HM89; leukocyte-derived seven-transmembrane receptor LESTR; re C;Species: Homo sapiens (man) (S;Species: Homo sapiens (man) (C;Species: Homo sapiens (man) (C;Species: 03-May-1994 #text change 05-Nov-1999 (C;Accession: A45747; A53103; I53006; I59444; I69203; S32761 (R;Redersppiel, B.; Melhado, I.G.; Duncan, A.M.V.; Delaney, A.; Schappert, K.; Clark-Lewin A;Ritle: Molecular cloning of the cDNA and chromosomal localization of the gene for a put A;Reference number: A45747; MUID:93315164; PMID:8325644
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R;Jazin, B.E.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Weng, G.; Walker, M.W.; Salon, J.; Lan
Regul. Pept. 47, 247-258, 1993
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R;Loetscher, M.; Geiser, T.; O'Reilly, T.; Zwahlen, R.; Baggiolini, M.; Moser, B.;
J. Biol. Chem. 269, 232-237, 1994
A;Title: Cloning of a human seven-transmembrane domain receptor, LESTR, that is highly A;Reference number: A53103; MUID:94103215; PMID:8276799
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R;Herzog, H.; Hort, Y.J.; Shine, J.; Selbie, L.A.
DNA Cell Biol. 12, 465-471, 1993
A;Title: Molecular cloning, characterization, and localization of the human homolog to A;Reference number: 153006; MUID:93319629; PMID:8329116
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    Length 706;
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DB 2;
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38.5%; Score 48.5; D 54.5%; Pred. No. 20; tive 1; Mismatches
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Gaps

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probable transporter protein Z4165 [imported] - Escherichia coli (strain O157:H7, subst. C.) Speciess Escherichia coli (5.) Speciess Escherichia coli (5.) Secession: A85937 Escherichia coli #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C.) Accession: A85937 Escherichia C.) Burkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, Nature 409, 529-533, 2001 Mature 409, 529-533, 2001 A.7 Eller, D. Dimalanta, E.; Potamousis, K.; Apodaca, A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosidues: 1-409 <STO>
A;Cross-references: GB:AE005174; NID:g12517337; PIDN:AAG57957.1; GSPDB:GN00145; UWGP:Z41
A;Experimental source: strain O157:H7, substrain EDL933
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Cispecies: Xenopus laevis (African clawed frog)
Cispecies: Xenopus laevis (African clawed frog)
Cibate: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
CiAccession: 151667
Rigerszten, R.E.; Chen, J.; Ishii, M.; Ishii, K.; Nanevicz, T.; Turck, C.W.; Vu, T.H.; C Rigerszten, R.E.; Chen, J.994
A;Title: Thrombin receptor's specificity for agonist peptide is determined by its extract A;Reference number: 151667; WUID:94195429; PMID:8145852
A;Accession: 151667
              A;Molecule type: DNA
A;Residues: 1-409 <HAX>
A;Ressidues: 1-409 <HAX>
A;Crossreferences: GB:BA000007; PIDN:BAB37125.1; PID:g13363174; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: BCB3702
C;Superfamily: threonine-serine permease
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Pred. No. 14;
3; Mismatches
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A;Residues: 1-420 <GER>
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38.1%; Score 48; DB 2;
Best Local Similarity 30.0%; Pred. No. 14;
Matches 6; Conservative 7; Mismatches
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14;
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Pred. No.
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C,Superfamily: threonine-serine permease
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Similarity 50.0%;
9; Conservative
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Best Local Similarity 50.0%;
Matches 9; Conservative
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81 YGKKIGNLITTLYFIAFF
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'Title: A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its human homold
Reference number: 159444; MUID:94052833; PMID:8234909
Accession: 159444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Discoult Limitation of Section 1. Sep-1997 #text_change ol-Mar-2002 C. Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change ol-Mar-2002 C. Accession: R65067

R. A.; Rose, D. J.; Mau, B.; Shao, Y.

A.; Rose, D. J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A. Title: The complete genome sequence of Escherichia coli K-12.

A. Reference number: A64720; MUD:97426617; PMID:9278503

A. Reference number: A64720; MUD:97426617; PMID:9278503

A. Residue: preliminary; nucleic acid sequence not shown; translation not shown
A. Residues: 1-409 calary
A. Superfamily: threonine-serine permease
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                                                                   A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1.352 < RE2>
A,GCOSS-references: GB:L01639; NID:g189313; PIDN:AAA16594.1; PID:g189314
R;Nomura, H.; Nielsen, B.W.; Matsushima, K.
Int. Immunol. 5, 1239-1249, 1993
A,Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leu A,Reference number: 1549; 1993
A,Feference number: 154751; MUD:94092629; PMID:7505609
A,Accession: 169203
A,Accession: 169203
A,Batus: preliminary; translated from GB/EMBL/DDBJ
A,Residues: 1-352 < RES>
A,Ccoss-references: GB:D10924; NID:g219868; PIDN:BAA01722.1; PID:g219869
C,Genetics:
A,Gene: GDB:NPY3R; NPY3
A,Ccoss-references: GB:D10924; NID:62643
A,Map position: 2q21-2q21
C,Superfamily: vertebrate rhodopsin
C,Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
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: 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 WYFGNFLCKAVHVIYTVNLYS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 WDFGNTMCQLLTGLYFIGFFS 22
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Job time : 13.075 secs

OM protein - protein search, using sw model

September 28, 2004, 08:55:11; Search time 6.875 Seconds (without alignments) 166.624 Million cell updates/sec Run on:

Title: US-10-084-813-12
Perfect score: 126
Sequence: 1 QWDFGNTMCQLLTGLYFIGFPS 22

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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P51678 mus musculu	P51677 homo sapien	018983 cercopithec	P51679 homo sapien	000574 homo sapien	O19024 macaca neme	O9tv16 pan troglod	Osbds6 macaca fasc	O9xt45 macaca mula	P51680 mus musculu	086917 capriboxvir	-	
CKR3 MOUSE	CKR3 HUMAN	CCR6 CERAE	CKR4 HUMAN	CCR6 HUMAN	CCR6 MACNE	CCR6 PANTR	CCR6 MACFA	CCR6 MACMU	CKR4 MOUSE	VQ3L_CAPVK	C3X1_MOUSE	
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE 999335215; PubMed=10408730; Multarine Trutumin M.C., Corbet S., Hansen J., Georges-Courbot M.-C., Multarion M.C., Corbet S., Hansen J., Georges-Courbot M.-C., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.; Stoulet J., Barre-Sinoussi F., Fomsgaard A.; Mutations in CCRS-coding sequences are not associated with SIV carries featus in African nonhuman primates."; ALS Res. Hum. Retroviruses 15:931-939(1999).

-1. FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-bet and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCRS).
CCRS OR CMKBRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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                                                                                                                                                                                                                                                                                                                                            Score 126; DB 1; Length 352;
Pred. No. 1e-11;
; Mismatches 0; Indels (
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SULPATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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                                                                             CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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(POTENTIAL)
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                  CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cercopithecinae; Cercopithecus.
NCBI_TaxID=60710;
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Les 22; Conservative
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InterPro, IPR000276; GPCR_Rhodpsn. Pfam; PF00001; 7tm_1; 1.

EMBL; AF035222; AAD44015.1; -

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"Primary SIVsm isolates use the CCR5 coreceptor from sooty mangabeys naturally infected in west Africa: a comparison of coreceptor usage of primary SIVsm. HV.2, and SIVmac.";
virology 246:113-124(1998).
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RAVIES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
          PROSITE; PS00237; G PROTEIN RECEP F1_1; 1.

PROSITE; PS0262; G PROTEIN RECEP F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

DOMAIN 31 58 CYTOPENTIAL).

TRANSMEM 59 68 CYTOPENTIAL).

TRANSMEM 69 89 2 (POTENTIAL).

DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         062743; 062744; 067745; 062746; 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey). Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercocebus.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
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SULFATION (BY SIMILARITY)
SULFATION (BY SIMILARITY)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (
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STRAIN=Isolate 079, 085, 087, and 089;
MEDLINE=98321155; PubMed=9656999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 OWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                              351 7
352 CC
178 BN
3 SI
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15 SU
PRINTS; PR00237; GPCRRHODOPSN
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1es 22; Conservative
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us-10-084-813-17.rgD

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ID _CKRS_HUMAN

RES_HUMAN

AC PSIGES, O14692; O14693; O14695; O14699; O14699;

AC O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707;

AC O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707;

AC O14709; O15538; Q9UPA4;

DT O1-OCT-1996 (Rel. 34, Lest equence update)

DT 15-MAR-2004 (Rel. 34, Last annotation update)

DT 15-MAR-2004 (Rel. 34, Last annotation update)

CC Chemokine receptor type 5 (C-C CKR-5) (CCR-S) (CCR-S)

CR CHOMOKINE receptor) (CHEMR13) (CD195 antigen).

CCRS OR CWKBRS.

OS HOMO sapiens (Human).

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

ON NCBI_TAXID=9606;
                    increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or
                                                                                                                                                                                                                                                                                                              EMBL, AF005659; AAB62553.1; -.
InterPro; IPR00276; GPCR_Rhodpsn.
Prints, PR00137; GPCRHCHODDEN.
PROSITE; PS00237; GPROTEIN RECEP_F1_1; 1.
PROSITE; PS00237; G PROTEIN RECEP_F1_2; 1.
PROSITE; PS00262; GPROTEIN RECEP_F1_2; 1.
DOMAIN COUPLED RECEP_F1_2; 1.
SO EXTRACELLULAR (POTENTAL).
                                                      differentiation.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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MEDLINE=96241590; PubMed=8639485;
Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;
"Molecular cloning and functional expression of a new human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 126, DB 1, Length 352, Pred. No. 1e-11; 0, Mismatches 0, Indels (
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EXTRACELLULAR (POTENTIAL)
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EMBL; AF051902; AAC39830.1; --
EMBL; AF051904; AAC39831.1; --
EMBL; AF051904; AAC39831.1; --
EMBL; AF051904; AAC39831.1; --
INTERPO: TER000276; GPCR_Rhodpsn.
Pfam; PR00021; 7tm 1, 1
PRINTS; PR00021; 7cm 1, 1
PROSITE; PS00237; GPROTEIN RECEP_F1.1; 1.
PROSITE; PS00262; GPROTEIN_RECEP_F1.2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN : 30
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT 2001 (CCR-5) (CCR-5) (CCR-5)
16-OCT 2001 (CCR-5) (CCR-5)
16-OCT 2001 (CCR-
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W -> G (IN ISOLATE 087).
L -> V (IN ISOLATE 089).
V -> G (IN ISOLATE 079).
V -> G (IN ISOLATE 079).
V -> G (IN ISOLATE 079).
T -> I (IN ISOLATE 079).
T -> I (IN ISOLATE 079).
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8 Y SIMLARITY.

9 Y SIMLARITY.

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9 Y SIMLARITY.

10 Y SULPATION (BY SIMLARITY).

11 SULPATION (BY SIMLARITY).

12 Y SULPATION (BY SIMLARITY).

13 Y SULPATION (BY SIMLARITY).

14 Y SULPATION (BY SIMLARITY).

15 Y SULPATION (BY SIMLARITY).

16 Y SIMLARITY.

17 Y SULPATION (BY SIMLARITY).

18 Y SIMLARITY.

19 Y SIMLARITY.

10 Y SULPATION (BY SIMLARITY).

20 Y SULPATION (BY SIMLARITY).

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25 Y SULPATION (BY SIMLARITY).

26 (IN ISOLATE 079).

27 Y SULPATION (BY SIMLARITY).
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MEDLINE=96291862; PubMed=8663314;
Raport C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.;
"Molecular Cloning and functional characterization of a novel human
"CC chemokine receptor (CCRS) for RANTES, MIP-lbeta, and MIP-lalpha.";
J. Biol. Chem. 271:17161-17166(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND POLYMORPHISMS.
MEDLINE=98022612; PubMed=9359654;
Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
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MEDLINE-98001387; Pubmed=9343222;
Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.;
"Polymorphisms in the CCR5 genes of African green monkeys and micimplicate specific amino acids in infections by simian and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K., Gnoj L., la Bastide M., Raplan N., Greco T., Touchman J., Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D., Sagripanti J.L., Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism."; AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Kopatz S.A., Aronstam R.S., Sharma S.V.;

"CDNA clones of human proteins involved in signal transduction sequenced by the Guthrie CDNA resource center (www.cdna.org)."; submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=96260017; PubMed=8649511;
Deng H., Liu R., Ellmeter W., Choe S., Unutmaz D., Burkhart M., di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B., Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
"Identification of a major co-receptor for primary isolates of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND VARIANT ARG-178.
Magierowska M., Barre-Sinoussi F., Issafras H., Theodorou I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
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CC-chemokine receptor gene.";
Biochemistry 35:3362-3367(1996),
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                                                                                                                                                                                                                             Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,
Gerard N.P., Gerard C., Sodroski J., Choe H.,
"Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glycosylation.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                   Paxton W.A., HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,
                                                                                                                                                       MEDLINE=99189752; PubMed=10089882;
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the Buropean Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
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RA MEDLINE-99416438; PubMed=10486970;

RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;

RGUENCE evolution of the CCRS chemkine receptor gene in primates.";

RI "Sequence evolution of the CCRS chemkine receptor gene in primates.";

RI "Sequence evolution of the CCRS chemkine receptor gene in primates.";

RL MOL Biol. Evol. 16:1145-1154(1999).

CC '- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

CC '- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

CC '- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

CC '- In the control of granulocytic lineage proliferation or

differentiation.

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-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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                                                                                                                                                                                                       EMBL, AF075451, AAD19863.1; -.
InterPro; IRR000276; GPCR_Rhodpsn.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP_F1 1; 1.
PROSITE; PS0262; G_PROTEIN RECEP_F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
EXTRACELLULAR (POTENTIAL).
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15-WAR-2004 (Rel. 43, Lost sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
15-WAR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5)
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hylobatidae, Hylobates.
MCBI_TaxID=81572;
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Matches
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CKR5_HYLML
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DR EMBL; AF011534; AAB65734.1; -.

DR EMBL; AF011534; AAB65735.1; -.

DR EMBL; AF011536; AAB65735.1; -.

DR EMBL; AF011536; AAB65737.1; -.

DR EMBL; AF011537; AAB65737.1; -.

DR GO; 00005769; C:endosome; TAS.

GO; 000015026; F:C-C chemokine receptor activity; NAS.

GO; 000016493; F:C-C chemokine receptor activity; NAS.

GO; 000016493; F:C-C chemokine response; TAS.

GO; 00000596; P:cellidar defense response; TAS.

GO; 00000596; P:cellidar defense response; TAS.

GO; 00000596; P:Cellidar defense response; TAS.

GO; 000001155; P:invasive growth; TAS.

GO; 000001155; P:invasive growth; TAS.

GO; 00001155; P:invasive growth; TAS.

GO; 00000125; P:invasive growth; TAS.

GO; 00001201; Tan, 1.

DR FRONITE; PRO0127; GPCRRHODOPSN.

PROSITE; PS00237; GPCRRHODOPSN.

PROSITE; PS00237; GPCRRHODOPSN.

PROSITE; PS00237; GPCRRIN RECEP FI 1; 1.

G-POTCHIN COUNTIAN.

THANSARNAN.

1 30 EXTRACELLULAR (POTENTIAL).

THANSARNAN.

21 DOMAIN

22 DOMAIN

23 EXTRACELLULAR (POTENTIAL).
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RA MEDLINE-99416438; PubMed=10486970;

RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;

RA Chang Y.-W., Ryder O.A., Zhang Y.-P.;

RI "Sequence evolution of the CCR5 chemokine receptor gene in primates.";

RL MAI. Brol. 16:1145-1154(1999).

CC '!-FUNCTION' Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

CC '!-FUNCTION' Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

CC '!-FUNCTION' Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

CC '!-FUNCTION' Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

CC '!-FUNCTION' Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

CC '!-FUNCTION' Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

CC '!-FUNCTION' Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

CC '!-FUNCTION' Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

CC '!-FUNCTION' Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

CC '!-FUNCTION' Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

CC '!-FUNCTION' Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

CC '!-FUNCTION' Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

CC '!-FUNCTION' Receptor for a C-C type chemokine.

CC '!-FUNCTION' RECEP
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
28-FBB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CRR-5) (CC-CRS-5) (CCRS).
Hylobates leucogenys (White-cheeked gibbon).
Hylobates leucogenys (Cordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hylobatidae; Hylobates.
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(VTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).
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Pred. No. 1e-11;
0; Mismatches (
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nes 22; Conservative
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DOMAIN
TRANSMEM
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097883;
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Gaps

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differentiation.
-!-SURCENTULAR LOCATION: Integral membrane protein.
-!-SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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the Ruropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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NEDLINE-99416438; PubMed=10486970;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Sequence evolution of the CREs chemokine receptor gene in primates.";
Mol. Biol. Evol. 16:1145-1154(1999).
-! FUNCTION: Receptor for a C.C type, chemokine. Binds to MIP-1-alpha,
-! FUNCTION: Receptor for a and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                           EMBL, AF177899, AAK43382.1; -.
InterPro; PR00276; GPCR_Rhodpsn.
PRAMPS, PR00237; GFCRHOOPSN.
PROSITE; PS0237; GFCRHOOPSN.
PROSITE; PS0237; G_PROTEIN_RECEP_FL_1; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN : BXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor type 5 (C-C CRR-5) (CC-CRR-5) (CCRS)
CCRS OR CMKBRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hylobates syndactylus (Siamang) (Symphalangus syndactylus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
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SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
9623CA98340CF274 CRC64;
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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(POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Les 22; Conservative
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166
198
198
223
240
277
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MOD RES
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CKR5_HYLSY
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                                                            EMBL, AF177884, AAK43367.1; -.

InterPro; IPR000276, GPCR_Rhodpsn.

Pfam, PF00001, 7tm 1; 1.

PRINTS, PR00237, GPCRHODDESN.

PROSITE; PS00237; GPROTEIN RECEP_F1_1; 1.

PROSITE; PS50262; GPROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

G-protein coupled receptor; Transmembrane; ROTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P793.5; C02746; 01.02746; 01.02746; 01.00V-1997 (Rel. 35, Created) 01.NOV-1997 (Rel. 35, Last sequence update) 01.NOV-1997 (Rel. 35, Last annotation update) 28-FBB-2003 (Rel. 41, Last annotation update) C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CC-CKR-5)
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Macaca mulatta (Rhesus macaque),

Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and

Macaca nemestrina (Pig-tailed macaque),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=M.mulatta;
MEDLINE=97184592; PubMed=9032394;
Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
Newman W., Gerard N., Gerard C., Sodroski J.;
"Utilization of C-C chemokine receptor 5 by the envelope
glycoproteins of a pathogenic simian immunodeficiency virus,
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0; Indels
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SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                       7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
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0; Mismatches
                                                                                                                                                                                            1 (POTENTIAL)
CYTOPLASMIC (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            40508 MW;
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NCBI_TaxID=9544, 9541, 9545;
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22; Conservative
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277
301
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352
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Matches
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MEDLINE=97268687; PubMed=9108095;
MEDLINE=97268687; PubMed=9108095;
MEDLINE=97268687; PubMed=9108095;
MEDLINE=97268687; PubMed=9108095;
MEDLINE=97268687; PubMed=9108095;
MEDLINE=97268687; PubMed=9108095;
MEDLINE=97268687; PubMed=8.0., Miller K., Doranz B.J., Endres M.,
Mandel M., Backer C.C., Doms R.W.;
MIPLIDIATION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIPLI-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
differentiation.
C. I- SUMLEARIY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation for Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
"Genetically divergent strains of simian immunodeficiency virus use CCRS as a coreceptor for entry."; J. Virol. 71:2705-2714(1997).
                                       SEQUENCE FROM N.A.
SPECIES=M.mulatta;
MEDLINE=21354176; PubMed=11461684;
Margulies B.J., Hauer D.A., Clements J.E.;
"Identification and comparison of eleven rhesus macaque chemokine
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SULFATION (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
M -> I (IN REF. 3).
I -> M (IN REF. 3).
58896C85909FACE2 CRC64;
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EXTRACELLUAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
SULFATION (BY SIMILARITY).
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352 AA;
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differentiation.
--- SUBCELLULAR LOCATION: Integral membrane protein.
--- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phylogeny.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCIION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
                                                     Gaps
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MEDLINE=98022612; PubMed=9359654;
Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
Fo D.D.;
                                                                                                                                                                                                                              P56440; 002778;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCRCR-5) (CCRS).
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MEDLINE=97426118; PubMed=92822;
Zacharova V., Zachar V., Goustin A.S.;
"Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=97268687; PubMed=9108095;
Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
Pelper S.C., Parmentier M., Broder C.C., Doms R.W.;
"Differential utilization of CCRS by macrophage and T cell tropic
simian immunodeficiency virus strains.";
Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
                                                                                                                                                                                                                                                                                                                                            Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism."; AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
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MEDILINE=98090115; PubMed=9430250;
Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;
"Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";
AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
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             Score 126; DB 1; Length 352;
Pred. No. 1e-11;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zimmerman P.A., Buckler-White A., Alkhatib G.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
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100.0%; Sco
100.0%; Pre
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       Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
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"Differential utilization of CCR5 by macrophage and T cell tropic

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EMBL; 097665; AAS55742.1; -
EMBL; AP6011540; AAB55740.1; -
EMBL; AP6011540; AAB55740.1; -
EMBL; AF77894; AAC03717.1; -
EMBL; AF77894; AAC03717.1; -
EMBL; AF77894; AAK43377.1; -
EMBL; AF77894; AAC03717.1; -
EMBL; AF77894; AAC03717.1; -
EMBL; AF77894; AAC03717.1; -
EMBL; AF77894; AAC03717.1; -
EMBL; PR000037; GFCRHODOPSN.
PROSTITE; PS000237; GFCRHODOPSN.
PROSTITE; PS00237; GFCRHOSTN. RECEPF1.1; 1.
PROSTITE; PS00237; GFCRHOSTN. RECEPF1.2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN.
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15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCRS).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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MEDLINE=97268687; PubMed=9108095;
Bdinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
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SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
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CYTOPLASMIC (POTENTIAL).
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EMBL; U94329; AAB58446.1; -.
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NCBI_TaxID=9557, 9555;
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                                                                                                                                                                                                     SPECIES=P.anubis;
Benton P.A., Thmanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
Benton P.A., Thmanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
                                                                          SPECIES=P.hamadryas;
MEDIJNE=99210133; PubMed=10195758;
Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;
"Species-specific changes in the CCR5 gene from African and Asian nonhuman primates.";
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EMBL; AF105287; AAD20556.1; --
EMBL; AF105289; AAD20557.1; --
EMBL; AF105299; AAD20557.1; --
EMBL; AF105299; AAD20559.1; --
EMBL; AF032452; AAC63830.1; --
EMBL; AF033452; AAC63830.1; --
EMBL; AF00207; GPCR_HOdpsn.
PRINTS; PR00217; GPCRRODOPSN.
PRINTS; PR00237; GPCRRODOPSN.
PROSITE; PS00237; GPCRED RECEPTION:
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
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-i- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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             simian immunodeficiency virus strains.";
Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
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93 QWDFGNTMCQLLTGLYFIGFFS 114

93 QWDFGNTMCQLLTGLYFIGFFS 114

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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang Y.-W., Ryder O.A., Zhang Y.-P.,
Sequence evolution of the CCR5 chemokine receptor gene in primates.";
"Sequence evolution of the CCR5 chemokine receptor gene in primates.";
Mol. Biol. Bvol. 16:1145-1154(1999).
-!-FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of gramulocytic lineage proliferation or
differentiation.
-!-SUBCELIULAR LOCATION: Integral membrane protein.
-!-SUBCELIULAR Elongs to family 1 of G-protein coupled receptors.
                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
38-FBB-2003 (Rel. 41, Last annotation update)
C-C chemokihe receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR5).
                                                                                                                                             Eukāryotā, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pongo.
NCBI_TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 (POTENTIAL).
EXTRAGELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
FXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
SULFATION (BY SIMILARITY).
                                 352 AA.
                                                                                                                                                                                       [1] SEQUENCE FROM N.A. MEDLINE=99416438; Pubmed=10486970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40527 MW;
                                                                                                                               Pongo pygmaeus (Orangutan)
                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              352 AA;
                CKRS PONPY
ID CKRS PONPY
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MOD_RES
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TRANSMEM
                                           097881;
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities ...

or send an email ...

or send an email ...

Dr. Ferd. AF075445; AAD19857.1; -..

DR. InterPro; IPR000276; GPCR.Rhodpsn.

DR. PRINTS; PR00237; GPCRHHODOPSN.

DR. PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.

DR. PROSITE; PS00262; GPROTEIN RECEP F1 2; 1.

KW. G-protein coupled receptor; Transembrane; Glycoprotein, Sulfation.

FT DOMAIN 31 58 1 (POTENTIAL).

TRANSMEM 31 59 68 CYTOPLASMIC (POTENTIAL).

SS GRANGELLULAR (POTENTIAL).

TRANSMEM 31 (POTENTIAL).

TRANSMEM 31 (POTENTIAL).

TRANSMEM (POTENTIAL).

TRANSMEM (POTENTIAL).

TRANSMEM (POTENTIAL).
                                                                                                                                                                                                                                                   MEDLINE=99416438; PubMed=10486970; Zhang Y.-P.; Zhang Y.-W., Ryder O.A., Zhang Y.-P.; Zhang Y.-P.; Zhang Y.-P.; Sequence evolution of the CCRS chemckine receptor gene in primates."; Mol. Biol. Evol. 16:1145-1154(1999).
-!- FUNCTION: Receptor for a C-C type chemckine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.
                                                                                                                                      Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae, Colobinae,
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                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5)
                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Integral membrane protein.
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Pred. No. 1e-11;
Mismatches 0; Indels
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELULAR (POTENTIAL).
7 (POTENTIAL).
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SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
4366F142730F938F CRC64;
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                                 352 AA
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100.0%;
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Best Local Similarity luccol
The 22; Conservative
                                 STANDARD;
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                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                        NCBI_TaxID=61621;
                                                                                                                          CCRS OR CMKBRS
                                           097880;
30-MAY-2000
                              PYGBI
                                                                                                                                                                                       Pygathrix.
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RESULT 13
CKRS_PYGBI
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Gaps

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1 OWDFGNTMCOLLTGLYFIGFFS 22

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93 QWDFGNTMCQLLTGLYFIGFFS 114
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Tue Sep 28 15:49:56 2004

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                                                                                                                                                                                                                                       MEDILINE=99416438; PubMed=10486970; Zhang Y.-W.; Ryder O.A., Zhang Y.-W.; Ryder O.A., Zhang Y.-P.; Sequence evolution of the CCRS polemekine receptor gene in primates."; Mol. Biol. Evol. 16:1145-1154(1999).

-!-FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or
                                                                                                                                 Pygathrix nemaeus (Dove langur).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae, Colobinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; irructi...
PRIMIS; PRO0001; TRIL; I. PRINTS; PRO0017; GFCRAHODPSN.
PROSITE; PS00237; GFROTEIN RECEP_FI_1; I.
PROSITE; PS50262; GFROTEIN RECEP_FI_2; I.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
EXTRACELLUIAR (POTENTIAL).
                                                       30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
38-FBB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCRS).
                                                                                                                                                                                                                                                                                                                                                                              -:- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N (BY SIMILARITY).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                               PRT; 352 AA
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40532 MW;
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Best Local Similarity 100.
Matches 22; Conservative
                             STANDARD;
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                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                 Pygathrix.
NCBI_TaxID=54133;
                               PYGNE
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RESULT 14
CKR5_PYGNE
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                                                                                                                                                                                                                                                                                              MEDLINE=99416438; PubMed=10486970;
MEDLINE=99416438; PubMed=10486970;
MEDLINE=99416438; PubMed=10486970;
Mang Y.-W., Ryder O.A., Zhang Y.-P.;
Sequence evolution of the CCRS chemokine receptor gene in primates.";
Mol. Biol. Bvol. 16:1145-1154(1999).
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
-!- FUNCTION: Receptor for a de subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Verrebrata; Euteleostom;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
Trachypithecus.
                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
38-FBB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type.5 (C-C CKR-5) (CC-CKR-5) (CCRS OR CMKBRS.
Trachypithecus francoisi (François' langur) (Indochinese langur)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEAM; PP00001; 7tm 1; 1.

PRINTS; PR00237; GPCRRIODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G PROTEIN TECEP F1 2; 1.

G-protein coupled receptor; Transmem5rane; Glycoprotein; Sulfation.

DOMAIN

EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF075442; AAD19854.1; -. InterPro; IPR000276; GPCR_Rhodpsn.
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097878;
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Gaps

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Score 126; DB 1; Length 352; Pred. No. 1e-11; le-11; --- 0; Indels

100.0%; Score 126; Di ilarity 100.0%; Pred. No. 1e-: Conservative 0; Mismatches

Best Local Similarity Matches 22; Conserv

Query Match

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0; Gaps

0; Indels

100.0%; Score 126; DB 1; Length 352;

100.0%; Pred. No. 1e-11; ive 0; Mismatches (

Gaps

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Mismatches

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22; Conservative
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P56484;
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REDLINE=99416438; PubMed=10486970;

RA Zhang Y.-W., Zyder O.A., Zhang Y.-P.;

RA Dang Y.-W., Zyder O.A., Zhang Y.-P.;

RI Sequence evolution of the CCRS chemokine receptor gene in primates.";

RI Sequence evolution of the CCRS chemokine. Binds to MIP-1-alpha,

RI Sequence evolution at G.1145-1154(1999).

CC -1- FUNCTION: Receptor for a G-C type chemokine. Binds to MIP-1-alpha,

CC -1- FUNCTION: Receptor for a G-C type chemokine. Binds to MIP-1-alpha,

CC -1- FUNCTION: Receptor for a G-C type chemokine. Binds to MIP-1-alpha,

CC -1- FUNCTION: Intagral membrane protein.

CC -1- SUBCELULAR LOCATION: Integral membrane protein.

CC -1- SUBCELULAR LOCATION: Integral membrane protein.

CC -1- SUBLAILY: Belongs to family 1 of G-protein coupled receptors.

CC -1- SUBLAILY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FWBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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modified ...

or send an email to liv...

or send an email to liv...

REMBL: AF075443; AAD19855.1; -..

DR InterPro; PR000276; GPCR_Rhodpsn...

Pfam; PF00001; Trm.!; 1...

DR PROSITE; P800237; GPCRTHODDSN...

DR PROSITE; P800237; GPCRTHODDSN...

PROSITE; P800237; GPCRTHODDSN...

DR PROSITE; P800237; GPCRTHODDSN...

PROSITE; P800237; GPCRTHODDSN...

FT DOMAIN

FT TRANSMEM 31 58 1 (POTENTIAL).

FT TRANSMEM 69 89 2 (POTENTIAL).

FT TRANSMEM 103 124 3 (POTENTIAL).

FT TRANSMEM 1125 141 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 142 166 4 (POTENTIAL).

FT TRANSMEM 142 166 4 (POTENTIAL).

FT TRANSMEM 142 166 GPOTENTIAL).

FT TRANSMEM 142 166 GPOTENTIAL).

FT TRANSMEM 142 166 GPOTENTIAL).

TRANSMEM 142 166 GPOTENTIAL).

TRANSMEM 199 218 EXTRACELLUAR (POTENTIAL).

TOMAIN 199 218 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trachypithecus phayrei (Phayre's leaf monkey).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae, Colobinae;
Trachypithecus.
                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
38-PEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CRR-5) (CC-CRR-5) (CCRS).
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Pred. No. 1e-11;
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
SULFATION (BY SIMILARITY).
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SULFATION (BY SIMILARITY).
3 (PATION (BY SIMILARITY).
3 (14366F148D3A5938F CRC64).
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                          40509 MW;
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352 AA;
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Best Local Similarity
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its montyfit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Singoni A., Soto H., Hedrick J.A., Stoppacciaro A., Storlazzi C.T., Singaglia F., D'Ambrosio D., O'Garra A., Robinson D., Rocchi M., Santoni A., Zlotnik A., Napolitano M.;

"The chemokine receptor CCR8 is preferentially expressed in Th2 but not Th1 cells."; Th751(1998).

"Immunol. 161:347-551(1998).

"IFUNCTION: Receptor for the TCA-3 chemokine.

"SUBCELLUAR LOCATION: Integral membrane protein.

"SUBCELLUAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
C-C chemine receptor type 8 (C-C CKR-8) (CC-CKR-8)
CCR8 OR CMKBR8 OR TERL.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                      Zaballos A., Goya I.I., Gutierrez J., Varona R., Marquez G., Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
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R EMBL; 298205; CAB10895.1; --

R EMBL; 298205; CAB10895.1; --

R EMBL; AF001277; AAC97598.1; --

R GO; GO:0016493; F:C-C chemokine receptor activity; IDA.

GO; GO:0005515; F:protein binding; IPI.

GO; GO:0005635; P:chemotaxis; IDA.

GO; GO:0006935; P:chemotaxis; IDA.

R GO; GO:0006935; P:chemotaxis; IDA.

R DITCEPTO; IPR000276; GPGR_Rhodpsn.

R PRINTS; PR00137; GPCRRHODOPSN.

R PROSITE; PS00237; GPRCRHODOPSN.

R PROSITE; PS50262; GPROTEIN RECEP_F1_1; 1.

R G-PCOLEMIN COUPLED F1_2; 1.
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                      353 A.A.
                          93 QWDFGNTMCQLLTGLYFIGFFS 114
1 QWDFGNTMCQLLTGLYFIGFFS 22
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STRAIN=129/Sv;
MEDLINE=98334001; PubMed=9670926;
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SEQUENCE FROM N.A.
Zaballos A., Goya
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MEDLINE=20501139; PubMed=11046064;
Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDIATE=97150864; PubMed=8995400;
MEDIATE=97150864; PubMed=8995400;
MODIA L.-M., Myers S.J., Tsou C.-L., Gosling J., Arai H., Charo I.F.;
"Organization and differential expression of the human monocyte
chemoattractant procein I receptor gene. Bvidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
J. Biol. Chem. 272:1038-1045(1997).
                                                                                                                                                          Gaps.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94195821; PubMed=8146186; Canci C., Connolly A.J., Charo I.F., Myers S.J., Herman A., Franci C., Connolly A.J., Consollin S.R., Myers S.J., Herman A., Franci C., Connolly A.J., "Molecular cloning and functional expression of two monocyte chemoattractant protein I receptors reveals alternative splicing of the carboxyl-terminal tails.", Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756 (1994).
                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOO(3) (Rel. 42, Last annotation update)
C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR2)
(Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ozuna M., Kuldanek S.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
Mnan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J.,
Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
Watanabe M., Doggett N., Garcia D., Sagripanti J.L.,
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL). 31EC4B642CDB9AE5 CRC64;
                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-94324942; PubMed=8048929; Tamaka H., Endo N.; Yamagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.; "cDhA cloning and functional expression of a human monocyte chemoattractant protein 1 receptor."; Biochem. Biophys. Res. Commun. 202:1156-1162(1994).
                                                                                                                        70.6%; Score 89; DB 1; Length 353; 63.6%; Pred. No. 4e-06;
                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND VARIANTS ILE.64 AND GLU-355.
Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuld
Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBU databases.
EXTRACELLULAR (POTENTIAL)
               SIMILARITY.
                                                                                                                                                                                                                                                                                                                         374 AA.
                                                                                                                                           Pred. No. 4e-0
5; Mismatches
                  7 (POTENTIAL)
CYTOPLASMIC (
                                                                                                                                                                                                                     1 OWDFGNTMCQLLTGLYFIGFFS 22
                                                                                        353 AA; 40045 MW;
                                                                                                                                                              Conservative
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   278
302
353
181
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Homo sapiens (Human)
                                                                                                                                               Local Similarity
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P41597;
   DOMAIN
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SEQUENCE
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CKR2_HUMAN
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MIN; 601267; --

BY GO: 00005887; C:integral to plasma membrane; TAS.

GO: 00005887; C:integral to plasma membrane; TAS.

GO: 00004559; C:integral to plasma membrane; TAS.

BY GO: 00004559; C:chemoxina receptor activity; TAS.

GO: 00004569; P:chemoxina response (sensu Inver. . .; TAS.)

BY GO: 00005889; P:chemotaxis; TAS.

GO: 00007204; P:chemotaxis; TAS.

GO: 00007205; P:chemotaxis; TAS.

GO: 00007205; P:chemotaxis; TAS.

GO: 00007205; GPCR-Nodosn.

Franty: PRO0071; FR.

FRAM: PRO0071; GPROFIEIN RECEP F1 1; 1.

FRAM: PS00027; GPROFIEIN RECEP F1 1; 1.

FROSITE; PS00227; GPROFIEIN RECEP F1 2; 1.
                                                                                                                                                                                                                                                                                               This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outsation-the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Chakravarty L., Kolattukudy P.E.;
"Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that has tyrosine sulfation in a conserved extracellular N-terminal
                                                          region.";

J. Immunol. 165:5295-5303(2000).

-!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.

-!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.

Transduces a signal by increasing the intracellular calcium ions

Transduces a signal by increasing the intracellular calcium.

Invel. Alternative correceptor with CD4 for HIV-1 infection.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                 :- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymorphism; Alternative splicing; 3D-structure.
DOMAIN 1 42 EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
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                                                                                                                                                                                                                                                       sold=P41597-2; Sequence=VSP_001893;
                                                                                                                                                                                                                    Isold=P41597-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, U03882, AAA19119.1; -. EMBL, U03905, AAA19120.1; -. EMBL, D29984; BAA06253.1; -. EMBL, U80924; AAC51637.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U80924; AAC51636.1; -. U95626; AAB57791.1; -. U95626; AAB57792.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U95626; AAB57791.1; -.
EMBL; U95626; AAB57792.1; -.
EMBL; AF545480; AAN16400.1;
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PIR, JC2443; JC2443.
PDB; IKAD; 14-AUG-02.
PDB; IKPI; 23-JAN-02.
Genew; HGNC11603; CCR2.
MIM; 601267; -

    -! - PTM: N-glycosylated.

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                                                            SLFHIALGGRIAPLOKPVCGGPGVRPGKNVKVTTQGLLDGR
GKGKSIGRAPEASLQDKEGA -> RYLSVFFRKHITKRFCK
QCPVFYRETVDGVTSTNTPSTGEQEVSAGL (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K., deFiebre C.M., Pennell N.A., Streit W.J., Harrison J.K., "Chemokine receptor expression in cultured glia and rat experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  allergic enceptalomyelitis.";
J. Neuroimmunol. 86:1-12(1998).
-!- FUNCTION: Receptor for the MCP-1 (JB), MCP-3 (FIC) and MCP-5 chemokines. Transduces signal by increasing the intracellular calcium ions level (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Expressed in lung, spleen, kidney, thymus and
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 2 (C-C CKR-2) (CCR.2) (CCR2)
CCR2 OR CMKBR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encephalomyelitis (EAE) has been induced.
    . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                  Query Match 69.0%; Score 87; DB 1; Length 374; Best Local Similarity 66.7%; Pred. No. 8.4e-06; Matches 14; Conservative 3; Mismatches 4; Indels
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InterPro; IPR000276; GPCR_Rhodpsn.
PROMITS; PR00237; GPCRHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP_F11; 1.
PROSITE; PS00262; GPROTEIN_RECEP_F12; 1.
G-protein coupled receptor; Transmembrane.
1 60 PRINGEN POTENTIAL.
DOMAIN 1 60 POTENTIAL.
DOMAIN 82 91 CYTOPLASMIC (POTENTIAL).
                                                                                                                                        /FTIG=WSP 01893.
V -> I (in dbSNP:1799864).
/FTIG=VAR_014339.
                                                                                                                                                                                                         G -> E. __
/FTId=VAR_014340.
F865E0D39E74CF0F_CRC64;
    (GLCNAC.
                       SULFATION.
BY SIMILARITY
                                                                                                                           isoform B)
                                                                                                                                                                                                                                                                                                                                                                                             1 OWDFGNTMCOLLTGLYFIGFF 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley;
MEDLINE-98318173; PubMed-9655467;
                                                                                                                                                                                                                                                374 AA; 41914 MW;
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    14
26
190
374
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                   MOD RES
DISULFID
VARSPLIC
  CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (MIP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=Wistar; TISSUB=Brain;
MEDLINE=98334064; PubMed=9670989;
Spleiss O., Gournala N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,
Berger M., Gebicke-Haerter P.J.;
"Clohing of rat HIV-1-chemCkine coreceptor CKR5 from microglia and
upregulation of its mRNA in ischemic and endotoxinemic rat brain.";
J. Neurosci. Res. 53:16-28(1998).
                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                      Length 373;
                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                      CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELLULAR (POTENTIAL).
                 EXTRACELLULAR (POTENTIAL)
                                                                           POTENTIAL.
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
                                                                                                                                                                                                                                            BY SIMILARITY.
2E7BB012F5D6FD09 CRC64;
                                      POTENTIAL. (POTENTIAL).
                                                                                                                                                                                                  POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                  68.3%; Score 86; DB 1; L
66.7%; Pred. No. 1.2e-05;
ative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 AA.
                                                                                                                                                                                                                                                                                                                                                                                                            1 QWDFGNTMCQLLTGLYFIGFF 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                 42763 MW;
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                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                               373 AA;
                                                                                                                                                                                                                                                                                                                       Local Similarity
es 14; Conserv
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92
113
1129
1120
1171
1192
221
221
227
302
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TRANSMEM
DOMAIN
TRANSMEM
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008556;
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CELA192CCAB999A3 CRC64;

31509 MW;

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Query Match
Best Local Similarity
269 AA;
                                                                                                                                                                                                                                  Suipoxvirus.
NCBI_TaxID=10277;
                                                                                                                                   VK02_SPVKA
Q08520;
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TRANSMEM
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CARBOHYD
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                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                Swinepox virus (strain Kasza) (SPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Virology 197:511-528(1993).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Massung R.F., Jayarama V., Moyer R.W.; "DAA sequence analysis of conserved and unique regions of swiner virus: identification of genetic elements supporting phenotypic observations including a novel G protein-coupled receptor
                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (POTENTIAL) 77EDB368AA4C868D CRC64;
                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                        66.7%; Score 84; DB 1; Length 354,
           PRINTS; PRO0237; GPCZRHODOPSN.
PROSITE; PS00237; GPCZRHODOPSN.
PROSITE; PS00207; G PROTEIN RECEP_F1_5; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_5; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN

EXTRACELLULAR (POTENTIAL).
                                                                                                              CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
                                                                 1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                             EXTRACELLULAR (POTENTIAL)
                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                  2.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
0-protein coupled receptor homolog C3.
                                                                                                                                                                                                                                                                                                                                                                            269 AA.
                                                                                                                                                                                                                                                                   Pred. No. 2.36
4; Mismatches
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PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane.
                                                                                                                                                             CYTOPLASMIC () 6 (POTENTIAL)
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                                                                                                         (POTENTIAL)
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CYTOPLASMIC (
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InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                   1 QWDFGNTMCQLLTGLYFIGFF 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94069924; PubMed=8249275;
                                                                                                                                                                                                                                     41030 MW;
                                                                                                                                                                                                                                                                     61.9%;
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                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
   PF00001; 7tm 1; 1
                                                                                                                                        Pfam; PF00001; 7tm
                                                                                                                                                                                                                                       354 AA;
                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suipoxvirus.
NCBI_TaxID=10277;
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P32229;
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                                                                                                                                                                                                                                                                              Matches
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                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Swinepox virus (strain Kasza) (SPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virology 197:511-528(1993).
-- FUNCTION: Putative chemokine receptor.
-- SUBCELLULAR LOCATION: Integral membrane protein.
-- SUBCELLULAR LOCATION: Integral membrane protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE=94069924; PubMed=8249275; Massung R.F., Jayarama V., Moyer R.W.; Massung R.F., Jayarama V., Moyer R.W.; Moyer B.W.; Moyer Conservations of Swinesty and Unique Appendix Applications including a novel G protein-coupled receptor
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
76D08613277B0CC0 CRC64;
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                       Score 83; DB 1; Length 269;
Pred. No. 2.4e-05;
7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, L21931; AAC37873.1; -.
InterPro; 1PR00276; GPCR_Rhodpen.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHNDOPSN.
PROSITE; PS00237; GPCRTEIN RECEP F1 1; 1.
PROSITE; PS00262; G_ROTEIN TRANSMEMBYANE; Glycoprotein.
G-protein coupled receptor; Transmembrane; Glycoprotein.
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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54.5%; Pred. No. 3.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
G-protein coupled receptor homolog K2.
                                                                                  7; Mismatches
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                                                                                                                                         1 QWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                       20 QWIFGNILCKIMSVLYYVGFFS 41
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                                65.9%;
54.5%;
Query Match

Query Match

Best Local Similarity 54....

Best Local 12; Conservative
                                                                                                                                                                                                                                                                                                                                     STANDARD;
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370 AA;
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(Human)
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MEDLINE=97026720; PubMed=8872898;
MEDLINE=97026720; PubMed=8872898;
MEDLINE=97026720; PubMed=8872898;
Meesen M., Tanabab S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,
Post T.W., Gerard C., Dorf M.E.;
"Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse
IT ranscriptase-polymerase chain reaction does not detect mRNA for the
IT canscriptase-polymerase chain reaction does not detect mRNA for the
IT Con new MCP-1 receptor.";
J. Neurosci. Res. 45:382-391(1996).

J. Neurosci. Res. 45:382-391(1996).

J. Neurosci. Res. 45:382-391(1996).

J. Neurosci. Res. 45:382-391(1996).

J. SEMITON: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5

Calcium ions level.

J. SEMILARITY: Detected in monocyte/macrophage cell lines,
but not in nonhematopoietic cell lines.

J. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=96205938; PubMed=8631787;
MEDLINE=96205938; PubMed=8631787;
Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L.,
Charo I.F.,
"Molecular cloning and functional expression of murine JE (monocyte chemoatractant protein 1) and murine macrophage inflammatory protein lalpha receptors: evidence for two closely linked C-C chemokine receptors on chromosome 9.";
J. Blol. Chem. 271:7551-7558(1996).
       Gaps
                                                                                                                                                                                                      CKR2_MOUSE STANDARD, PRT, 373 AA.

91-0GT-1996 (Rel. 34, Created)
01-0GT-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
CC chemoxine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2)
CJF/FIC receptor) (MCP-1 receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) MCT:10618; CCT2.
GO:0016493; F:C-C chemokine receptor activity; IDA.
GO:0016493; F:C-C chemokine binding; IPI.
GO:001606; P:CPIDULAL defense response (sensu Vertebrata); IMP.
GO:0030097; P:hemopolesis; IMP.
GO:0006959; P:humoral immune response; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kurihara T., Bravo R.;
Cloning and functional expression of mCCR2, a murine receptor for
the C-C chemokines JB and FIC.";
J. Biol. Chem. 271:11603-11606(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
    ;
0
       Indels
    ж
Э
  Mismatches
                                                                         121 QWIFGNILCKIMSVLYYVGFFS 142
                                              1 QWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=BALB/c;
MEDLINE=96216064; PubMed=8662823;
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EMBL; U51717; AAC52557.1; -.
EMBL; U56819; AAC52784.1; -.
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
12;
                                                                                                                                                                                     MOUSE
Matches
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(GPR-CY6)
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J. Immunol. 160:1975-1981(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CCR-8) (G
(CMKBRL2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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Tiffany H.L., Lautens L.L., Gao J.-L., Pease J., Locati M., Combadiere C., Modi W., Bonner T.I., Murphy P.M.;
"Identification of CCR8: a human monocyte and thymus receptor: CC chemokine I-309.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=97040707; PubMed=8886020;
Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 373;
                                                                                                                                                                                                                    1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                        PERINTS; PRO0237; GFCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS02625; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane.
1 55
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y -> H (IN REF. 1).
A -> G (IN REF. 1).
V -> G (IN REF. 1).
FA012C10F4C9325A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1936 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 8 (C-C CKR-8) (GRC-CKR-8)
(GPRCYG) (Chemokine receptor-like 1) (CKR-L1) (TER1)
C-CR8 OR CMXBR8 OR CKRL1.
GO; GO:0006954; P:inflammatory response; IMP.
GO; GO:0013314; P:regulation of cell migration; IMP.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.9%; Score 83; DB 1; I
61.9%; Pred. No. 3.4e-05;
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MEDLINE-98129363; PubMed=9469461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21
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Best Local Similarity
These 13; Conserve
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receptors.";
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 25
CKR8_MACMU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration the between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@lsb-sib.ch).
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GO; GO:0004950; F:chemokine receptor activity; TAS.
GO; GO:0004950; F:chemokine receptor activity; TAS.
GO; GO:00155; P:cell adhesion; TAS.
GO; GO:0006935; P:cell adhesion; TAS.
GO; GO:0006935; P:chemoctaxis; TAS.
GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.
InterPro; IPR004068; CC & receptor.
InterPro; IPR004068; CC & receptor.
InterPro; IPR000276; GPGR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification of the CC chemokines TARC and macrophage inflammatory protein-1 beta as novel functional ligands for the CCR8 receptor.";

Fur. J. Immunol. 28:58-588(1998).

-!- FUNCTION: Receptor for the chemokines SCYA1/I-309, SCYA4/MIP-1-beta and SCYA1/TARC. May regulate monocyte chemotaxis and thymic cell line apoptosis. Alternative coreceptor with CD4 for HIV-1
                                                                                SEQUENCE FROM N.A.
MEDLINE=97131825; PubMed=8977299;
MEDLINE=97131825; PubMed=8977299;
Bamson M., Stordeur P., Labbe O., Soularue P., Vassart G.,
Parmentier M.;
"Molecular cloning and chromosomal mapping of a novel human gene,
"Molecular cloning and chromosomal mapping of a novel human gene,
"Molecular cloning and chromosomal mapping of a novel human gene,
chomR1, expressed in T lymphorytes and polymorphonuclear cells and
encoding a puterive chemokine receptor.";
Eur. J. Immunol. 26:3021-3028(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
      "Molecular cloning and RNA expression of two new human chemokine
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InterPro; IFR...

R PEAM; PROMOO1; 7tm_1; 1.

R PEAM; PROMOO1; 7tm_1; 1.

DR PROSTTS; PRO1530; GHENCHONDEN.

DR PROSTTS; PSO1237; G_ROTEIN_RECEP_F1_1; 1.

DR PROSTTE; PSO262; G_ROTEIN_RECEP_F1_2; 1.

DR PROSTTE; PSO262; G_ROTEIN_RECEP_F1_2; 1.

TO PROSTTE; PSO262; G_ROTEIN_RECEP_F1_2; 1.

TO PROSTTE; PSO262; G_ROTEIN_RECEP_F1_2; 1.

TO G_TOPIC TABLE CONTINENTIAL OF THE CON
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Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
Napolitano M.;
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Nakajima T., Yoshida R., Harada S.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                receptor-like genes.";
Biochem. Biophys. Res. Commun. 227:846-853(1996)
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98180363; PubMed=9521068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EWBL, 162556, AAB05542.1; --
EWBL, 179782, CAB02142.1; --
EWBL, Y08456, CAA69712.1; --
EWBL, D49919, BAA23377.1; --
EMBL, AF005210, AAB62547.1; --
EMBL, AC5067, JC5067, GCR8.
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-!- FUNCTION: Receptor for the chemokines SCYA1/I-309, SCYA4/MID-1-beta and SCYA1/TARC. May regulate monocyte chemotaxis and thymic call line apoptosis (By similarity).

-!- SUBCELLUIAR LOCATION: Integral membrane protein.

-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Spleen; MEDLINE-21354176; PubMed=11461684; MEDLINE-21354176; PubMed=11461684; Margulies B.J., Hauer D.A., Clements J.E.; Margulies B.J., Hauer comparison of eleven rhesus macaque chemokine "Identification and comparison of eleven rhesus
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 8 (C-C CKR-8) (CCR-8)
                                                                                                                                                                                                                       Length 355;
                                                                                EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                        C SIMILARITY.
BC14A153CF695361 CRC64;
                                       CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                  Score 82; DB 1; 1
Pred. No. 4.5e-05;
6; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              356 AA.
                         5 (POTENTIAL)
CYTOPLASMIC (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AF100205; AAC72403.1; -.
INTEPPC, IPR004068; CC 8 receptor.
INTERPRO, IPR000276; GPCR Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                   98 QWVFGTVMCKVVSGFYYIGFYS 119
                                                                                                                                                                                                                                                                                                            1 QWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macaca mulatta (Rhesus macaque).
                                                                                                                                                                               40844 MW;
                                                                                                                                                                                                                    Match 65.1%;
Local Similarity 54.5%;
les 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                               355 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9544;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptors.",
AIDS Res. Hum. Retroviruses 17:981-986(2001).
-!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
Transduces a signal by increasing the intracellular calcium ions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCCR-2) (CCCR-2) (CCR-2) (CCR-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=A;
IsoId=018793-2; Sequence=Not described;
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF013958; AAD11572.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINYS; PR00237; GFCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G-PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=21354176; PubMed=11461684;
Margulies B.J., Hauer D.A., Clements J.E.;
"Identification and comparison of eleven rhesus macaque chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                          Length 356;
  S (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                       1979628DEE44845B CRC64;
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                   Score 82; DB 1; I
Pred. No. 4.6e-05;
5; Mismatches 4;
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IsoId=O18793-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                             1 OWDFGNTMCQLLTGLYFIGFFS 22
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                                                                                                                                                                       41210 MW;
                                                                                                                                                                                                                   65.1%;
54.5%;
                                                                                                                                                                                                                                         Local Similarity 54.5
les 12; Conservative
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     223
233
264
281
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1856
1856
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70
100
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356 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=9544;
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Matches
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"Molecular cloning and functional expression of murine JE (monocyte chemcattractant protein 1) and murine macrophage inflammatory protein lalpha receptors: evidence for two closely linked C-C chemckine receptors on chromosome 9.1;
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                       CRRS MOUSE STANDARD, PRT, 354 AA.
PS1662; 035313; 035891; P97308; P97405; Q61867;
01-0CT-1996 (Rel. 34, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (MIP-1 CCR5 OR CMKBRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Makaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6, and NIH Swiss; TISSUE=Kidney, Liver, and Spleen; MEDLINE=98001387; PubMed=934322; Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.; "Polymorphisms in the CORS genes of African green monkeys and mice implicate specific amino acids in infections by simian and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Power C.A.;
                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDIANE=962781/6 X CBA; TISSUB=Thymus;
MEDIANE=96278910: PubMede8662890;
Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power
Cloning and characterization of a novel murine macrophage
inflammatory protein-1 alpha receptor.";
J. Biol. Chem. 271:14445-14451(1996).
                                                                                                                                                                                                  Length 360;
                                                   S (POTENTIAL).
CYTOPLASNIC (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASNIC (POTENTIAL).
CYTOPLASNIC (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kuziel W.A., Beck M.A., Dawson T.C., Maeda N., Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                           4 (POTENTIAL). EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                      4B2552BCE913FE9F CRC64;
               (POTENTIAL)
                                                                                                                                                                                           Score 81; DB 1; I
Pred. No. 6.5e-05;
                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptors on chromosome 9."; J. Biol. Chem. 271:7551-7558(1996).
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STRAIN-129/SvJ; TISSUE-Spleen;
MEDLINE-96205938; PubMed-8631787;
                                                                                                                                                                                                                                                                1 OWDFGNTMCQLLTGLYFIGF 20
                                                                                                                                                                        41139 MW;
                                                                                                                                                                                                            65.0%;
                                                                                                                                                                                               64.3%;
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J. Virol. 71:8642-8656(1997)
                                                                                                                                                                                                                        13; Conservative
  1136
1153
1153
1153
1156
1156
1156
                                                                                                                                                                      360 AA;
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126
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                                                                                                                                                                                                                                                      MEDLINE-97404635; PubMed-9261347;
Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,
Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;
"Two distinct CCR5 domains can mediate coreceptor usage by human
j. Wirol. 71:6305-6314(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD, MGI:107182; Ccr5.
GO: 60:0016493; F:C-C chemokine receptor activity; IDA.
GO: GO:0006952; P:defense response; IMP.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
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CYTOPLASMIC (POTENTIAL).
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EMBL; AP019772; AAB71183.1; -...
EMBL; D83648; BAA12024.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U47036; AAC52454.1; -.
EMBL; X94151; CAA63867.1; -.
EMBL; U6865; AAB3727.1; -.
EMBL; U83327; AAC53386.1; -.
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                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINES99049845; PubMed=9834099; MEDLINES99049845; PubMed=9834099; MEDLINES99049845; PubMed=9834099; MEDLINES99049845; PubMed=9834099; J. Y., Collins P.D., Post T.W., Jose P.J., Williams T.J., Gerard C.J., Ponath P.D.; "Cloning and characterization of the guinea pig ecsinophil ectaxin acceptor. Cc Chemokine receptor.3: blockade using a monoclonal anticody in vivo "; Jummunol. 161:6139-6147(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -I. FUNCTION: Receptor for a C-C type chemokine. Binds to ectaxin, MCP-3, MCP-4 and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level (By similarity).
-I. SUBCELLULAR LOCATION: Integral membrane protein.
-I. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                 CKR3 CAVPO STANDARD; PRT; 358 AA.
092213;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)
                                                                                                                                                                                                                                                                                                                                                                          Cavia porcellus (Guinea pig).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
                                                                                                           .
0
                                                                           63.5%; Score 80; DB 1; Length 354; 57.1%; Pred. No. 9.1e-05;
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INTERPO. AF060698; AAC80428.1; -.
INTERPO. PRO00276; GPCR_Rhodpsn.
PRINTS; PRO0237; GFRATEDOPEN.
PROSITE; PSO0237; G PROTEIN RECEP F1 1; 1.
PROSITE; PSO0262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane.
43 EXTRACELLULAR (POTENTIAL).
145 N -> I (IN REF. 5).
190 H -> Y (IN REF. 3).
208 P -> S (IN REF. 1).
40863 MW, B4A6B942E88F9CF0 CRC64;
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EXTRACELLULAR (POTENTIAL)
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                                                                                                             5; Mismatches
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                                                                                                                                         1 OWDFGNTMCQLLTGLYFIGFF 21
                                                                                                             12; Conservative
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 145
190
208
354 AA;
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                                                                                                                                                                                                                                                                                                                                                              CCR3 OR CMKBR3.
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CKR3 CAVPO
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SUBCELLULAR LOCATION: Integral membrane protein
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WEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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Hopkins R.F., Jordan H., Moorer T., Max S.I., Wang J., Haieh F.,

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Batchench C., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Asha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., Nofernan K.J., Marason R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,

Nilalon D.K., Muxry D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Yallalon D.K., Muxry D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rachey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.M., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A., Schein J.E., Jones S.J.W., Marra M.A.,

Rodriguez A., Schein J.E., Jones S.J.W., Marra M.A.,

Rodriguez A. S., Grimwood S.I., Schmutz J., Myers R.M.,

Rodriguez A. S., Grimmood S.I., Schmutz J., Myers R.M.,

Rodriguez A., Schein J.E., Jones S.J.W., Marra M.A.,

Rodriguez A. S., Grimwood S.I., Sanstoner S., Sunchra M.A.,

Rodriguez A. S., Grimwood S.I., Sanstoner S., Sunchra M.A.,

Rodriguez A. Schein J.E., Jones S.J.W., Marra M.A.,

Rodriguez A. S., Grimwood S.I., Sanstoner S., Sunchra M.A.,

Rodriguez A. S., Sunchra S. S.I. Sanstoner S., Sanchra M.A.,

Rodriguez A. S., Sunchra S. S.I. Sanstoner S., Sanstoner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gao J.-L., Murphy P.M.;
"Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.";
J. Biol. Chem. 270:17494-17501(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular characterization of two murine eosinophil beta chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=129/Sv; TISSUE=Peritoneal macrophage;
MFDLINE=96072806; PubMed=7594543;
Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
Gerard C.;
                                                                                                                 ö
                                                           Length 358;
                                                                            0.00013;
ches 3; Indels
358 AA; 41623 MW; 7B73FAB7A3BC3670 CRC64;
                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                        355 AA.
                                                   62.7%; Score 79; DB
50.0%; Pred. No. 0.00
iive 8; Mismatches
                                                                                                                                                                                              102 KWVFGHFMCKIISGLYYVGLFS 123
                                                                                                                                                         1 OWDFGNTMCOLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=129/SvJ;
MEDLINE=95340546; PubMed=7542241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptors.";
J. Immunol. 155:5299-5305(1995).
[2]
                                             Ouery Match
Best Local Similarity 50.0°
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCR1 OR CMKBR1.
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SEQUENCE
                                                                                                                                                                                                                                                                                               RESULT 29
CKR1_MOUSE
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Bukaryota, Metazoa; Chordata; Cramiata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCSI_Taxil=10116;
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-1- TISSUE SPECIFICITY: Detected in the heart, spleen, lung, peritoneal exudate cells and leukocytes.
-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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054814; 055169;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)
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REMEL; U29604; AAA86119.1; -.

REMEL; U29604; AAA811092.1; -.

REMEL; BC011092; AAH11092.1; -.

REMEL; BC011092; AAH11092.1; -.

REMEL; BC010059; AGH11092.1; -.

RGO; GO:001515; F:C-C chemokine receptor activity; IDA.

GO; GO:001515; F:prote cin binding; IPI.

RGO; GO:001515; F:prote cin binding; IPI.

RGO; GO:001515; F:prote cin binding; IPI.

RGO; GO:001959; P:myeloid blood cell differentiation; IMP.

RGO; GO:00101; 7tm 1; 1.

RPININI: PRO0277; GPCRHODOSN.

RPININI: PRO0277; GPCRHODOSN.

RPROSITE; PS00227; GPROTEIN_RECEP_F1 1; 1.

RROSITE; PS00227; GPROTEIN_RECEP_F1 2; 1.

ROSITE; PS00227; GPROTEIN_RECEP_F1 2; 1.

REMENTAL
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CYTOPLASMIC (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
3 (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
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40901 MW;
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Matches
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TID CKR3

AC 0548

DT 30-M

DT 30-M

DT 10-C

DE C-C

CKR

GN CKR

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                                                             Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K., Defiebre C.M., Pennell N.A., Streit W.J., Harrison J.K., "Chemokine receptor expression in cultured glia and rat experimental allergic encephalomyelitis.";
J. Neuroimmunol. 86:1-12(1998).
                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=Wistar; TISSIB=Spleen;
STRAIN=Wistar; TISSIB=Spleen;
Harrington P.M., Wewton D.J., Coleman J.W., Flanagan B.F.;
Harrington P.M., Mewton D.J., Coleman J.W., Flanagan B.F.;
Submitted (JAN-1998) to the EMEL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to ectaxin,
MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Expressed in spleen but not in astrocytes or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-00T-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor 1-like protein 1 (Macrophage inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .,
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880F682984F501DA CRC64;
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45.5%; Pred. No. 0.00052;
             SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
STRAIN=Wistar; TISSUE-Spleen;
MEDLINE-98318173; PubMed=9655467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 356 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF003954; AAC03337.1; --
EMBL; Y13400; CAA73830.1; --
INTELPRO, IPR000276; GPCR_Rhodpsn.
PEfam; PF00001; Tem 1; 1.
PRINTS; PR00237; GPCREHODOPSN.
PROSITE; PS00237; GPCREHODOPSN.
PROSITE; PS50237; GPCREHORIN RECEP_F1 1; 1.
G-protein coupled receptor; Transmembrane.
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102 EWGFGHCMCKMLSGLYYLALYS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41643 MW;
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Best Local Similarity 45.5
Matches 10; Conservative
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359 AA;
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P51676;
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TRANSMEM
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TRANSMEM
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                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
15-MR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor type 1 (C-C CKR-1) (CC-CKR-1) (CCR-1) (MP-1alpha-R)
(Macrophage inflammatory protein-1 alpha receptor) (MIP-lalpha-R)
                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.7%; Score 74; DB 1; Length 356; 47.6%; Pred. No. 0.00073; rive 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
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EXTRACELIULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0237; GFCRHODOPSN.
PROSITE; PSO0237; G PROTBIN RECEP F1 1; 1.
PROSITE; PSE0262; G PROTBIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                          PIR; 149340; 149340.
MGD; MG1:104617; CCr111.
InterPro; IPR000276; GFCR-Rhodpsn.
Pfam; PP00001; 7tm 1, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 WIFGNAMCKFVSGFYYLGLYS 120
                                                                                                         STRAIN=129/SvJ;
MEDLINE=95340546; PubMed=7542241;
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protein-1 alpha receptor-like 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40934 MW;
                                                                                                                                                                                                                                                                                                                                                                             EMBL; U28405; AAA89154.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                          Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        356 AA;
                                                                                          SEQUENCE FROM N.A.
             CCRILI OR CMKBRILI
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                                                                   NCBI_TaxID=10090;
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P32246;
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TRANSMEM
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W. MEDLINE=94095629; PubMed=7505609;

W. MEDLINE=94095629; PubMed=7505609;

W. MEDLINE=94095629; PubMed=7505609;

W. Nolecular Cloning of CDNAs encoding a LD78 receptor and putative

T "Molecular cloning of CDNAs encoding a LD78 receptor and putative

T "Molecular cloning of CDNAs encoding a LD78 receptor and putative

W. Molecular cloning of CDNAs encoding a LD78 receptor and putative

W. Molecular cloning of CDNAs encoding a LD78 receptor and putative

W. Molecular cloning of CDNAs encoding a LD78 receptor and putative

MIP-1 delta, RANTES, and MCP-3 and, less efficiently, to MIP-1-

MIP-1 delta, RANTES, and MCP-3 and, less efficiently, to MIP-1-

Deta or, MCP-1 and subsequently transduces a signal by increasing the intracellular calcium ions level. Responsible for affecting stem cell proliferation.

C -- SUBCELLULAR LOCATION: Integral membrane protein.

C -- TISCE ESPECIFICITY: Widely expressed in different hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=93240122; PubMed=7683036;

Gao J.-L., Kuhns D., Tiffany H.L., McDermott D., Li X., Francke U.,

Murphy P.M.,

"Structure and functional expression of the human macrophage
inflammatory protein 1 alpha/RANTES receptor.";

J. Exp. Med. 177:1421-1427(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors
                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                             SEQUENCE FROM N.A.
MEDLINE=93161416; PubMed=7679328;
Neote K., Digregorio D., Mak J.Y., Horuk R., Schall T.J.;
"Molecular cloning, functional expression, and signaling characteristics of a C-C chemokine receptor.";
Cell 72:415-425(1993).
(RANTES-R) (HM145) (LD78 receptor) CCR1 OR CMKBR1 OR CMKR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L09220; AAAS8408.1; -.
EMBL; L10918; AAA36543.1; -.
EMBL; D10925; BAA01723.1; -.
PIR; A45177; A45177.
Genew; HGNC:1602; CCR1.
                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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TRANSMEM 65 91 2 (POTENTIAL). DOMAIN 106 129 3 (POTENTIAL). DOMAIN 108 129 3 (POTENTIAL). TRANSMEM 107 12 197 EXTRACELLULAR (POTENTIAL). TRANSMEM 147 171 4 (POTENTIAL). TRANSMEM 198 223 (POTENTIAL). TRANSMEM 240 25 197 EXTRACELLULAR (POTENTIAL). TRANSMEM 240 25 197 EXTRACELLULAR (POTENTIAL). TRANSMEM 240 264 6 (POTENTIAL). TRANSMEM 265 281 EXTRACELLULAR (POTENTIAL). TRANSMEM 265 281 TRANSMEM (POTENTIAL). TRANSMEM 265 281 EXTRACELLULAR (POTENTIAL). TRANSMEM 265 281 EXTRACELLULAR (POTENTIAL). TRANSMEM 306 355 CYTOPLASMIC (BOTENTIAL). CARROHAN 306 355 CYTOPLASMIC (BOTENTIAL). DISULIED 106 183 BY SIMILARITY. SEQUENCE 355 AA, 41172 MM, B2C100FFED275985 CRC64;	Query Match Best Local Similarity 47.6%; Pred. No. 0.0021; Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;	2 WDFGNTWCQLLTGLYFIGFFS 22 :: : : :	CKRI_MACMU CCC Chemokine receptor type 1 (C-C CKRI_L) (CCCRI_L) CCC Chemokine receptor type 1 (C-C CKRI_L) CCC Chemokine receptor type 1 (C-C CKRI_L) CCC CONTINE DELIBERATOR PRIMATE CRITERIAL CONTINE THE TAIL CRITERIAL CONTINE THE TAIL CRITERIAL CRITERIAL CONTINE THE TAIL CRITERIAL CRITERIA CRITERIAL CRITERIAL CRITERIAL CRITERIAL CRITERIA
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EMBL, U29677; AAA86118.1; -. EMBL; U28406; AAA89155.1; -. MGD; MGI:104616; CCr3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR-3) (Macrophage inflammatory protein-1 alpha receptor-like 2) (MIP-1 alpha RL2).
CCR3 OR CMKBR3 OR CMKBR1L2.
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95340546; PubMed=7542241;
Gao J.-L., Murphy P.M.;
"Cloning and differential tissue-specific expression of three mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular characterization of two murine eosinophil beta chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amounts in Leukocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                         Length 355;
                                                                                                                                                                                                                                                          Score 71; DB 1; Length 355
Pred. No. 0.0021;
Fred. No. 5; Indels
                                                                  6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                      BY SIMILARITY.
41CAEA7CC19D23D4 CRC64;
            EXTRACELLULAR (POTENTIAL)
                                   3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                          41198 MW;
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Best Local Similarity 47.6%;
Matches 10; Conservative
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 91
107
1129
1171
1197
2223
233
264
281
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306
5
106
355 AA;
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P51678;
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TISSUE=Monocytes;
MEDLINE=95348056; PubMed=7622448;
Combadiere C., Ahuja S.K., Murphy P.M.;
"Cloning and functional expression of a human eosinophil CC chemokine
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CKR3 HUMAN STANDARD; Q9ULY8;

D1677-1996 (Rel. 34, Created outlete)

15-MAR-2004 (Rel. 34, Last sequence update)

C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CC-CKR3)

(CKR3) (EOSINOPhil ectaxin receptor).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo
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GO; GO:0016493; F:C-C chemokine receptor activity; IDA. GO; GO:005515; F:protein binding; IPI.
GO; GO:006935; P:chemocaxis; IDA.
InterPro; IRR00027; GPCR_Rhodpsn.
PRINITS; PR00237; GPCR_RHODPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1_1; I.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; I.
G-protein coupled receptor; Transmembrane.
                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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AC11ED66E283CEAF CRC64;
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CYTOPLASMIC (POTENTIAL).
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Pred. No. 0.003;
                                                                                                                                                                                                                                                                                                              (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
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Local Similarity 40.9%;
les 9; Conservative
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276 S
41043 MW;
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Best Local Similarity 52.4%;
Matches 11; Conservative
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355 AA;
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REAL SETABLE SEASON ST. PubMed=1247932;

REAL SETABLE SEASON ST. PubMed=1247932;

REAL SETABLE R.D., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang L.,

RA Bornstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Parage C.,

RA Raha S.S., Loquallano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gab L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gab L.J., Hulyk S.W.,

RA Nilalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A.,

RA Phey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Niting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Richards S., Worley W. Schwurz J., Myers R.M.,

RA Blakesley R.W., Touchman J.W., Scheutz J., Myers R.M.,

RA Schriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Schriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra D., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra D., Shegequently

R. Proc. Natl. Acad. Sci. U.S.A., 99:1689-16903 (2002).

-!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,

c. -- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,

c. -- FUNCTION: Receptor for a C-C type chemokine.

eotaxin.-3, MCP-3, MCP-4, RANTES and MIP-1 delta. Subsequently

transduces a signal by increasing the intracellular Subsequently

c. -- FUNCTION: Receptor for a C-C type chemokine.

--- SUBELLULAR LOCATION: Integral membrane protein.

--- TISSUE SPECIFICITY: In eosinophils as well as trace amounts in

neutrophils and monocytes.

--- SIMILAR STREE SPECIFICITY: In eosinophile as well as trace amounts in

--- SIMILAR STREE SPECIFICATION To C. STREET STREET STREET STREET STREET STREET STREET
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                                                           MEDLINE=96281895; PubMed=8676064; Pont D., Gerard N.P., Pont T.W., Wang J., Wu L., Gerard N.P., Pont T.W., Wang J., Wu L., Gerard N.P., Nackay C.R.; Modecular cloning and characterization of a human ectaxin receptor expressed selectively on eosinophils."; Exp. Med. 183:2737-2748(1996).

SEQUENCE FROM N.A. Xiao L., Weiss S., Qari S., Rudolph D., Hodge T., Lal R.; Xiao L., Weiss S., Qari S., Rudolph D., Hodge T., Lal R.; Startial resistance to infection by syncytium-inducing primary HIV-1 in exposed uninfected individuals homozygous for CCR5 32bp deletion."; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLITE=22074933; PubMed=12079287;
With S., Dayhoff D.E., Wang C.E., Imam Z., Ehrenberg P.K.,
Michael N.L.;
"Transcription regulation of human chemokine receptor CCR3: evidence
for a rare TATA-less promoter structure conserved between Drosophila
and humans.";
                                                                                                                                                                                                                                                        [6]
SEQUENCE FROM N.A., AND VARIANT SER-218.
MEDLINE=21040311; PubMed=11196669;
Kato H., Tsuchlya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki Hirai K., Tokunaga K.;
"New variations of human CC-chemokine receptors CCR3 and CCR4.";
Genes Immun. 1:97-104(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kopatz S.A., Aronstam R.S., Sharma S.V.; arons clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdma.org)."; Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
eotaxin receptor.";
J. Exp. Med. 183:2349-2354(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomics 80:86-95(2002).
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                                               SEQUENCE FROM N.A.
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C -> S (polymorphism found in about
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Pred. No. 0.0083;
4; Mismatches 6; Indels
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CYTOPLASMIC (POTENTIAL).

4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
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S -> T (IN REF. 4 AND 5).
E95DCD7A6C643874 CRC64;
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15-JUL-1998 (Rel. 36, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
C-X-C chemokine receptor type 6 (CXC-R6) (CXR-6)
receptor bonzo).
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CCR6 CERAB
TO CCR6 CE
TO CCR6 CE
DT 15-JUL
DT 15-JUL
DT 15-JUL
DE C-C CE
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2.7 5 - a

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              NCBI_TaxID=9606;
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                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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P51679; Q9ULK6; Q9ULX7;
01-OCT-1996 (Rel. 34, Last sequence update)
15-PAR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor type 4 (C-C CKR-4) (CCR-4) (CCR4)
                                                                                                                                           -i-FUNCTION: Receptor for the C-X-C chemokine CXCL16. Used as a coreceptor by SIVs and by strains of HIV-2 and m-tropic HIV-1.
-i-SUBCELLULAR LOCATION: Integral membrane protein.
-i-SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCR4 OR CMKBR4.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Cercopithecus aethiops (Green monkey) (Grivet).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
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                                                                           SEQUENCE FROM N.A.
MEDLINE=97373958; PubMed=9230441;
Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;
"Expression oloning of new receptors used by simian and human immunodeficiency viruses.";
Nature 388:296-300(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.4%; Score 66; DB 1; Length 342; 45.5%; Pred. No. 0.011;
                                                                                                                                                                                                                                                                          EMBL, AF007859; AAB6425.1; ...
InterPro, IPR00276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHODPSN.
PROSITE; PS00237; GPROTEIN RECEP_F1_1; 1.
PROSITE; PS00262; G_ROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                 Cercopithecinae; Cercopithecus.
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Best Local Similarity 45.5
Warrhes 10, Conservative
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342 AA;
                                                             NCBI_TaxID=9534;
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HUMAN
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FUNCTION, TISSUE SPECIFICITY, AND PHOSPHORYLATION.

RAY

MEDLINE=20219238; PubMed=10754297;

RA Imngjerdingen M., Damaj B., Maghazachi A.A.;

Inngjerdingen M., Damaj B., Maghazachi A.A.;

Innmunon K. Cells express CC chemokine receptors 4 and 8 and respond to require the express CC chemokine, macrophage-derived and 1-309 ";

Inmunon Infation-regulated chemokine, macrophage-derived themokine, and 1-309 ";

Inmunon Infation receptor for the C-C type chemokines

TARC/SCYA17 and MDC/SCYA22. The activity of this receptor is mediated by Gil proteins which activate a phosphatidylnositol-calcium second messenger system. Can function as a chemoatractant carried by Gil proteins which activate a phosphatidylnositol-calcium second messenger system. Can function as a chemoatractant carried by primary HIV-2 isolates. In the CNS, could mediate hippocampal-neuron survival.

C-I- SUBCELLULAR LOCATION: Integral membrane protein.

C-I- SUBCELLULAR LOCATION: Integral membrane protein.

C-I- TISSUE SPECIFICITY: Predominantly expressed in the thymus, in peripheral blood Leukocytes, including T cells, moselly the and basophils, and in platelets; at lower levels, in the spleen and basophils, and in platelets; at lower levels, in the spleen and basophils, and in platelets; at lower levels, including memory T cells, moselly the ones expressing the cutaneous lymphocyte antigen (CLA). Expressed in brain microvascular and coronary artery endothelial cells.

C-I- PTM. IN NATURAL KILLER CELLS, SCYA22 BINDING INDUCES

PHOSSHORYLAIDNO NY YET UNDEFINED SER/THR RESIDUES, MOST PROBABLY BY BY ADRENBERGIC RECEPTOR KINASES I AND 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99104168; PubWed=9430724; MEDLINE=99104168; PubWed=9430724; Mood C.L., Nishimura M., Godiska R., Yoshie O., Gray P.W.; Macrophage-derived chemokine is a functional ligand for the CC
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21040311; PubMed-11196669; Kabonene H., Nakajima T., Kawasaki H., Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H., Hirai K., Tokunaga K.; Indunaga K.; Indunasa K.; Indunasa K.; Indunasa K.; Indunasa K.; Indunasa C. Chemokine receptors CCR3 and CCR4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-99394604; PubMed=10466728; Campbell J.J., Qin S., Fonath P., Campbell J.J., Haraldsen G., Pan J., Rottman J., Qin S., Fonath P., Andrew D.P., Warnke R., Ruffing N., Kassam N., Wu L., Butcher E.C.; "The chemokine receptor CCR4 in vascular recognition by cutaneous but not intestinal memory T cells.";
MEDLINE-95370289; PubMed=7642634;

MEDLINE-95370289; PubMed=7642634;

Proudfoot A.E.I., Wells T.N.C.;

"Molecular cloning and functional expression of a novel CC chemokine receptor CDNA from a human basophilic cell line.";

J. Biol. Chem. 270:19495-19500(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97313486; PubMed-9169480; Imai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yoshie O.; Imai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yoshie O.; The T cell-directed CC chemokine TRC is a highly specific biological ligand for CC chemokine receptor 4."; J. Biol. Chem. 272:15036-15042(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kopatz S.A., Aronstam R.S., Sharma S.V.; "Copatz S.A., Aronstan B.S., Sharma S.V.; "cNR clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org)."; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND VARIANTS VAL-130 AND SER-178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       emokine_receptor 4.";
Biol. Chem. 273:1764-1768(1998)
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C-X-C chemokine receptor type 6 (CXC-R6) (G protein-coupled receptor bonzo) (G protein-coupled receptor STRL33). CXCR6 OR BONZO OR STRL33 OR TYMSTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97431687, PubMed-9285716;
Doctscher M., Amara A., Oberlin E., Brass N., Legler D.F.,
Loetscher P., D'Apuzzo M., Meese E.U., Rousset D., Virelizier J.L.,
Baggiolini M., Arenzana-Seisdedos F., Moser B.;
"TYMSTR, a putative chemokine receptor selectively expressed in
activated T cells, exhibits HIV-1 coreceptor function.";
Curr. Biol. 7:652-660(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                   "STRL33, A novel chemokine receptor-like protein, functions as a fusion cofactor for both macrophage-tropic and T cell line-tropic HIV-1.";
                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kopatz S.A., Aronstam R.S., Sharma S.V.; "cDM clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org)."; Submitted (UUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-97373958; PubMed=9230441;
Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;
"Expression cloning of new receptors used by simian and human immunodeficiency viruses.";
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DISDLINE-97311099; PubMed=9166430;
Liao F., Alkhatib G., Peden K.W.C., Sharma G., Berger E.A.,
Farber J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Exp. Med. 185:2015-2023(1997)
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                                                                     (Human)
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                                                                                                                                           NCBI_TaxID=9606
                                                                             sapiens
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BRE EMBL; AB023889; BAA68656.1; ---
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BRE EMBL; AB023890; BAA68666.1; ---
BRE EMBL; AB023891; BAA68668.1; ---
BRE EMBL; AB023891; BAA68668.1; ---
BRE EMBL; AB023891; BAA68696.1; ---
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EXTRACELULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
EXTRACELULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
7 (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
BY SIMILARITY.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors
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Pred. No. 0.012;
8; Mismatches 5; Indels
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PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G-PROTEIN RECEP F1 2; 1.
PROSITE; PS50262; G-PROTEIN RECEP F1 2; 1.
PROSITE; PS50262; G-PROTEIN RECEP F1 2; 1.
Phosphorylation; Polymorphism: CREACELLULAR (POTENTIAL).
DOMAIN
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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51EBE12AD1FAFABF CRC64;
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CCR6_HUMAN STANDARD; PRT; 342 AA.
AC 000574; 000575;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
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Matches 9; Conservative
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MEDINE-2388257; PubMed=12477932;

RESUBLE-Pancreas,

RESUBLE-Pancreas,

RECORDER F. Foligold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Feligold E.A., Grouse L.H., Schemen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heng L.,

Ra Diatchenko L., Warnes M.B., Bonaldo M.F., Carninci P., Parage C.,

RA Diatchenko L., Widin T.B., Toshiyuki S., Carninci P., Parage C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Parage C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Rolards S.W., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gab L.J., Hilyk S.W.,

Rahesley S.W., Mazuy D.W., Sodergren B.J., Lu X., Gibbs R.A.,

Rhiting M., Madan A., Young A.C., Schwultz J., Myers R.M.,

Rakesley R.W., Touchman J.W., Creen E.D., Dickson M.C.,

RA Scheiner A., Schein J.E., Jones S.J.M., Marra M.A.,

Rodriquez A.C., Grimwood J., Schwultz J., Mers R.M.,

Rodriquez A.C., Grimwood J., Schwultz J., Skalska U., Smailus D.E.,

Ronerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Ronerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Ronerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Rutherfield Y.S.N. Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences.",

"Froc. Natl. Acad. Sci. U.S. A. 9916899-16903 (2002).

"FRUKTION: Receptor for the C-x.C chemokine CxCL16. Used as a

correceptor by SIVs and by strains of HIV-2 and m-tropic HIV-1.

"TISSUE SPECIFICITY: Expressed in lymphoid tissues and activated T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                GO, GO:0015026; F:coreceptor activity; TAS.
GO; GO:0015026; F:coreceptor activity; TAS.
GO; GO:000186; F:G-protein coupled receptor activity; TAS.
GO; GO:000186; F:G-protein coupled receptor protein signalin. .; TAS.
GO; GO:000186; P:viral replication; TAS.
InterPro; PRO02076; GPRR.Rhodpsn.
PROSITE; PS00237; GPRR.Rhodpsn.
PROSITE; PS00237; GPRR.Rhodpsn.
PROSITE; PS00237; GPROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
DOMAIN
TRANSMEM
GO G CYTOPLASMIC (POTENTIAL).
DOMAIN
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15-UUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-X-C chemokine receptor type 6 (CXC-R6) (G protein-coupled
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Eukaryota, Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
D -> A (in STRL33.3).
/FILG-VAR 003506.
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MEDLINE=97373958; PubMed=9230441;
Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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5; Mismatches
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                                                                                                                            EMBL, AF007545; AAB64221.1; -.
EMBL, U73529; AAB61456.1; -.
EMBL, U73531; AAB61457.1; -.
                                                                                                                                                      EMBL, U73529, AAB61456.1; -...
EMBL, U73531, AAB61457.1; -..
EMBL, Y13248, CAA73698.1; -..
EMBL, AX322543; AAP84356.1; -..
EMBL, BC033584; AAH33584.1; -..
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45.5%;
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Best Local Similarity 45.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                               HGNC:16647; CXCR6.
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CXCR6 OR BONZO.
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CCR6_MACNE
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MEDLINE=99433499; PubMed=10505680;
Brussel A., Prefet J.-L., Girard M., Butor C.;
Brussel A., Prefet G.-L., Girard M., Butor C.;
gradences and predicted structures of chimpanzee STRL33 (Bonzo) and gpr15 (BOB).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                    -i- FUNCTION: Receptor for the C-X-C chemokine CXCL16. Used as a coreceptor by SIVs and by strains of HIV-2 and m-tropic HIV-1. SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .) (POTENTIAL).
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Expression cloning of new receptors used by simian and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 65; DB 1; Length 342; Pred. No. 0.016;
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InterPro; IPR000276; GPCR_Rhodpsn.
Primr; PR00037; GPCRRHODOPSN.
PROSITE; P800237; GPCRHODOPSN.
PROSITE; P850262; GPROTEIN RECEP_F1_1; 1.
PROSITE; P850262; GPROTEIN RECEP_F1_2; 1.
PROSITE; P850262; GPROTEIN RECEP_F1_2; 1.
TRANSMEM 33 CPC F1 EXTRACELULIAR (POTENTIAL).
TRANSMEM 33 CPC F1 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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N-LINKED (GLCNAC.
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CYTOPLASMIC (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39297 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 45.5%;
Matches 10; Conservative
                            immunodeficiency viruses.";
Nature 388:296-300(1997).
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16
342 AA;
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Q9TV16;
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CCR6_PANTR
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coreceptor by SIVs and by strains of HIV-2 and m-tropic HIV-1.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
5B58003797806B2A CRC64;
                                                                                                                                                                                                                                                                                            entillocar endillocar send an email or send or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.6%; Score 65; DB 1; Length 342; ilarity 45.5%; Pred. No. 0.016; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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39273 MW;
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342 AA;
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Search completed: September 28, 2004, 09:04:05 Job time : 7.875 secs

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The L., Ehrenberg P.K., Chang G., Michael N.L.;

RT Transcription Unit for the Chemokine Receptor CCR-5, a Major Entry Co-10 C
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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SEQUENCE 215 AA; 23946 MW; 3C9146C76BA416F7 CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
CC-chemokine receptor.
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014694 homo sapien
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09un25 homo sapien
09un27 homo sapien
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09tux4 macaca neme
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               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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1 QWDFGNTMCQLLTGLYFIGFFS 22
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Submitted (JUL-1999) to the EWBL/GenBank/DDBJ databases.
Submitted (JUL-1999) to the EWBL/GenBank/DDBJ databases.
BMBL; AF161920; AAD47677.1; -
GO; GO:00016021; C:integral to membrane; IEA.
GO; GO:0001887; F:receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001886; P:G-protein coupled receptor protein signalin. . .; IEA.
PF00001; 7Fm_1; 1.
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bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 339;
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339 AA, 39066 MW, 8BAF02E19423BF79 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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100.0%; Pred. No. 3.1e-11;
Live 0; Mismatches 0;
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Pred. No. 3.1e-11;
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PROSITE; PRO0237; G PROTEIN RECEP FI 1; 1.

PROSITE; PS50262; G PROTEIN RECEP FI 2; 1.
PROSITE, PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sen
01-UTN-2003 (TrEMBLrel. 24, Last and
C-C chemokine receptor 5 (Fragment).
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....hes 22; Conservative
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339 AA;
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A Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
A D.D.;
Hubtypes, co-receptor usage, and CCR5 polymorphism.";
A LDS Res. Hum. Retroviruses 0:0-0(1997).

R MALL, FROILSOH, AABSTO41.1.

R GO; GO:00016021; F:receptor activity; IEA.

GO; GO:0001634; F:rindopshin-like receptor activity; IEA.

GO; GO:0001864; F:rindopshin-like receptor protein signalin. ..; IEA.

InterPro; IPR000276; GPCR_Rhodpsn.

R PROILS: PR000277; GPCRRHODPSN.

PRINTS; PR000277; GPCRRHODPSN.

PROSITE; PS00237; GPCRRHODPSN.

PROSITE; PS00237; GPCRRHODPSN.

PROSITE; PS00237; GPCRRHONEN_RECEP_FL1; 1.
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EMBL; AF161919; AAD47676.1; -.

EMBL; AF161919; AAD47676.1; -.

GO; GO:0004672; F: receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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0; Mismatches 0; Indels C
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01-WAY-2000 (TrEWBLrel. 13, Created)
01-WAY-2000 (TrEWBLrel. 13, Last sequence update)
01-UNY-2003 (TrEWBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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Last annotation update)
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                                                                                                                                                            333 AA
                                                                                                                                                                                                                   Created)
               QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                            PRT;
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Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
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Best Local Similarity 100.0%;
Matches 22; Conservative 0
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                                                                                                                                                                                                                                                                                                      CCR5 receptor (Fragment).
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Local Similarity 100.
1es 22; Conservative
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Homo sapiens (Human)
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Q9UN27
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinkay S.;
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinkay S.;
T. Sequences of the CCR5 genes from diverse simian and prosimian

R. Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AB161918; AAD47675.1; -.

R. Shoitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AR161918; AAD47675.1; -.

R. Opi GO:0016021; C::ntegral to membrane; IEA.

GO: GO:001684; F::receptor activity; IEA.

R. Opi GO:001184; F::receptor activity; IEA.

GO: GO:001186; P::-protein coupled receptor protein signalin. .; IEA.

InterPro: IRR00027; GPCR_Rhodpsn.

P. FANTY: PRO00237; GPCRRHODOPSN.

R. PROSITE; PS00237; GPCRRHODOPSN.

R. PROSITE; PS00237; GPCRRHON_RECEP_FI_1; 1.
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SEQUENCE FROM N.A.

A Shibata R., Tohen Z., Korber B., Oprondek J., Stanton J., Agy M.,
A Shibata R., Yoden A., Pillai S., Kuiken C., Marx P., Wolinkey S.,
T Sequences of the CCR5 genes from diverse simian and prosimian
species."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

E RMBL, APIG1921, AAD47678.1; --
SR EMBL, APIG1921, AAD47674.1; --
SR GO; GO:00016021, Cintegral to membrane, IEA.
GO; GO:00016021, Gintegral to membrane, IEA.
GO; GO:00016021, GF-protein coupled receptor protein signalin. . .; I
DR RAINYS; PRO02237, GFCRRHODOPSN.
DR PROSITE; PSSO2237, GFCRRHODOPSN.
DR PROSITE; PSSO262; G_PROTEIN_RECEP_FI_2; I.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.16-11;
Matches 22; Conservative 0; Mismatches 0; Indels (
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100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels (
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339 339
339 Aa; 39128 MW; 9C3369FFF1F2F27A CRC64;
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339 339
339 AA; 39146 MW; 10PEO5FE5371D4B3 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment)
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PRELIMINARY;
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339 AA

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606; Homo sapiens (Human). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. NCBI_TaxID=9606; SECUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.
Shipate S. of the CCR5 genes from diverse simian and prosimian species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. 100.0%; Score 126; DB 4; Length 339; 100.0%; Pred. No. 3.1e-11; ive 0; Mismatches 0; Indels (01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) C-C chemokine receptor 5 (Fragment) EMBL, AF161915, AAD47672.1; -.
EMBL, AF161909, AAD47666.1; -.
EMBL, AF161910, AAD47667.1; -.
EMBL, AF161911, AAD47669.1; -.
EMBL, AF161912; AAD47669.1; -.
GO, GO:0016021; C:integral to membrane; IEA. PRT;

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C-C chemokine receptor 5 (Fragment).
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Les 22; Conservative
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GO; GO: 0016872; F: receptor activity; IEA.
GO; GO: 0001884; F: rhodopsin-like receptor activity; IEA.
GO; GO: 0001886; F: rhodopsin-like receptor protein signalin. . .; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
PRINTS; PR000217; GPCRRHODPSN.
PROSITE; PS000237; GPCRRHODPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_1; 1.
                                                             . ., IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
GO, GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor protein signalin.
InterPro; IPR00027; GF-protein coupled receptor protein signalin.
Pfam; PF00001; 7tm 1; 1.
PROMI; PRO00137; GPCRHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN RECEP_F1 2; 1.
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Pred. No. 3.1e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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339 339
339 AA, 39114 MW, 3C6369F92C29F4A7 CRC64;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Best Local Similarity
Matches 22; Conserv
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF161887; AAA47644.1; -.
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:00018872; F:receptor activity; IEA.
GO, GO:0001884; F:rhodopsin-like receptor activity; IEA.
GO, GO:0001885; P:G-protein coupled receptor protein signalin. . .; IEA.
InterPro; IPRO00276; GFCR_Rhodpsn.
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EMBL; AF162024; AAD47779.1; -...

EMBL; AF16189; AAD47646.1; -...

EMBL; AF16189; AAD47646.1; -...

GO; GO:0016872; F:receptor activity; IEA.

GO; GO:0001584; F:rhodopsin.like receptor activity; IEA.

GO; GO:0001584; F:rhodopsin.like receptor protein signalin. .; IEA.

Interpro; IPR000276; GPCR_Rhodopsn.

PRINTS; PR00237; GPCR*HODOPSN.

PROSITE; PR00237; GPCR*HODOPSN.

PROSITE; PS50237; GPCR*HODOPSN.
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Hylobates concolor (crested gibbon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hylobatidae, Hylobates.
                                                                                                                                                                   Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; Squences of the CCR5 genes from diverse simian and prosimian species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hylobates concolor (crested gibbon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hylobatidae, Hylobates.
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Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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339 339
339 AA, 39075 MW, 09257FBFB834C4AE CRC64;
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339 339
339 AA, 39036 MW, 5555FEAF2614D35C CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 126; DB 6;
Pred. No. 3.1e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     339 AA.
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PRINKS: PR00231; GPCMFHODPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; PROSITE; PS0262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 QWDFGNTMCQLLTGLYFIGFFS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

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Gaps

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Match
Local Similarity 100.0%; Score 126; DB 6; Length 339;
Local Similarity 100.0%; Pred. No. 3.1e-11;
es 22; Conservative 0; Mismatches 0; Indels

1 OWDFGNTMCQLLTGLYFIGFFS 22

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1 1 339 339 339 AA, 39092 MW, 84B51B9548E0703C CRC64,

Receptor. NON TER NON TER SEQUENCE

Query Match

Best Loca Matches

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The Sep 28 13:49:56 2004
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                                                                       Gaps
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gorilla gorilla gorilla (Lowland gorilla).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCRS genes from diverse simian and prosimian
spectes.";
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates; Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; E:receptor activity; IEA.
GO; GO:000186; F:receptor activity; IEA.
GO; GO:000186; F:receptor activity; IEA.
InterPro; IPR000276; GPCR.Rhodpsn.
PETM: PR00017; Tem 1; 1.
PROSITE; PS00027; GPCRRHODPSN.
PROSITE; PS00027; GPCRRHODPSN.
PROSITE; PS00027; GPROTEIN RECEP F1 1; 1.
PROSITE; PS00027; GPROTEIN RECEP F1 2; 1.
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Query Match 100.0%; Score 126; DB 6; Length 339; Best Local Similarity 100.0%; Pred. No. 3.1e-11; Matches 22; Conservative 0; Mismatches 0; Indels (
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100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels
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339 339
339 AA; 39079 MW; A4A79753DA2F7AAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UDN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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01-MAY-2000 (TrEMBirel. 13, Last sequence update)
01-UJN-2003 (TrEMBirel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                          339 AA
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                                                                                                                                                                      QWDFGNTMCQLLTGLYFIGFFS 107
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                                                                                                                          1 OWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Q9TUW8
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209TUT4
1D 09TUT9
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                                                                                                                                                                                                                                                                                                                                                                                                                        Hylobates concolor (crested gibbon).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hylobatidae, Hylobates.
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339 AA; 39024 MW; BC4CE48DEEEF107E CRC64;
                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UDN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                              339 AA
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86 QWDFGNTMCQLLTGLYFIGFFS 107
                                                                                                                                                                                              PRT;
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                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 22; Conservative
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Q9TUW9;
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Q9TUU8;
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Q9TUU8
1D Q9TUU
AC Q9TUU
                                                                                                                     RESULT 14
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CONSTRUCTION OF THE PROPERTY OF THE PROPER
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Gaps

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Cercopithecus nictitans (white-nosed guenon).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
NCBI_TaxID=36228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sub-Lets. (1)
Submitted (1)
Su
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
NCBI_TaxID=9598;
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Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy F.
"Sequences of the CCRS genes from diverse simian and prosimian species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 339;
                                                                                                                                Length 339;
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                                              1
339 339
339 AA; 39129 MW; 4A88F8BB601D46A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O9TQU7;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 100.0%; Score 126; DB 6; Similarity 100.0%; Pred. No. 3.1e-11; 22; Conservative 0; Mismatches 0;
                                                                                                                              100.0%; Score 126; DB 6;
100.0%; Pred. No. 3.1e-11;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      339 AA
                                                                                                                                                                                                                                                                                                                                                                                          339 AA
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                                                                                                                                                                                                                                                         86 QWDFGNTMCQLLTGLYFIGFFS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 OWDFGNIMCOLLIGLYFIGFFS 22
                                                                                                                                                                                                                            1 OWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                           1 Similarity 100.0%; 22; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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Q9TUW4
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Species.")
Submitteed (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF161905; AAD47662.1; ---
EMBL; AF161905; AAD47662.1; ---
EMBL; AF161904; AAD47658.1; ---
GO; GO:0016804; F:receptor activity; IEA.
GO; GO:0015804; F:receptor activity; IEA.
GO; GO:0001806; P:receptor activity; IEA.
GO; GO:0001806; P:receptor activity; IEA.
GO; GO:0001806; P:receptor activity; IEA.
FEAN; F:RECONDI, 7Tm 1; IEA.
FEAN; PRO0021; GECRRHODOPSN.
FFAN; PRO0021; GECRRHODOPSN.
PROSITE; PS000237; GERRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                               Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                   species.";
Submitted (UTL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (UTL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (UTL-1999) to the EMBL/GenBank/DDBJ databases.
GO; GO:001681; Cantegral to membrane; IEA.
GO; GO:001684; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001786; P:rhodopsin-like receptor protein signalin.
InterPro; IPR002276; GPCR_Rhodpsn.
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Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
"Sequences of the CCRS genes from diverse simian and prosimian
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; Pred. No. 3.1e-11;
0; Mismatches 0; Indels C
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339 AA; 39049 MW; 6D1A93F66270F3ED CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTM-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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PROMINS, PRO0237, GPCRHODOSN.
PROSITE; PS00137, G PROMEIN RECEP F1 1, 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2, 1.
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                                                                                                                           Cercopithecus diana (Diana monkey)
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100.0%;
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                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                     TaxID=36224;
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RESULT 20
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P SEQUENCE FROM N.A.

A KURDERMAN K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
A Kunbara R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
T "Sequences of the CCR5 genes from diverse simian and prosimian
T species.",
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF162047; AAD47797.1; -.

R EMBL; AF162042; AAD47797.1; -.

R EMBL; AF162042; AAD47797.1; -.

R EMBL; AF162042; AAD47799.1; -.

R GO; GO:00016021; C:integral to membrane; IEA.

GO; GO:0001684; P:rhodopsin-like receptor activity; IEA.

GO; GO:0001586; P:rhodopsin-like receptor activity; IEA.

GO; GO:0001586; P:rhodopsin-like receptor protein signalin. ..; I
DR PROSITE; PSS00237; GPCRRHODOPSN.

P RNNTS; PR00237; GPCRRHODOPSN.

PROSITE; PSS50262; G-PROTEIN_RECEP_FI_2; 1.
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EMBL, AFIGIDIST, AAD47716.1;

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0001882; F:receptor activity; IEA.

GO; GO:0001886; F:rhodoppin-like receptor activity; IEA.

GO; GO:00071886; F:rhodoppin-like receptor protein signalin...

InterPro; IPR000276; GFCR_Rhodopsn.

PRGM; FO00001; Thm 1, 1.

PRAINTS; PR000237; GFCRRHODOPSN.

PROSITE; PS00237; GFCRRHODOPSN.

PROSITE; PS00227; GFCRENCEP_F1 1; 1.
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macaca mulatta (Rhesus macaque).
Bukaryota, Metazoa; Chordata; Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 1
339 339
339 AA, 39150 MW, 847D5F92BB03E6E2 CRC64;
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Best Local Similarity 100...
Local 22; Conservative
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Platyrrhini, Callitrichidae, Saguinus.
NCBI_TaxID=100754;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; T. Sequences of the CCRS genes from diverse simian and prosimian species."; Coloude (JUL-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AF16,2015; AAD47770.1; Coloude Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Bukaryota, Metazota, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCR5 genes from diverse simian and prosimian
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR161954; AAD47101.1; -.
EMBL; AR161955; AAD47706.1; -.
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339 339
339 AA; 39063 MW; 78BCE7A84B877085 CRC64;
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Q9TQT0;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
Q9TUR9 PRELIMINARY; PRT; 339 AA.
Q9TUR9;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2003 (TrEMBLrel. 13, Last sequence update)
01-UMY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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Matches 22; Conserv
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18-10-064-613-17.rBDC

Matches

RESULT 22

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Carbonic From N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Sibbata R., Venen Z., Fullai S., Kuiken C., Marx P., Wolinksy S.;
Shibata R., Venen Z., Fullai S., Kuiken C., Marx P., Wolinksy S.;
Shibata R., Tenen S., Fullai S., Kuiken C., Marx P., Wolinksy S.;
Shibata R., Line Carb S., Fullai S., Kuiken C., Marx P., Wolinksy S.;
Shibata R., Line Carb S., Line Carb S., Carb 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cercopithecus aethiops vervet.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele:

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 AA; 39137 MW; 9E626ED3288607C1 CRC64;
01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) C-C chemokine receptor 5 (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNAY-2003 (TrEMBLrel. 24, Last annotation update)
0-C chemokine receptor 5 (Fragment).
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Pred. No. 3.1e-11;
0; Mismatches 0;
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O9TUR6;
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161972; AAD47727.1; -
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:000186; P:rhodopsin-like receptor activity; IEA.
GO, GO:000186; P:rhodopsin-like receptor protein signalin. .; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
PRINTS; PR000273; GPCRRHODOPSN.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
  GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:000184; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; F:rhodopsin-like receptor protein signalin. .; IEA.
InterPro; IPR000276; GPCR Rhodopsu.
PRINTS; PR000217; GPCRRHODOPSN.
PRINTS; PR000237; GPCRRHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP FI.; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_FI.2; 1.
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Local Similarity 100.0%; Pred. No. 3.1e-11;
hes 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                Match 100.0%; Score 126; DB 6; Length 339; Local Similarity 100.0%; Pred. No. 3.1e-11; es 22; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                 339 339 34; C576E7AA492D7080 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 339 AA.
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                                                                                                                                                                                                                                                                                                                                                             Query Match
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339 AA.

Q9TSN2 PRELIMINARY; PRT; Q9TSN2; 01-MAY-2000 (TrEMBLrel. 13, Created)

RESULT 23 Q9TSN2

Matches

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Gaps

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Indels

Length 339;

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A KUNDER FROM N.A.

A KUNDER R., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Subbata R., Yoder A., Pillais S., Kulken C., Marx P., Wolinksy S.;

T. Scquences of the CCRS genes from diverse simian and prosimian

T. Sequences of Library CCRS genes from diverse simian and prosimian

T. Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

R. Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

R. MGD; GO:0001601; Cintegral to membrane; IEA.

R. GO; GO:0001802; F:receptor activity; IEA.

R. GO; GO:000186; F:rhodopsin-like receptor activity; IEA.

R. GO; GO:000186; F:rhodopsin-like receptor protein signalin. ..;

R. InterPro; IPR00027; GPC-Rhodopsn.

R. PROSITE; PS00237; GPCRHODOPSN.

R. PROSITE; PS00237; GPCRHODOPSN.

R. PROSITE; PS00237; GPCRTEIN REGEP F1 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 126; DB 6; Length 339; 100.0%; Pred. No. 3.1e-11; ive 0; Mismatches 0; Indels 0
    Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 1
339 339
339 AA; 39103 MW; 4038C132D024C5A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 QWDFGNTMCQLLTGLYFIGFFS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
les 22; Conservative
                 NCBI_TaxID=9598;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCR5.
Colobus guereza (Black-and-white colobus monkey).
Colobus guereza, Metazoa, Chordeta, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae, Colobinae,
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinkey S.; "Sequences of the CCR5 genes from diverse simian and prosimian species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
C-CSCR5.
Pan troglodytes (Chimpanzee).
Bukaryota, Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi;
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                                                                          Length 339;
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                                                                                                                    Indels
'339 339
339 AA; 39178 MW; 9DF2A6F446C55AED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339 339 34; 39168 MW; 6A4BF72FBBFF566F CRC64;
                                                                                                                                                                                                                                                                                                                                                OFICAGO (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                  Query Match
100.0%; Score 126; DB 6;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                 PRT; 339 AA.
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                                                                                                                                                                                              QWDFGNTMCQLLTGLYFIGFFS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 OWDFGNIMCOLLIGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OWDFGNTMCOLLTGLYFIGFFS 22
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Best Local Similarity 100.0
Best Local Similarity 200.0
                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colobus.
NCBL_TaxID=33548;
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                                                                                                                                                                                                                                                                        RESULT 25
109 TQV6
100 TQPTOV
AC Q9TQVV
AC Q9TQVV
AC Q9TQVV
AC Q9TQVV
AC Q0 TQPTOV
AC 
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Gaps

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18-10-064-613-17:TBDC

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EQUENCE FROM N.A.

Xunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., A Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; Stanton S. St
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Cercopithecus mona.

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
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339 339
339 AA; 39019 MW; 7176F940AF11F3ED CRC64;
                                                     097009;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
PRT;
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Best Local Similarity 100.
Matches 22; Conservative
PRELIMINARY;
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us-10-084-813-12.rspt

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Submitted (UTL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (UTL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161988; AAD47744.1;
EMBL; AF161988; AAD47743.1;
EMBL; AF161988; AAD47743.1;
EMBL; AF161988; AAD47743.1;
EMBL; AF161988; AAD47744.1;
EMBL; AF161988; AAD47744.1;
EMBL; AF161988; AAD47744.1;
EMBL; AF161988; AAD47744.1;
EMBL; EMBL
GO, GO:0004872; F:receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:000186; P:G-protein coupled receptor protein signalin. . .; IEA.

InterPro; IPR000276 GPCR Rhodpsn.

PFam; PF00001; 7tm 1; 1.

PROSITE; PR00237; GPCRPHODOPSN.

PROSITE; PS00237; GPROTEIN RECEP FI 1; 1.

PROSITE; PS00262; G_PROTEIN_RECEP_FI_2; 1.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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339 339
339 AA, 39097 MW, C576E7AA492D7080 CRC64;
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339 AA; 39113 MW; 7F9803EA0E0AF9ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 126; DB 6; Similarity 100.0%; Pred. No. 3.1e-11; 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 126; DB 6;
100.0%; Pred. No. 3.1e-11;
Live 0; Mismatches 0;
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01-MAY-2000 (TrEMBLrel. 13, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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Best Local 9
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Q9TQV0;
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K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                       Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 species.";
Submitred (JUL-1999) to the EMBL/GenBank/DDBJ databases.
Submitred (JUL-1999) to the EMBL/GenBank/DDBJ databases.
Submitred (JUL-1999) to the EMBL/GenBank/DDBJ databases.
GO; GO:001681; C:integral to membrane; IEA.
GO; GO:001584; F:receptor activity; IEA.
GO; GO:00011884; F:rhodopsin-like receptor activity; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
FF00001; 7tm 1: 1.
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100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AFT61955; AAD47711.1; -.
GO, GO:0016021; C:integral to membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     339 AA; 39098 MW; F0132E8BC44EF829 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                         01-WAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                          339 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0237; GPCRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1, 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
                                               86 QWDFGNTWCQLLTGLYFIGFFS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                          PRT;
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               1 QWDFGNTMCQLLTGLYFIGFFS 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339
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NON TER
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                                                                                                                                                                                                                          O9TSN3
                                                                                                                                                                 RESULT 28
Q9TSN3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 29
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Query Match 100.0%; Score 126; DB 6; Best Local Similarity 100.0%; Pred. No. 3.1e-11; Matches 22; Conservative 0; Mismatches 0;
                                                                                                               86 QWDFGNTMCQLLTGLYFIGFFS 107
                                                                                               1 OWDFGNIMCQLLIGLYFIGFFS 22
                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor.
NON TER
NON TER
SEQUENCE
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF162046; AAD47801.1; ...

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor protein signalin. .; IEA.

InterPro; IRR000276; GPCR_Rhodops.

PEAN; PRO0037; GPCRRHODOPSN.

PROSITE; PSS00237; GPRRHODOPSN.

PROSITE; PSS00237; GPROTEIN_RECEP_F1_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF161995; AAD47750.1; -.

GO, GO.0016021; C.integral to membrane; IEA.

GO, GO.0001884; F:rhodopsin-like receptor activity; IEA.

GO, GO.0001886; P:G-protein coupled receptor protein signalin. . .; IEA.

Interpre, IPR00021; GPCRRHODOPSN.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                  Cercopithecus nictitans (white-nosed guenon).
Subaryotas, Metazoca; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCR5 genes from diverse simian and prosimian species.";
                                                                                                                                       SEQUENCE FROM N.A.

K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Papio papio (Guinea baboon).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Papio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 126; DB 6; Length 339; 100.0%; Pred. No. 3.1e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           339
39178 MW; 847F8F936B00E6E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            339 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 OWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 100.
22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 Receptor.
NON_TER 1
NON_TER 339 33
SEQUENCE 339 AA; 3
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NON_TER
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Gaps
                                                                                                                                                      CCR5.
Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pongo pygmaeus (Orangutan).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                             Species.';
Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR161899; AAD47656.1;
GO; GO:0016021; C:1ntegral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:000186; P:rhodopsin-like receptor activity; IEA.
GO; GO:000186; P:rhodopsin-like receptor protein signalin.
InterPro; IPR000276; GPCR_Rhodpsn.
FRAM; PR00037; GFCR_Rhodpsn.
PROSITE; PS000237; GFCR_RHODPSN.
PROSITE; PS000237; GFCR_RHODPSN.
PROSITE; PS000237; GFCR_RHODPSN.
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
"Sequences of the CCR5 genes from diverse simian and prosimian
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Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 126; DB 6; Length 3 Best Local Similarity 100.0%; Pred. No. 3.1e-11; Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1
339 339
339 AA, 39157 MW, 4A9EBAD183E8E72D CRC64;
                     QUIUN7;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UMY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9TUW3;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
     339 AA
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PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 QWDFGNTMCQLLTGLYFIGFFS 107
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Gaps

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Indels Length

339 339 343 39068 MW; 84EB018085DC0A62 CRC64;

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Best_Local Matches 2

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Q9TUS5

RESULT 35 Q9TUS5

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species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFF61970; AAA47725.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:00018872; F:receptor activity; IEA.
GO; GO:000186; F:receptor activity; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
PRINTS; PR000217; GPCR_Rhodpsn.
PRINTS; PR00217; GPCRRHODPSN.
PROSITE; PS00237; GPCRRHODPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF161997, AAD47748.1; --
EMBL, AF161990, AAD47745.1; --
EMBL, AF161991, AAD47746.1; --
EMBL, AF761991, AAD47746.1; --
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0004872; F:receptor activity; IEA.
GO, GO:0001884; F:rhodopsin-like receptor activity; IEA.
GO, GO:0001886; F:G-protein coupled receptor protein signalin. .; IEA.
                                                                                                                                                                                                                 Macaca mulatta (Rhesus macaque).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Papio papio (Guinea baboon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
Shibate R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
Sequences of the CCRS genes from diverse simian and prosimian
Species.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1
339 339
339 AA; 39155 MW; 3D1B5039B9E24C82 CRC64;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UMY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 126; DB 6;
100.0%; Pred. No. 3.1e-11;
trive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 OWDFGNTMCOLLIGLYFIGFFS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 OWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22; Conservative
                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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NCBI_TaxID=100937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor.
NON TER
NON TER
SEQUENCE
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                               ð
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                      species.";
submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161908; AAD47665.1;
GO: GO: 0016021; C:integral to membrane; IEA.
GO: GO: 001681; F:receptor activity; IEA.
GO: GO: 001884; F:rhodopsin-like receptor activity; IEA.
GO: GO: 0001884; F:rhodopsin-like receptor protein signalin. .; IEA.
GO: GO: 0001886; P:Crotein coupled receptor protein signalin. .; IEA.
InterPro: PR000216; GPCR_Rhodops.
Ffam; PF00001; 7tm 1; 17m 1; 17m 1; IPA.
PRINTS; PR00227; GPCRRHODOPSN.
PROSITE; PS00227; GPRRHODOPSN.
PROSITE; PS00227; GPROTEIN_RECEP_F1_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Papio papio (Guinea baboon).
Bukaryota, Metazota, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Papio.
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species...;
Submitted (ULL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (ULL-1999) to the EMBL/GenBank/DDBJ databases.
BMBL, API61997; AAA1752.1;
GO, GO:00016021; C:integral to membrane; IEA.
GO; GO:0001584; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor protein signalin.
InterPro; IPR000276; GPCR_Rhodopsn.
Pfam, PF00001; 7tm_1; 1.......
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"Sequences of the CCR5 genes from diverse simian and prosimian
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339 339
339 AA, 39103 MW, 4350C4625FB0657C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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22; Conservative (
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es 22; Conservative
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Indels

RESULT 36

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Best Loc Matches

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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kulken C., Marx P., Wolinksy S., "Sequences of the CCR5 genes from diverse simian and prosimian
                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Cercopithecus.
                                                                                                                                                                                                                                           Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR162045 (And47800.1;
GO; GO:0016021; C:nteeptal to membrane; IEA.
GO; GO:0018872; F:receptor activity; IEA.
GO; GO:0001886; F:gerctein coupled receptor protein signalin.
InterPro; IPR000276; GPCR_Rhodpsn.
PFAm; PR00037; Trul; 1.
PRINTS; PR00037; GPCRRHODOFN.
PROSITE; PS00237; GPCRRHODOFN.
PROSITE; PS00237; GPCRHODOFN.
PROSITE; PS00237; GPROTEIN_RECEP_FI_1; 1.
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339 339
339 AA; 39148 MW; 0CA289CDDEEDE831 CRC64;
                              Cercopithecus nictitans (white-nosed guenon)
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Best Local Similarity 100.
Matches 22; Conservative
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339 AA;
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                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                     NCBI_TaxID=36228;
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S.; T. Sequences of the CCRS genes from diverse simian and prosimian species.";

EMEL; AF162040; AAD47795.1; -.

REMEL; AF162040; AAD47795.1; -.

RO; GO:00016021; C:integral to membrane; IEA.

GO; GO:0001887; F:receptor activity; IEA.

GO; GO:000188; F:rhodopsin-like receptor activity; IEA.

GO; GO:000188; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001186; F:rhodopsin-like receptor protein signalin. ..; I

RIMER: PRO001; 7tm 1; 1.

DR FEANTE; PS00237; GPRRAHODOPSN.

PROSITE; PS00237; G-RROTEIN RECEP_FI_2; 1.
                                                                                                                                                                                                                                                                       Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Cercopithecus.
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Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels C
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.339 339 MW; 7176E3EAOE00F3ED CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          339 AA.
Interpro, IPR000276, GPCR_Rhodpsn.
Pfam; PF00001, 7tm 1, 1.
PRINTS, PR000237, GPCRRHODOPSN.
PROSITE; PS00237, G PROTEIN RECEP F1 1, 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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Q9TUQ8
ID Q9TUQA
AC Q9TUQ
DT 01-MAN
DT 01-MAN
DT CC C
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1091073
1001074
AC 0910V
AC 0910V
DT 01-MA
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         SET KEN BER
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Gaps

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Length 339;

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National Property (Chem 2.) Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; Sequences of the CCRS genes from diverse simian and prosimian pecies.";

Submitted (ULL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; APIG1907; ADAP4664.1;

EMBL; AF161907; ADAP4664.1;

CO; GO:00016021; C:integral to membrane, IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

CO; GO:0001586; P:G-protein coupled receptor protein signalin. ..; IEA.

InterPro; IPR000276; GPCR_Rhodpsn.

PROSITE; PS00237; GPCR_Rhodpsn.

PROSITE; PS00237; GPCR_RHOGPSP.11; 1.
                                                                                                                                                                                              Pongo pygmaeus (Orangutan).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pongo.
NCBI_TaxID=9600;
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39117 MW; 4C4E35825BD54E9C CRC64;
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      339 AA
PRT;
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0; Gaps Best Local Similarity 100.0%; Pred. No. 3.1e-11; Matches 22; Conservative 0; Mismatches 0; Indels

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Search completed: September 28, 2004, 09:06:18 Job time: 36.2 secs

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September 28, 2004, 08:51:21; Search time 42.975 Seconds (without alignments) 118.345 Million cell updates/sec
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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1586107 segs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 US-10-084-813-13 96 1 SQYQFWKNFQTLKIVILG 18 Title: Perfect score: Sequence: Scoring table: Searched:

1586107 Total number of hits satisfying chosen parameters: seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

genesagn1990s:* genesagn200s:* genesagn2001s:* genesagn2001s:* genesagn2002s:* genesagn2002s:* genesagn2003bs:* A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES * Ouerv Result

	Description		Aab88995 HIV gp120		Aaw27123 Human che	Aaw07602 Human G-p	Aaw23835 Human CC	Aaw88232 HIV-1 co-		Amino	Human	Aae07048 Human G-p	Aag80111 Human CCR	Human	Aae07037 Human G-p	Aae07039 Human G-p	Human	Abb56342 Non-endog	Aab83354 Human CCR	Aab82948 Human HIV	Aau97150 Human G-p	Aau97152 Human G-p	Aam52829 Human CCR	Aam52828 Human CC	Abg70597 Human G-p	Abg92883 Human imm
	ID	AAB88954	AAB88995	AAW27407	AAW27123	AAW07602	AAW23835	AAW88232	AAY80128	AAG79089	AAE07046	AAE07048	AAG80111	AAE04321	AAE07037	AAE07039	AAB46858	ABB56342	AAB83354	AAB82948	AAU97150	AAU97152	AAM52829	AAM52828	ABG70597	ABG92883
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Kienz	Match]	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0		100.0	100.0	100.0	100.0	100.0
	Score	96	96	96	96	96	96	96	96	96	96	96	96	96	96	96	96	96	96	96	96	96	96	96	96	96
ממחור	No.	н	7	m	4	Ŋ	9	7	80	0	10	11	12	13	14	15	16	17	18	19					24	25

	AbbB1054 G-protein Abb08343 Human che Abg75540 Human G-p Abr58602 Human can	Aao29514 Human C-C Abu61654 Human G-p Abp97728 Amino aci	Abp81933 Human C-C Adc03341 Human che Aaw23834 Human CC Aav21280 Finsion pr		Aag80087 Chemokine Aaw43018 Synthetic Aaw39912 Peptide r
ABG92880 AAE25808 AAE25811	ABB81054 ABB08343 ABG75540 ABR58602	AAO29514 ABU61654 ABP97728	ABP81933 ADC03341 AAW23834	AAW27125 ADC03359 AAW50141	AAG80087 AAW43018 AAW39912
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25 25 28 28 28 28	339 339 350 350 350 350 350 350 350 350 350 350	33 34 35	3 3 4 3 4 4 8 7	9444 014	4 4 4 ይ 4 ሺ

ALIGNMENTS

Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist; replication; CCR5; CXCR4; CD4; STRL33. (USSH) US DEPT HEALTH & HUMAN SERVICES. HIV gp120 protein binding peptide #47. Ş AAB88954 standard; peptide; 18 25-AUG-2000; 2000WO-US023505. 99US-0151270P. (first entry) WPI; 2001-244398/25 WO200116182-A2. 27-AUG-1999; Homo sapiens. 23-MAY-2001 08-MAR-2001. Saxinger C;

Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gpl20 under physiological conditions.

Example 1; Page 37; 114pp; English.

The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCR5, CXCR4 and STR133, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus. The present sequence is an example of a peptide of the invention

Sequence 18 AA;

Gaps ö 100.0%; Score 96; DB 4; Length 18; 100.0%; Pred. No. 4.2e-08; Live 0; Mismatches 0; Indels Query Match Best Local Similarity 100. Matches 18; Conservative

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1 SQYQFWKNFQTLKIVILG 18

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SQYQFWKNFQTLKIVILG 18

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                                                                                                              Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist; replication; CCR5; CXCR4; CD4; STRL33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention; inflammatory disease; rheumatorid arthritis; glomerulonephritis; asthma; idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer; atherosclerosis; autoimmune disorder.
                                                                                                                                                                                                                                                                                                                                                                                          Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gp120 under physiological conditions.
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100.0%; Pred. No. 4.2e-08;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                   HIV gp120 protein binding peptide #88.
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AAB88995 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 21; Page 38; 114pp; English.
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                                                                                                                                                                                                                                                  25-AUG-2000; 2000WO-US023505
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                                                       23-MAY-2001 (first entry)
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nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-244398/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18 AA;
                                                                                                                                                                                        WO200116182-A2.
                                                                                                                                                                                                                                                                              27-AUG-1999;
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                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                    08-MAR-2001
                                                                                                                                                                                                                                                                                                                                      Saxinger C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human CCR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
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                             AAB88995;
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AAW27407
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                                                                                                                                                                                                                                                                                   The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5), which is estimulated by MIP-1 alpha, MIP-1 beta or RANTES chemokines, but not by monocyte chemoattractant protein 1 (MCP-1), MCP-2, MCP-3, interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha) chemokines, Active CCR-5 is also a receptor of human immunodeficiaency virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its CDNA can used to diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid psoriaeis, iral infections, especially HIV-1 or HIV-2 infection, cancer, atherosclerosis and autoimmune disorders
                                                                                                                                                                                                         Active and inactive forms of human CC chemokine receptor CCR-5 - useful to diagnose, prevent and/or treat inflammatory disorders, autoimmune disease and viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 352;
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100.0%; Pred. No. 8.9e-07;
                                                                                                                                               Libert F;
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/label= Extracellular_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                               Vassart G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW27123 standard; protein; 352 AA
                                                                                                                                                                                                                                                             Claim 4; Fig 1b-c; 94pp; English.
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                                                            97WO-BE0000023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human chemokine receptor 88C.
                                                                                   96EP-00870021.
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/label= Int
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/label= E
                                                                                                                                                 Parmentier M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                        (EURO-) EUROSCREEN SA.
                                                                                                                                                                         WPI; 1997-479829/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                      N-PSDB; AAT90117.
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 352 AA;
                                                            28-FEB-1997;
                                                                                   01-MAR-1996;
06-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                  04-SEP-1997
                                                                                                                                                 Samson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW27123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Domain
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95WO-US007173.
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N-PSDB; AAT44042.
                                                                                                                                                         Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 352 AA;
                                       06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens,
                                                                           06-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW23835;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This polypeptide sequence comprises novel human chemokine receptor 88C, a grotein coupled receptor that is involved in leukcoyte trafficking. Its amno sequence was deduced from a cDNA clone (AAAT85161) isolated from a macrophage library. Its shows 62% identity to CCCKR1. Chemokine receptor 88-2B (see AAW27124) has also been identified. 88C and 88-2B receptors and their polypeptide fragments can be produced in transformed host cells. The receptors, peptides comprising one or more of the extracellular or intracellular domains, and anti-receptor antibodies can be used to modulate receptor activities, particularly ligand and G protein binding, and are potentially potentially useful in the treatment of atheroslerosis, inheumatoid arthritis, tumours, asthma, viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G-protein chemokine receptor; HDGNR10; signal transduction;
haematopoiesis; leukaemia; inflammation; rheumatoid arthritis; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammatory conditions, pathological immune response,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding chemokine receptors 88-2B and 88C - used to modulate leukocyte trafficking, e.g. for treatment of inflammation, tumours, viral infections, auto-immune diseases, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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213. .235
/label= Intracellular_domain
259. .280
/label= Extracellular_domain
301. .352
                                                                                            301. .352
/label= Intracellular domain
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                                                                                                                                                                                                                                                                                                                                                                           Raport CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 16; Page 47-48; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW07602 standard; protein; 352 AA
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96US-00661393
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                                                                                                                                                                                                                                                                                                                                                                           Gray PW, Schweickart VL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-341689/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT85161
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                                                                                                                                                         409722698-A2
                                                                                                                                                                                                                                    20-DEC-1996;
                                                                                                                                                                                                                                                                          20-DEC-1995;
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                                                        Domain
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                                                                                                                                                                                                                                                                                                                                                    Novel human mature G-protein chemokine receptor HDGNR10 (AAW07602) is a 7-transmembrane protein involved in signal transduction. Its amino acid sequence was deduced from a cDNA clone (AAT44042) isolated from a human monceyte library. Isolation of the cDNA allows prodn. of recombinant HDGNR10 in host, e.g. E. coli, COS or Sf9, cells. The recombinant creeptor can be used to identify agonists or antagonists of the receptor; such cpds. can be used to identify agonists or antagonists of the receptor; expression of G-protein chemokine receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC chemokine receptor 5; CCR5; G-protein coupled receptor;
human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.
                                                                                                                                                                                    Human G-protein chemokine receptor, HDGNR10 - useful to identify (ant)agonists, for treatment of haematopoiesis, leukaemia, chronic and acute inflammation, rheumatoid arthritis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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94. .219
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note= "transmembrane domain"
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note= "transmembrane domain"
04. .126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human CC chemokine receptor 5 (CCR5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW23835 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                          Claim 1; Page 44-46; 61pp; English.
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(HUMA-) HUMAN GENOME SCI INC.
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/label= IV
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Best Local Similarity 100.
Matches 18; Conservative
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This is the amino acid sequence of wild-type human CCR5, which serves as a co-receptor for infection by macrophage-tropic (M-tropic) strains of HIV-1. The invention relates to the identification of a CCR5 variant (see AW88211), designated CCR5m303, comprising the first two transmembrane domains of wild-type CCR5, but lacking transmembrane domains of wild-type CCR5, but lacking transmembrane domains of the CCR5m303 variant with the wild type CCR5 allele shows a positive correlation with resistance to infection with M-tropic HIV-1 carains, and may indicate slower progression of the disease. The detection of CCR5 variants may be used to identify individuals at lower crisk of infection relative to the general population who, if infected, may exhibit slower progression to ALDS. Probes and primers (see ANV84127-36) are provided for use in diagnostic methods for detecting the presence of such variants. A method is provided for inhibiting HIV-1 infection of a cell expressing the CCR5 receptor. This involves introducing a nucleic acid encoding a CCR5 variant into the cell, thereby reducing the number of functional CCR5 molecules present on the cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; G-protein coupled receptor; G-protein chemokine receptor; HDGNR10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   New CCRS variant protein of the HIV-1 co-receptor - useful in developing resistance of CCRS-expressing cells to {
m HIV-1} infection.
        /note= "corresponds to TGT (Cys) in wild-type CCR5, (Stop) in CCr5m303"
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                                                                                                                                                                                                                                                                                                                                                                          Braun J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human G-protein chemokine receptor HDGNR10 SEQ ID NO:2.
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100.0%; Score 96; DB 2; I
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0;
                                      103. .124 /note= "transmembrane domain 3" 142. .167 /note= "transmembrane domain 4"
                                                                                                                                      236. .260
/note= "transmembrane domain 6"
275. .301
                                                                                                                       domain 5"
                                                                                                                                                                                  /note= "transmembrane domain 7"
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                                                                                                                                                                                                                                                                                                                                           (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
                                                                                                                          "transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 34-35; 55pp; English
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                                                                                                                                                                                                                                                                                 98WO-EP003437.
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                                                                                                        .223
                                                                                                                                                                                                                                                                                                                                                                          Quillent C,
                                                                                                                          'note=
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-059835/05.
N-PSDB; AAV84126.
 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 352 AA;
                                                                                                                                                                                                                     WO9854317-A1
                                                                                                                                                                                                                                                                                 29-MAY-1998;
                                                                                                                                                                                                                                                                                                               30-MAY-1997;
                                                                                                                                                                                                                                                     03-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                            Beretta A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185
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                                                                                                                                                                                                                                                                                                                                                                                                                      This protein sequence comprises of a novel human macrophage-selective CC chemokine receptor that has been designated CCR5. The sequence was deduced from an isolated DNA clone (see APT/620). An Ala127Leu variant (see WA38810 of CCR5 as a slow identified. The susceptibility of human macrophages to HIV infection depends on cell surface expression of CD4 protein coupled cell surface molecules. The susceptibility of for protein coupled cell surface molecules. It plays an essential role in the membrane fusion step of infection by some HIV isolates. The establishment of stable, non-human cell lines and transgenic mammals having cells that coexpress human CD4 and CCR5 provides valuable tools for research of HIV infection. Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding agents capable of blocking membrane fusion between HIV and target cells represent potential anti-HIV therapeutics for macrophage tropic strains
                                                                                                                                                                                                                                                                                                                                              CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;
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                                                                                                                                                                                                                                                     Murphy PM;
261. .276
/note= "extracellular loop-3 (Claim 19)"
77. .300
/label= VII
/note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                   Berger EA, Alkhatib G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "transmembrane domain 2"
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                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                           Claim 68; Fig 1C; 70pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SOYOFWKNFQTLKIVILG 18
                                                                                                                                                                                                                                                                                                                                                               between HIV and a target cell
                                                                                                                                                           97WO-US009586.
                                                                                                                                                                                         96US-0018508P
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/note= "
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Broder CC, Kennedy PE;
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Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT76920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene therapy;
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Domain
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Gaps

Homo sapiens.

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The present sequence represents a human G-protein chemokine receptor designated HDGNR10 polymucleotides are useful in methods of screening for compounds which bind to and either: (1) activate the HDGNR10 polypeprides causing stimulation of haematopoiesis, wound healing, coagulation, and angiogenesis; treatment of solid tumours, chronic infections, leukaemia, T-cell mediated autoimmune diseases, parastic infections, psoriasis, and to stimulate growth factor activity, or (2) inhibit activation of the HDGNR10 polypeptides which is useful for preventing and/or treating allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histamine and immunoglobulin B-mediated allergic reactions, prostaglandin-independent fever, bone marrow failure, silicosis, sarcoidosis, rheumatois arbhits shock and hyper-eosinophilia syndrome. The polymucleotides are also useful for diagnostic assays for detecting the polypeptides and for detecting an nucleic acid sequences encoding the polypeptides and for detecting an altered level of the soluble form of the receptor polypeptides. The polymucleotides are also useful for in vituro purposes related to micro polymolectics securicity for in vituro purposes related to scientific research, synthesis of DNA and manufacture of DNA vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, receptor; DC-SIGN, dendritic cell; T lymphocyte; HIV; gpl20;
C-type lectin; ICAM3; HIV entry; T cell; macrophage; HIV infection; CCR5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acid encoding human G-protein chemokine receptor useful for diagnostic assays, scientific research and screening for compounds which bind to and activate or inhibit activation of the receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
diagnosis; haematopoiesis; wound healing; coagulation; angiogenesis;
                    tumour, infection, leukaemia, psoriasis, allergy, r-cell mediated autoimmune disease, atherogenesis, anaphylaxis, inflammation, allergic reaction, sillcosis, sarcoidosis, rheumatoid arthritis, hyper-eosinophilia syndrome.
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nes 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAZ91481.
                                                                                                                                                                                                                                                                                                                                                          Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 352 AA;
                                                                                                                                                                                                                                        06-JUN-1995;
                                                                                                                                                                                                                                                                              06-JUN-1995;
                                                                                                                                                           US6025154-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; yctostatic; immunosuppressive; nootropic; neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcona; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative collitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.
                                                                                                                                                                                                                                                                                                                   An antibody for the treatment or prevention of HIV-infection comprises a gpl20 portion which binds to DC-SIGN or is exposed upon gpl20 binding of DC-SIGN due to concomitant conformational change.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 352;
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100.0%; Pred. No. 8.9e-07;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                              Geijtenbeek T;

    .36
    /label= Extracellular_domain

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                                                                                                                                                                                                                                            Van Kooyk Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE07046 standard; protein; 352 AA.
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                                                                                                              28-FEB-2001; 2001WO-US006322.
                                                                                                                                                  02-MAR-2000; 2000US-00517605.
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                                                                                                                                                                                      (UYNY ) UNIV NEW YORK STATE.
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Best Local Similarity 100.
Matches 18, Conservative
                                                                                                                                                                                                                                              Kwon D,
                                                                                                                                                                                                                                                                                WPI; 2001-602565/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 352 AA;
                                      WO200164752-A2
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                                                                          07-SEP-2001
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label= Transmembrane domain

Domain Domain

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The invention relates to human G-protein chemokine receptor (CCR5) HDGNR10 polypeptides and polymuclectides. CCR5 HDGNR10 antibodies are useful for treating, preventing or ameliorating a disease or disorder associated with inflammation, defective or aberrant chemotaxis of immune cells, HIV infection (such as Pheumocystis carini; pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen presenting cell interaction. The disease or disorder may also be an infections disease (e.g. a viral infection such as an early stage HIV infection, a cytomegalovirus infection, or a poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The disease or disorder may be associated with aberrant CCR5 expression, lack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleic acid encoding a human G-protein chemokine receptor (CCRS) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
                                                         59. 67
/label= Intracellular_loop_1
68. 88
/label= Transmembrane_domain
/note= "Segment 2"
                                                                                                                                                                                                                                                                                                                                                                                                                 .87. .305
|label= Transmembrane_domain
|note= "Segment 7"
                                                                                                                                                                  label= Transmembrane_domain
note= "Segment 3"
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| Jabel = Transmembrane_domain
                                                                                                                                                                                                                                                                                   .96. .223
|Tabel= Transmembrane_domain
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| label= Transmembrane_domain
note= "Segment 6"
                                                                                                                                                                                                                                                                                                                                                                                       61. .274 [label= Extracellular_loop_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Intracellular domain
                       17. .58
|label= Transmembrane_domain
                                                                                                                                          Extracellular_loop_1
                                                                                                                                                                                                        label= Intracellular loop 2
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                                                  "Segment 1"
                                                                                                                                                                                                                                                                                                              note= "Segment 5
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                                                                                                                                                                                                                                             note= "Segment
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09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
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/label= Ex
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'label= In
                                                                                                                           19. .102
|Jabel= E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        352
                                                    note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-488966/53.
N-PSDB; AAD13282.
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of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein is used as a food additive or preservative to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists are also useful in the diagnosis, treatment and prevention of cancer (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract, liver, lung, urogenital); immune disorders (Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's histosa, multiple sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular disorders (Mpocardial ischaemias) and wound healing. The present sequence is human CCR5 HDGNR10 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostetic; immunosuppressive; nootropic; neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.
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                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE07048 standard; protein; 352
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09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
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                                                                                                                                                                                                                                                                                                                                                       18; Conservative
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N-PSDB; AAD13299.
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Best Local Similarity
                                                                                                                                                                                                                                                                         Sequence 352 AA;
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cells, HIV infection (Such as Pneumocystic carinii pneumonia or Kaposi's cells, HIV infection (Such as Pneumocystic carinii pneumonia or Kaposi's carcoma) or defective or aberrant -cell antigen presenting cell interaction. The disease or disorder may also be an infectious disease (e.g. a viral infection, or a poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The disease or disorder may be associated with aberrant CCR5 expression, lack of CCR5 function. aberrant CCR5 ligand expression, or lack of CCR5 ligand function. CCR5 HOCKNIO procein is used as a food additive or preservative to increase or decrease storage capabilities. CCR5 HDGNRIO DNA, protein, antibodies, agonists and antagonists are also useful in the disease in autoimmune disorders and prevention of cancer (breast, ovary, adrenal diand, bone, bone marrow, gastrointestinal tract, liver, lung, cropmised in autoimmune thyroiditis, disease, allergies, autoimmune thyroiditis, disease, allergies, autoimmune thyroiditis, disease, allergies, rheumatoid arthritis and ulcerative colitis); cardiovascular disorders (Myocardial isohaemias) and wound healing. The present sequence is human CCR5 HDGNRIO protein Sequence 352 AA; \$

100.0%; Score 96; DB 4; Length 352; 100.0%; Pred. No. 8.9e-07; 0; Indels Mismatches 185 SQYQFWKNFQTLKIVILG 202 . 1 SQYOFWKNFQTLKIVILG 18 Conservative Local Similarity Les 18; Conserv Query Match Matches Dp

AAG80111 standard; protein; 352 AAG801:

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AAG80111;

(first entry)

17-JAN-2002

Human CCR5 protein.

Chemokine, tumour diagnosis, colorectal, prostatic, organ rejection, inflammation, autoimmune disease, metastasis, bronchial asthma, lupus, chronic bowel inflammation, rheumatoid arthritis, cytostatic, antiinflammatory, antiasthmatic, immunosuppressive, dermatological, antirheumatic; antiarthritic.

Homo sapiens

WO200172830-A2.

04-OCT-2001,

02-APR-2001; 2001WO-EP003708.

31-MAR-2000; 2000DE-01016013.

IPF PHARM GMBH. FORSSMANN U.

(IPFP-) IPF (FORS/) FORS

Spodsberg N; Heitland A, Forssmann W, Adermann K,

WPI; 2001-626256/72.

Diagnostic agent containing two or more receptor-specific ligands, useful for detecring tumors, inflammation etc., also therapeutic use of ligand inhibitors.

Disclosure, Page 10; 26pp; German.

at least in This invention describes a novel diagnostic agent (A) comprising two different ligands (I) for receptors (II) that are implicated

or prostatic), organ rejection, inflammation and autoimmune diseases.
Also inhibitors of (I) are used therapeutically against tumors (and their metastases), inflammation (particularly bronchial asthma or chronic bowell inflammation), or autoimmune diseases (rheumatcoid arthritis or lupus), where the (cardio) vascular, lymphatic, respiratory, nervous, digestive, endocrine, motor or urogenital systems or skin are affected, and bone marrow diseases. The products of the invention are chemokine derivatives which have cytostatic, antiinflammatory, antisthmatic, chemokine derivatives immunosuppressive, dermatological, antitheumatic, antiarthritic. Chemokines act on specific tumor and inflammatory cells through a conscellation of chemokine receptors (CR), which control migration and proliferation of these cells. AAG80045 AAG80128 represent human chemokine (A) are used for the diagnosis of tumors (especially colorectal fragments used to illustrate the method of the invention 888888888888888888888

Sequence 352 AA;

Gaps . 0 Length 352; 0; Indels 100.0%; Score 96; DB 4; I 100.0%; Pred. No. 8.9e-07; Live 0; Mismatches 0; Local Similarity 100. Query Match Best Loca Matches

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185 SQYQFWKNFQTLKIVILG 202 1 SOYOFWKNFOTLKIVILG 18 à

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Gaps

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RESULT 13 AAE0432 AAE04321;

AAE04321 standard; protein; 352 AA

(first entry) 04-SEP-2001

Human; transformed mammalian cell; CD4; reporter gene; translocation; human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy; chemokine receptor; CKR; cellular dysfunction; HIV infection; cofactor; CC-CKR-5; envelope glycoprotein; anti-HIV. Human chemokine receptor (CKR), CC-CKR-5 related protein #2.

Homo sapiens.

US6258527-B1

10-JUL-2001.

97US-00861105 21-MAY-1997; 96US-0017157P. 96US-0020043P. 97US-00858660. 20-MAY-1996; 19-JUN-1996; 19-MAY-1997;

(AARO-) AARON DIAMOND AIDS RES CENT. (UYNY) UNIV NEW YORK STATE.

Ellmeier W, Landau NR, Littman DR,

Deng H,

Liu R;

WPI; 2001-417127/44. N-PSDB; AAD08577 mammalian cell (I) that contains a CD4 gene, reporter gene for identification of drugs and antibodies for treatment of Transformed and HIV LTR

Disclosure; Col 47-50; 37pp; English.

The present invention relates to a transformed mammalian cell that contains a gene encoding CD4, a construct encoding a reporter gene under the regulation of an human immuno deficiency virus (HIV) long terminal repeat (LTR) and that has been transduced with a vector encoding a human chemokine receptor (CKR) where the CD4 and the CKR are present on the cell surface of transformed mammalian cell. The invention is useful for

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AAE07039 standard; protein; 352 AA.
                                                                                                          WO200158915-A2
                                                                                                                            16-AUG-2001
                      Domain
                                            Domain
                                                                            Domain
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identifying drugs or antibodies that interfere with the translocation of HIV into transformed mammalian cell or for identifying a human chemokine receptor that facilitates the infection of a particular HIV strain into the transformed mammalian cell. Compounds identified can be used to tract cellular dysfunction and to prevent or combat HIV infection. The present ccludar dysfunction and to prevent or combat HIV infection. The present CC-CKR-5 is the principal cofactor for entry mediated by the envelope glycoproteins of primary macrophage-tropic strains of HIV-1
                                                                                                                                                                                                                                                                                                                       Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostatic; immunosuppressive; nootropic; neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative collitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.
                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                      Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.
                                                                                                                      Length 352;
                                                                                                                                          0; Indels
                                                                                                                       100.0%; Score 96; DB 4; I
100.0%; Pred. No. 8.9e-07;
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/label= Transmembrane_domain
/note= "Segment 3"
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/label= Transmembrane_domain
/note= "Segment 5"
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[label= Transmembrane_domain
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/label= Extracellular_loop_2
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/label= Intracellular_loop_3
236. .260
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|Tabel= Extracellular_domain
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/label= Transmembrane_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane domain
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                                                                                                                                          Mismatches
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                                                                                                                                                                 1 SOYOFWKNFOTLKIVILG 18
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/label= T
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                                                                                                                                           Conservative
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/label= 7
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                                                                                                                               Local Similarity
es 18; Conserv
                                                                                                   Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                               AAE07037;
                                                                                                                        Query Match
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Matches
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The present sequence is human G-protein chemokine receptor (CCRS) HDGNR10 protein. CCRS HDGNR10 cDNA is included in ATCC Deposit No: 97183. CCR5 HDGNR10 antibodies are useful for treating, preventing or amaliorating a disease or disorder associated with inflammation, defective or aberrant chemotaxis of immune cells, HTV infection (such as Pneumocystis carini premotaxis of immune cells. HTV infection (such as Pneumocystis carini presenting cell interaction. The disease or disorder may also be an infectious disease (e.g. a viral infection such as an early stage HIV infection, a cytomegalovirus infection, or a poxvirus infection, an automane disease (e.g. rheumatoid arthritis) or a neurodegenerative containmune disease or disorder may be associated with aberrant CCRS disorder. The disease or disorder may be associated with aberrant CCRS cxpression, lack of CCRS function. CCRS HDGNR10 protein is used as a food additive or preservative to increase or decrease storage capabilities. CCRS HDGNR10 DNA are useful for chromosome identification and in gene conternation or such an early adrenal gland, bone, bone marrow, gastrointestinal tract, breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract, cubic mune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, collitis), cardiovascular disorders (Mayocardial ischaemias) and wound colling collitis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid encoding a human G-protein chemokine receptor (CCRS) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.
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label= Transmembrane_domain
note= "Segment 6"
161. .274
                                                                                                                                                                                                                                                   306, .352
/label= Intracellular_domain
                                                                             261. .274
/label= Extracellular_loop_3
                                                                                                                                        187. .305
| Transmembrane_domain
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09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosen CA, Roschke V,
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Best Local Similarity
Matches 18; Conserv
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AAE07039;
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16-OCT-2001 (first entry)

Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.

human immunodeficiency virus; antimicrobial; vasodilator; valnerary; cytostatic; immunosuppressive; nootropic; neuroprotective; gene therapy; neurodegenerative disorder; Raposi's sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic namemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crobin's disease; wound healing; cardiovascular disorder; myocardial ischaemia. Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;

Homo sapiens.

WO200158915-A2,

16-AUG-2001,

09-FEB-2001; 2001WO-US004152.

09-FEB-2000; 2000US-0181258P. 09-MAR-2000; 2000US-0187999P. 22-SEP-2000; 2000US-0234336P.

(HUMA-) HUMAN GENOME SCI INC

Li Y, Ruben SM; Roschke V, Rosen CA,

WPI; 2001-488965/53. N-PSDB; AAD13198.

Isolated nucleic acid encoding a human G-protein chemokine receptor (CCRS) HDGNRIO polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.

Example 40; Page 486-487; 495pp; English.

The present sequence is human d-protein chemokine receptor (CCR5) HDGNR10

C protein. CCR5 HDGNR10 antibodies are useful for treating, preventing or
ameliorating a disease or disorder associated with inflammation,

C defective or aberrant chemotaxis of immune cells, HTV infection (such as
C decrein antigen presenting cell interaction. The disease or
C disorder may also be an infectious disease (e.g. a viral infection such
cs an early stage HIV infection, a dytomegalovirus infection, or a
CC disorder may also be an infection, a dytomegalovirus infection, or a
CC disorder may also be an intection, a dytomegalovirus infection, or a
CC disorder may also be an intection, a dytomegalovirus infection, or a
CC disorder may be associated
CC a neurodegenerative disorder. The disease or disorder may be associated
CC with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5
CC ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein
CC is used as a food additive or preservative to increase or decrease
CC storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome
CC identification and in gene therapy. CCR5 HDGNR10 DNA, protein,
CC antibodies, agonists and antagonists are also useful in the diagnosis,
CC treatment and prevention of cancer (breast, ovary, adrenal gland, bone,
CC disorders (Addison's disease, allergies, autoimmune haemolytic anaemia,
CC disorders (Addison's disease, allergies, autoimmune haemolytic anaemia,
CC disorders (myocardial ischaemias) and wound healing

Sequence 352 AA;

ö 100.0%; Score 96; DB 4; Length 352; 100.0%; Pred. No. 8.9e-07; tive 0; Mismatches 0; Indels Conservative Query Match Best Local Similarity Matches 18; Conserva

1 SQYQFWKNFQTLKIVILG 18

185 SQYQFWKNFQTLKIVILG 202

RESULT 16 AAB46858

AAB46858 standard; protein; 352 AA

(revised) 02-AUG-2001 04-MAY-2001 AAB46858;

Human HDGNR10 protein.

(first entry)

HDGNR10; human; G-protein chemokine receptor; antiinflammatory; immunosuppressive; cylamurocagulant; antialregic; immunosuppressive; cytostatic; antiparatitic; antialregic; antirheumatic; antiarthritic; vasotropic; gne therapy; haematopolesis; wound healing; coagulation; vasotropic; gne therapy; haematopolesis; wound healing; coagulation; anapidegenesis; old tumnour; infection; leukemia; growth factor activity; r-ceil mediated autoimmune disease; psoriasis; allergy; atherogenesis; anaphylaxis; malignancy; inflammation; histamine; IgE; silicosis; shock; prostaglandin-independent fever; bone marrow failure; sarcoidosis; hyper-eosinophilic syndrome; vulnerary.

Homo sapiens.

US2001000241-A1.

12-APR-2001.

29-NOV-2000; 2000US-00725285

95US-00466343. 98US-00195662. 99US-00339912. 06-JUN-1995; 18-NOV-1998; 25-JUN-1999;

(LIYY/) LI Y. (RUBE/) RUBEN S M.

Li Y, Ruben SM;

WPI; 2001-226317/23. N-PSDB; AAF26390.

New human G-protein chemokine receptor polypeptides and polynucleotides, useful for identifying (ant)agonists to the G-protein chemokine receptor

Claim 1a; Page 15; 22pp; English.

This invention describes a novel receptor polypeptide (1) selected from (1) a fully defined 329 amino acid sequence (II) fully disclosed in the specification, and (ii) a polypeptide encoded by the DNA contained in a plasmid, and fragments, analogs and derivatives of the polypeptide. The products of the invention have antiinflammatory, immunomodulatory, anticoagulant, antiallergic, immunosupressive, vulnerary, cytostatic, antiparastitic, antipocriatic, antiinflammatory, immunomodulatory, continged can be used for gene therapy. The d-protein chemokine activity and can be used for gene therapy. The d-products of the invention can also be used for stimulating haematopoiesis, wound healing, coagulation, and operation of the invention of activate or inhibit activation of (1). The products of the invention can also be used for stimulating haematopoiesis, wound healing, coagulation, and operation of activity and can be used for stimulating solid tumours, chronic infections, psoriasis, and stimulating growth factor activity. HDGNRIO is useful for treating stimulating growth factor activity. HDGNRIO is useful for treating stimulating arowth factor activity. HDGNRIO is useful for treating callergy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histamine and immunoglobulin B (IgB)-mediated allergic reactions, prostaglandin-independent fever, bone marrow fallure, cosinophilic syndrome. (N.B. This record was resubmitted to correct errors in the keyword formatting)

Sequence 352 AA;

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This sequence represents the human CCRS protein sequence. The invention relates to a method for determining whether an agent is capable of modulating the interaction of chemotractic chemokine receptor 5 (CCR5) with gpl20, comprising incubating the agent with CCRS and gpl20 and determining whether the agent modulates the interaction, where gpl20 as sociated with CD4, and where the interaction is a low affinity binding. The method is used to identify an agent capable of modulating the interaction of CCRS with gpl20, an agent identified by the method is used to prepare a pharmaceutical composition for the treatment of a disease or condition associated with CCRS and gpl20 interaction, to treat a subject with a disease or condition associated with CCRS and gpl20 interaction, and for preparing a pharmaceutical for treating human immunodeficiency virus (HIV). It can also be treat anti-inflammatory diseases. The method is commercially useful, amenable to high throughput screening, and cetects interaction of gpl20 with cells expressing only CCR5.
                                                                                                                                                                                                                                                                                                                                                                                                                Determining if an agent can modulate CCR5-gp120 interaction, comprises incubating the agent with CCR5 and gp120 and determining if the agent modulates the interaction.
                                       Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5; human immunodeficiency virus; anti-inflammatory disease; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB82948 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 110; 113pp; English.
                                                                                                                                                                                                                                                                                                                                         Rickett GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 SQYQFWKNFQTLKIVILG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQYQFWKNFQTLKIVILG 18
                                                                                                                                                                                                                       12-JAN-2000; 2000GB-0000659.
12-JAN-2000; 2000GB-0000661.
12-JAN-2000; 2000GB-0000663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human HIV-1 co-receptor CCR5.
                                                                                                                                                                                          03-JAN-2001; 2001EP-00300020
             Human CCR5 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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Best Local Similarity 100...
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                       Dobbs S, Perros M,
                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-477088/52
                                                                                                                                                                                                                                                                                       (PFIZ ) PFIZER LTD (PFIZ ) PFIZER INC
                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAF87099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                            EP1118858-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-DEC-2001
                                                                                                                                                           25-JUL-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying agonists of G protein-coupled receptors (GPCRs) for use in disease treatment, comprises contacting candidate compounds with versions of GPCRs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to G protein-coupled receptors (GPCRs) for which the endogenous ligand has been identified. Non-endogenous constitutively activated versions of known GPCRs are used in the invention for the direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists. Such agonists are useful as therapeutic agents for diseases or disorders associated with GPCRs. The present sequence is a non-endogenous version of a known human GPCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                              Gaps
                                                                                                                                                                                                                                                                                                                        Human, G protein-coupled receptor; GPCR; non-endogenous; mutant; constitutively activated GPCR; agonist; disease.
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             100.0%; Score 96; DB 4; Length 352;
100.0%; Pred. No. 8.9e-07;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 96; DB 4; Length 352; Best Local Similarity 100.0%; Pred. No. 8.9e-07; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                          Non-endogenous human GPCR protein, SEQ ID NO: 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 277-278; 394pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lin I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB83354 standard, protein; 352 AA
                                                                                                                                                                                               ABB56342 standard; protein; 352 AA.
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                                                                                                                185 SOYOFWKNFOTLKIVILG 202
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                                                                                 1 SOYOFWKNFOTLKIVILG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liaw CW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-APR-2001; 2001WO-US011098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-APR-2000; 2000US-0195747P
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                                                                                                                                                                                                                                                             (first entry)
                 Query Match
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AREN-) ARENA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lehmann-Bruinsma K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-648759/74.
N-PSDB; ABI97978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                          WO200177172-A2.
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                               18-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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                                                                                                                                                                                                                              ABB56342;
                                                                                                                                                              RESULT 18
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                                                      Gaps
                                                      .
0
100.0%; Score 96; DB 4; Length 352; 100.0%; Pred. No. 8.9e-07; tive 0; Mismatches 0; Indels
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The present sequence is that of human HIV-1 co-receptor CCR5. Amino acids 2-18 in the N-terminal region of CCR5 comprise an HIV-1 gpl20-binding 2-18 in the N-terminal region of CCR5 comprise an HIV-1 gpl20-binding 2.18 HIV-1 gpl20. Post-translational sulfation of the interaction between CCR5 and HIV-1 gpl20. Post-translational sulfation of the tyrosine residues in the CCR5 N-terminal is required for gpl20 binding and may critically modulate the susceptibility of target cells to HIV-1 infection in vivo. The invention provides claimed sulfated peptides (see AAB8294) that are based on the CCR5 N-terminal region and which are effective for inhibiting HIV-1 binding to CCR5. These oppides are used in claimed methods of inhibiting HIV infection of CD4+ cells, of preventing CD4+ cells are infected with HIV, of treating a subject, whose CD4+ cells are infected with HIV, and of identifying an agent which inhibits binding of a CCR5 ligand to a CCR5 receptor. The methods may be carried out in a subject, especially a human, infected (therapeutic method), not infected with, but has been exposed to, HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel compounds comprising specific amino acids within CCR5 (HIV 1 coreceptor) amino terminal domain including negatively charged and two sulfated tyrosine residues is useful for treating HIV infection in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; immune call chemotaxis; autoimmune disease; rheumatoid arthritis; neurodegeneration; viral infection; Kaposi sarcoma; cancer; hyperproliferative disease; neurological disease; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 96; DB 4; Length 352; Best Local Similarity 100.0%; Pred. No. 8.9e-07; Matches 18; Conservative 0; Mismatches 0; Indels
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    18 // note = "binds to HIV-1 gp120"

                                                                                                                                                                                                                                                                                        (PROG-) PROGENICS PHARM INC. (AARO-) AARON DIAMOND AIDS RES CENT.
                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU97150 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 30; 163pp; English.
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                                                                                                                                                                                                            29-FEB-2000; 2000US-0185657P.
19-MAY-2000; 2000US-0205839P.
07-FEB-2001; 2001US-0267231P.
                                                                                                                                                                       28-FEB-2001; 2001WO-US006699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                  Dragic I, Olson WC;
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-611273/70.
                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAH26903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 352 AA;
                                                                                            WO200164710-A2
                  Key
Binding-site
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                                                                                                                                    07-SEP-2001
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The present invention relates to the isolation of a novel human G-protein chemokine receptor (CCR5) designated HDGNR10, and polynucleotide sequences encoding it. The invention also describes antibodies that bind human G-protein chemokine receptor (CCR5) HDGNR10 and polynucleotide chuman G-protein chemokine receptor (CCR5) HDGNR10 and polynucleotide sequences encoding the antibodies. The antibodies are useful for treating or preventing inflammation, defective or aberrant chemotaxis of immune cells and T-cell/antigen-presenting cell interactions, infections and autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral infections depecially early-scage human immune deficiency virus (HIV), cytomegalovirus or pox virus infections, Kapoei sarcoma, or conditions associated with aberrant or deficient expression of the CCR5 receptor or its ligands. The antibodies are also useful to determine CCR5 expression, e.g. for diagnosis, prognosis and monitoring of accer and other combinant receptor, and in the treatment of a wide range of diseases such as infectious diseases (e.g. influenza), neurological diseases (e.g. combinant requence represents human G-protein chemokine receptor (CCR5) HDGNR10 er ecceptor (CCR5) HDGNR10 #10.

Parkinson's diseases (e.g. influenza), neurological diseases (e.g. HDGNR10 #1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding an antibody specific for the G-protein chemokine receptor CCR5, useful for treatment and diagnosis of e.g. inflammation.
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100.0%; Pred. No. 8.9e-07;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human G-protein chemokine receptor (CCR5) HDGNR10 #2.
                                                                                                                                                                                                                                                                                                                                  Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU97152 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 61; Fig 1; 180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 SÓYOFWKNFOTLKIVILG 202
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                                                                                                                                                     09-FEB-2000; 2000US-0181258P.
09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
                                                                                                                09-FEB-2001; 2001US-00779879.
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                  Rosen CA, Roschke V,
                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-434754/46.
                                                                                                                                                                                                                                (ROSE/) ROSEN C A. (ROSC/) ROSCHKE V.
                                                                                                                                                                                                                                                                      (LIYY/) LI Y.
(RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ABK51853.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 352 AA;
                                     US2002048786-A1
Homo sapiens.
                                                                          25-APR-2002
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human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome; drug screening; identification; variant.
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                                                                                                                                                                                                                                                                                                                                        See RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 SQYQFWKNFQTLKIVILG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SOYOFWKNFOTLKIVILG 18
                                                                                                                                                                                                                       21-MAR-2000; 2000US-0190946F.
21-MAR-2000; 2000US-0190996F.
21-MAR-2000; 2000US-0191299F.
20-MAR-2001; 2001US-00813613.
20-MAR-2001; 2001US-00813653.
                                                                                                                                                                                              21-MAR-2001; 2001WO-US009155.
                                                                                                                                                                                                                                                                                                               CONS-) CONSENSUS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                      Wilson CJ,
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-010610/01.
                                                                              Misc-difference 55
                                                                                                        Misc-difference 58
                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABA02318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 352 AA;
                                                                                                                                              WO200171346-A2
                                           Homo sapiens
                                                                                                                                                                        27-SEP-2001
                                                                                                                                                                                                                                                                                                                                          Westor JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM52828;
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AAM52828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding an antibody specific for the G-protein chemokine receptor CCRS, useful for treatment and diagnosis of e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 96; DB 5; Length 352; 100.0%; Pred. No. 8.9e-07;
     hyperproliferative disease; neurological disease; receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 165-166; 180pp; English
                                                                                                                                                                                                                                                     Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM52829 standard; protein; 352 AA
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                                                                                                                                                                                                                                                     Li Y,
                                                                                                                                              09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
                                                                                                           09-FEB-2001; 2001US-00779879
                                                                                                                                     09-FEB-2000; 2000US-0181258P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human CCR5 Gln 55 variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18; Conservative
                                                                                                                                                                                                                                                      Rosen CA, Roschke V,
                                                                                                                                                                                                                                                                             WPI; 2002-434754/46.
N-PSDB; ABK51870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                      (ROSE/) ROSEN C A. (ROSC/) ROSCHKE V.
                                                                                                                                                                                                                            RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 352 AA;
                                                           JS2002048786-A1
                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                            inflammation
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                                                                                                                                                                                                  (ROSC/) |
(LIYY/) |
(RUBE/) |
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AAM52829
ID AAM52X
XX
AC AAM52X
XX
DT 22-FEI
XX
DB Human
XX
KW CCR5;
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The invention relates to a method for identifying a binding compound for chemokine receptor 5 (CCR5). The method involves screening a library of test molecules (particularly peptides) with immobilised CCR5, and then identifying those molecules which bind. The invention also relates to identifying those molecules which bind. The invention also relates to complete a identifying consensus motifs for CCR5-binding peptides, a transfer vector encoding tagged CCR5, a computer-aided methods for transfer vector encoding tagged CCR5, a computer-aided methods for a computer aided drug screening assay that utilises the three-dimensional structure of CCR5. Compounds identified using the methods of the invention are useful for treating or preventing HJV (human structure of CCR5. Compounds identified using the methods of the invention may also be used to invention in a patient. The methods of the interaction of CCR5. The present containing and the interaction of CCR5. The present sequence represents a naturally courring variant of human CCR5. The present sequence represents a naturally a leucine, at position 55 the invention 55 there is a glutamine, rather than a leucine, at position 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                         note= "Glu replaces wild-type Leu; encoded by CTG"
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Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tan Hehir CA;
                                                                                                                                                                                                       /note= "Encoded by AGC"
Location/Qualifiers
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Human; G-protein chemokine receptor; HDGNR10; CCR5 receptor;

99US-00339912, 95US-00466343

25-JUN-1999; 06-JUN-1995;

25-JUL-2002

(RUBE/) RUBEN S M.

(TIXX/) TI

antipyretic, receptor

Homo sapiens.

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haematopolesis, wound healing; coagulation; angiogenesis; solid tumour; chronic infection; leukaemia; T-cell mediated autoimmune disease; parasitic infection; leukaemia; T-cell mediated autoimmune disease; atheritic infection; psoriasis; growth factor activity; allergy; atherogenesis; anaphylaxis; malignancy; inflammation; histamine; immunoglobulin E; IgE-mediated allergic reaction; sarcoidosis; prostaglandin-independent fever; bone marrow failure; shock; rheumatoid arthritis; hyper-cosinophilic syndrome; cytostatic; immunosuppressive; antiparastic; antiparastic; antiparastic; antiparastic; antiparateriosclerotic; antinflammatory; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human G-protein chemokine receptor polypeptide useful for identifying modulators for stimulating hematopoiesis, wound healing, leukemia, for treating allergy, rheumatoid arthritis, shock and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-690494/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li Y, Ruben SM;
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     BXXXE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for identifying a binding compound for CC chemokine receptor 5 (CCR5). The method involves screening a library CC chemokine receptor 5 (CCR5). The method involves screening a library of test molecules (particularly peptides) with immobilised CCR5, and then identifying those molecules which bind. The invention also relates to CCR5-binding molecules identified using the method of the invention, methods for identifying consensus motifs for CCR5-binding peptides, a transfer vector encoding tagged CCR5, a computer-aided methods for determining that relative binding affinity of a test molecule to CCR5 and a computer aided drug screening assay that utilises the three-dimensional structure of CCR5. Compounds identified using the methods of the invention are useful for treating or preventing HIV (human immunodeficiency virus) infection or AIDS (acquired immunodeficiency syndrome) in a patient. The methods of the invention may also be used to identify agonists or antagonists of the interaction of CCR5. The present sequence represents human CCR5.
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                                                         CCR5; CC chemokine receptor 5; human; HIV infection; human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome; drug screening; identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying CC chemokine receptor 5 binding compound for treating AIDS, comprises binding a molecule from library to a molecule having binding property corresponding to CCR5 and identifying bound molecule.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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100.0%; Pred. No. 8.9e-07;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tan Hehir CA;
                      Human CC chemokine receptor 5 (CCR5).
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                                                                                                                                                                                                                                                                                                                                                                                                                21-WAR-2000; 2000US-0190996P.
21-WAR-2000; 2000US-019129P.
20-WAR-2001; 2001US-00813448.
20-WAR-2001; 2001US-00813651.
20-WAR-2001; 2001US-00813653.
                                                                                                                                                                                                                                                                                                                                     21-MAR-2001; 2001WO-US009155
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Best Local Similarity 100.
Matches 18; Conservative
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N-PSDB; ABA02317.
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                                                                                                                                                                                Homo sapiens.
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ABG70597
NAME OF THE PROPERTY OF THE PR
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leukemia, for tr research agents.

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The present invention relates to the isolation of human G-protein chemokine receptor, HDGNR10 (CCRS receptor), and the polynucleotide sequence acquence encoding it. HDGNR10 polypeptide and the polynucleotide sequences are or useful for diagnoshing a disease or a susceptibility to a disease or classes of the polynucleotide sequences are or useful for identifying modulators for stimulating haematopoiesis, wound healing, coagulation, angiogenesis, to treat solid tumours, chronic infections, leukaemia, Tocall mediated autoimmune diseases, parasitic infections, psoriasis, or preventing and/or treating allergy, atherogenesis, anaphylaxis, preventing and/or treating allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histamine and immunoglobulin E (IgE)-mediated allergic reactions, protaglandin-independent fever, bone marrow failure, sarcoidosis, rheumatoid arthritis, shock and hyperessinophilic syndrome. Polynucleotide sequences encoding HDGNR10 can be used in gnee therapy to treat conditions related to underexpression of HDGNR10. The present sequence represents human G-protein chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Claim 7; Fig 1; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SOYOFWKNFOTLKIVILG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor, HDGNR10
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Matches
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Human G-protein chemokine receptor, HDGNR10.

(first entry)

03-DEC-2002

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Immunoglobulin, variable heavy chain, variable light chain, human, G-protein chemokine receptor; CCR5, HDGNR10; cancer; inflammation; immunologic deficiency syndrome; blood protein disorder; nephritis; ataxia telangiectasia; endorcaxia lethality; inflammatory bowel disease; histocytosis; chemotaxis; infectious disease; autoimmune disease; hadison's disease; dermatitis; rheumatoid arthritis; allergy; neurodegenerative disorder; viral infection; poxvirus infection; HIV; human immunodeficiency viral; cytomegalovirus; Kaposi's sarcoma; pheumocystis carnii infection; cardiovascular disorder; atherosclerosis;
Human immunoglobulin variable heavy domain #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lymphocytopenia
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WO200264612-A2 Homo sapiens.

22-AUG-2002

08-FEB-2002; 2002WO-US003634 09-FEB-2001; 2001US-00779880

09-FEB-2001; 2001WO-US004153. 12-UUN-2001; 2001US-0297257P. 08-AUG-2001; 2001US-0310478P. 12-OCT-2001; 2001US-03447P.

(HUMA-) HUMAN GENOME SCI INC.

Roschke V, Rosen CA, Ruben SM;

WPI; 2002-643455/69. N-PSDB; ABS68606 New human G-protein Chemokine Receptor gene (HDGNR10) useful for treating, preventing, ameliorating or monitoring diseases or disorders associated with aberrant expression of HDGNR10 e.g. cancer.

Example 55; Fig 4; 562pp; English.

The invention describes an isolated polynucleotide encoding a first antibody at least 95-100% identical to a second antibody consisting of antibody at least 95-100% identical to a second antibody consisting of antibody at least 95-100% identical to a second antibody consisting of a variable heavy (VH) or variable light (VL) domain of thee antibody expressed by a hybridoma cell line consisting of XF3.5F1, XF11.F8, XF3.662, XF3.661, XF2.3C9.6, XF2.3C9.6, XF2.7C8.36110 or XF3.7C8.18B2, XF3.7C9.18B2, XF3. sequence of humagainst HDGNR10

Sequence 352 AA;

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                                                            0; Gaps
Query Match 100.0%; Score 96; DB 5; Length 352; Best Local Similarity 100.0%; Pred. No. 8.9e-07; Matches 18; Conservative 0; Mismatches 0; Indels
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Immunoglobulin; variable heavy chain; variable light chain; human; G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation; immunologic deficiency syndrome; blood protein disorder; nephritis; ataxia telanglectasia; endotoxin lethality; inflammatory bowel disease; histiocytosis; chemotaxis; infectious disease; autoimmune disease; Addison's disease; dermatitis; rheumatoid arthritis; allergy, neurodegenerative disorder; viral infection; poxvirus infection; HIV; human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma; pneumocystis carnii infection; cardiovascular disorder; atherosclerosis;
                                                                                                            Human G-protein chemokine receptor (CCR5) HDGNR10 #1.
                                                       ABG92880 standard; protein; 352 AA.
185 SQYQFWKNFQTLKIVILG 202
                                                                                            19-NOV-2002 (first entry)
                                                                                                                                                                                                                       lymphocytopenia
                                                                                                                                                                                                                                         Homo sapiens.
                                                                           ABG92880;
                                      RESULT 26
                                                 ABG92880
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09-FEB-2001; 2001WO-US004153. 12-JUN-2001; 2001US-0297257P. 08-AUG-2001; 2001US-0310458P. 08-FEB-2002; 2002WO-US003634 09-FEB-2001; 2001US-00779880 21-DEC-2001; 2001US-0341725P. (HUMA-) HUMAN GENOME SCI INC. 12-OCT-2001; 2001US-0328447P

WO200264612-A2.

22-AUG-2002.

Roschke V, Rosen CA, Ruben SM;

WPI; 2002-643455/69. N-PSDB; ABS68553. New human G-protein Chemokine Receptor gene (HDGNR10) useful for treating, preventing, ameliorating or monitoring diseases or disorders associated with aberrant expression of HDGNR10 e.g. cancer.

Disclosure, Fig 1A-B; 562pp; English.

The invention describes an isolated polynucleotide encoding a first antibody at least 95-100% identical to a second antibody consisting of antibody at least 95-100% identical to a second antibody consisting of a maino acid sequence comprising at least one, two or three CDR regions of a variable heavy (VH) or variable light (VL) domain of the antibody conversed by a hybridoma cell line consisting of XB3.5F1, XF11.1F8, CC XF2.3C2, XF2.1G2, XF2.7C8.7D5, XF2.7C8.1D5, XF2.7

72

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Gaps

.. 0

Indels

Pred. No. 8.9e-07; Mismatches 0;

ilarity 100.0%; F Conservative 0;

Best Local Similarity Matches 18; Conser

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us-10-084-813-13.rag

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The invention relates to human G-protein chemokine receptor (CCR5), HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5 antibodies are used for the treatment or prevention of inflammation, defective or aberrant chemotaxis of immune cells or T cell antigenpresenting cell interaction, viral infections (specifically human immune deficiency (including its early stages), cytomegalo or pox viruses), autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis carinii infection, Kaposi's sarcoma or any condition associated with deberrant expression of CCR5 or their ligands. They are also used for the detection, diagnosis, prognosis and monitoring of cancers or other hyperproliferative diseases. The present sequence is human G-protein chemokine receptor (CCR5), HDGNR10 DNA
protein chemokine receptor (CCRS) HDGNR10. This is an amino acid sequence of Human G-protein chemokine receptor (CCRS) HDGNR10 #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10, useful for treatment, prevention and diagnosis of e.g. cancer, also related antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                  Human; G-protein chemokine receptor; CCRS; HDGNR10 protein; cancer;
inflammation; viral infection; autoimmune disease; neurodegeneration;
rheumatoid archirits; Pneumocystis carinii infection; Kaposi's sarcoma;
hyperproliferative disease; receptor.
                                                                                                                   Gaps
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                                                                                    Length 352;
                                                                                                                  0; Indels
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                                                                                100.0%; Score 96; DB 5; I
100.0%; Pred. No. 8.9e-07;
ive 0; Mismatches 0;
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09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
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                                                                       Query Match
Best Local Similarity 100.0
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ROSE/) ROSEN C A.
(ROSC/) ROSCHKE V.
(LIYY/) LI Y.
(RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2002-499674/53.
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N-PSDB; AAD42409.
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                                                 Sequence 352 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10, useful for treatment, prevention and diagnosis of e.g. cancer, also
                                                                                                                                                                                                                         Human, G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer; inflammation; viral infection; autoimmune disease; neurodegeneration; rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma; hyperproliferative disease; receptor.
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                                                                                                                                                                                             Human G-protein chemokine receptor (CCRS), HDGNR10 #2.
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100.0%; Pred. No. 8.9e-07;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 170; 186pp; English.
                                                                                                    AAE25811 standard; protein; 352 AA
               185 SQYQFWKNFQTLKIVILG 202
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18
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09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
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1 SOYOFWKNFOTLKIVILG
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                                                                                                                                                               (first entry)
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Best Local Similarity 100.
Matches 18; Conservative
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(ROSC/) ROSCHKE V.
(LIYY/) LI Y.
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RUBEN S M.
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(RUBE/)
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Length 352;

5, В

100.0%; Score 96;

The invention relates to a novel human 7-transmembrane receptor, HDGNR10, which has been identified as a G-protein chemokine receptor. The dPCR HDGNR10 polypeptide can be expressed by standard recombinant methodology. Compounds that activate or inhibit the receptor polypeptide, optionally expressed from DNA in gene therapy vectors, are used to treat diseases that requires (a) activation of the receptor (e.g. stimulation of haematopoiseis, treatment of solid tumours, T-cell mediated autoimmune diseases, parasitic infections, psoriasis etc.); or (b) inhibition of the receptor (e.g. allergy, inflammation, rheumatoid arthritis, silicosis etc.). The present sequence represents the human HDGNR10 receptor Claim 7; Fig 1; 22pp; English.

Sequence 352 AA;

Gaps . 0 100.0%; Score 96; DB 5; Length 352; 100.0%; Pred. No. 8.9e-07; 0; Indels Mismatches 100.0%; Fr. 18; Conservative Query Match Best Local Similarity Matches 18; Conser

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SOYOFWKNFOTLKIVILG 202 SOYOFWKNFOTLKIVILG 18 185

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ABB08343 standard; protein; 352 ABB08343; ABB08343 LID ABB083 XX ABB08: XX ABB08: XX ABB08: XX DT 18-JUD XX DE Human

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(first entry)

18-JUN-2002

Human chemokine (C-C motif) receptor 5 polypeptide.

Human chemokine C-C motif receptor 5; CCR5; haplotype pair; isogene; single nucleotide polymorphism; SNP; human immunodeficiency virus 1; HIV-1 infection; acquired immunodeficiency syndrome; AIDS; antiviral; genotype; polymorphic variant; transgenic; drug screening; gene therapy; chromosome 3p21

Homo sapiens

Location/Qualifiers label= Leu, /label= Arg, /label= Phe, Key Misc-difference Misc-difference Misc-difference

WO200177125-A2

18-OCT-2001

04-APR-2001; 2001WO-US010708

05-APR-2000; 2000US-0194361P.

(GENA-) GENAISSANCE PHARM INC.

Choi JY, Kliem SE,

WPI; 2002-041282/05

N-PSDB; ABA97318, ABA97319.

New haplotypes of the human chemokine (C-C motif) receptor 5 gene, useful to diagnose and treat diseases associated with its abnormal expression or function, including human immunodeficiency virus-1 infection.

Claim 29; Fig 3; 61pp; English

The present sequence is that of a polypeptide encoded by the human chemokine (C-C motif) receptor 5 (CCR5) gene of the invention (see ABA97318, ABA97318). The specification describes haplotyping the CCR5 cene of an individual by determining if the individual has one of the CCR5 haplotypes or haplotype pairs fully defined in the specification.

CC CR5 haplotypes or haplotype pairs fully defined in the specification.

The specification also describes an isolated polymucleotide comprising a nucleotide sequence which is a polymorphic variant of the reference CCR5 in the specification and its encoded polypeptide. The methods of the interpretation are useful to diagnose and develop treatment for diseases associated with abnormal expression or function of the gene. The CCR5 isogenes and the screened compounds are useful for treating human immunodeficiency virus (HIY)-1 infection and the progression to acquired immunodeficiency syndrome (AIDS). The invention has antiviral applications. The specification describes genotyping the CCR5 gene of an individual; identifying an association between a trait and a haplotype or individual; identifying an association between a trait and a haplotype or composition comprising a genotyping oligomucleotide for detecting a CCR5 polymorphism, a recombinant non-human organism transformed with CCR5 polymucleotide expressing a CCR5 polypeptide and a method for screening drugs targeting the CCR5 polypeptide and a method for screening drugs targeting the CCR5 polypeptide.

Sequence 352 AA;

Gaps .; 0 100.0%; Score 96; DB 5; Length 352; 100.0%; Pred. No. 8.9e-07; ive 0; Mismatches 0; Indels Local Similarity 100. 1es 18; Conservative Query Match Best Loc Matches

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185 SQYQFWKNFQTLKIVILG 202 SOYOFWKNFQTLKIVILG 18 н

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RESULT 31

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RESULT 32

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ABG75540 standard; protein; 352 AA.
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ABG75540;

(first entry) 16-APR-2003

Human G-protein chemokine receptor, HDGNR10, protein.

Human; receptor; G-protein chemokine receptor; 7-transmembrane receptor; HDGNR10; signal transduction; gene therapy; haematopoiesis; wound healing; coagulation; angiogenesis; tumour; chronic infection; leukaemia; T-cell mediated auto-immune disease; parasitic infection; psoriasis; growth factor; allergy; atherogenesis; anaphylaxis; malignancy; inflammation; histamine; IgE-mediated; prostaglandin-independent fever; bone marrow failure; silicosis; sarcoidosis; rheumatoid arthritis; shock; hyper-eosinophilic syndrome.

Homo sapiens.

US2002132269-A1.

19-SEP-2002

11-FEB-2000; 2000US-00502783

95US-00466343 06-JUN-1995; (HUMA-) HUMAN GENOME SCI INC

Li Y, Ruben SM;

WPI; 2003-208944/20. N-PSDB; ABX10635.

Novel human G-protein chemokine receptor polypeptide useful for diagnostic purposes and for identifying modulators of the polypeptide useful for treating leukemia, autoimmune diseases, psoriasis and allergic reactions.

Claim 7; Fig 1; 22pp; English

The invention discloses a G-protein chemckine receptor (sometimes referred to as a 7-transmembrane receptor) polypeptide, HDGNR10, and the polymucleotide encoding it. G-protein chemckine receptors are involved in signal transduction pathways. The polymucleotide and polypeptide can be protein and these compounds which activate or inhibit activation of the compounds are useful for treating a patient having need to activate or inhibit a G-protein chemckine receptor. The compound is administered by providing to the patient DNA encoding the agonist or administered by providing to the patient DNA encoding the agonist or an expressing them in vivo (gene therapy). The compound is disease or susceptibility to a disease related to an under-expression of the protein, for chromosome identification or as immunogens for producing antibodies. Agonists are useful in stimulating haematopolesis, wound healing, coagulation, angiogenesis, to treat solid tumours, chronic infections, learkeamia T-cell mediated auto-immune diseases, parasitic infections, psoriasis and to stimulate growth factor activity allergy, anthropolated allergic reactions, or activity anaphylaxis, anaphylax

Sequence 352 AA;

Gaps ô Length 352; Query Match 100. Best Local Similarity 100. Matches 18; Conservative

SQYQFWKNFQTLKIVILG

Ą ABR58602 standard; protein; 352 ABR58602; ABR58602

(first entry) 09-JUL-2003 Human cancer related protein SEQ ID NO:259.

Human, cancer; diagnosis; screening; modulator; leukaemia; ischaemia; heart disease; atherosclerosis; endometriosis.

Homo sapiens.

WO2003025138-A2

27-MAR-2003

17-SEP-2002; 2002WO-US029560.

20-SEP-2001; 2001US-0323887P. 13-NOV-2001; 2001US-0350666P. 08-FEB-2002; 2002US-0355145P.

12-APR-2002; 2002US-0372246P. 08-FEB-2002; 2002US-0355257P

(EOSB-) EOS BIOTECHNOLOGY INC.

Mack DH, Hevezi PA, Gish KC, Aziz N, Zlotnik Mfar D,

2003-354600/33. N-PSDB; ACC72740. New genes that are up-regulated or down-regulated in cancers, useful a markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.

Claim 12; Page 745; 767pp; English.

The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down-regulated in specific cancers (e.g. about 1013 genes up-regulated in cutellymphocytic leukemia). ACC72641 to ABC702860 represent cancer related gene nucleotide sequences which encode the proteins given in ABRS8109. Also described: (1) determining the presence or absence of a pathological cell in a patient; (2) an expression vector comprising a nucleic acid molecule described above; (3) a host cell comprising the vector; (4) an isolated polypeptide, which is encoded by the nucleic acid; (5) an antibody that specifically binds the polypeptide of (1); (6) specifically targeting a compound to a pathological cell in a patient by administering to the patient the antibody above; and (7) a patient by administering to the patient the antibody above; and (7) a patient by administering to the patient, the nucleic acid is useful for therapeutic targets. In particular, the nucleic acid is useful for diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow, bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary, bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary, and cancer of anorreas, prostate, skin and uterus), wounds, ischaemia, heart diseases, atherosclerosis and endometriosis. The nucleic acid is also useful in a pathology, e.g. cancer is nucleic acid is also useful in a pathology, e.g. cancer is nucleic acid is also useful in a pathology. pathologies

Sequence 352 AA;

ö 100.0%; Score 96; DB 6; Length 352; 100.0%; Pred. No. 8.9e-07; ive 0; Mismatches 0; Indels Query Match 100. Best Local Similarity 100. Matches 18; Conservative

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1 SOYOFWKNFOTLKIVILG 18

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Human G-protein chemokine receptor (HDGNR10) polypeptide Human; G-protein chemokine receptor; receptor; HDGNR10;

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The invention relates to a method for treating an urological disorder which comprises assaying the ability of the compound to modulate 313, 313, 5464, 188717 or 3354 mucleic acid expression or polypeptide activity. The method is useful for identifying a compound for treating urological disorder comprising urinary incontinence e.g., overactive/oversemaitive bladder, overflow urinary incontinence, stress urinary incontinence caused by defunction of the bladder, urethra or central/peripheral nervous system prostatitis, benign prostatic hyperplasia, prostate cancer or kidnay disorders. It is also used in gene therapy. The present sequence is human C-C chemokine receptor type 5 (CCRS, 333) protein. This sequence is used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                        Human; urological disorder; stress urinary incontinence; prostate cancer; benign prostatic hyperplasta; overactive bladder; oversensitive bladder; oversilow urinary incontinence; gene therapy, nephrotropic; prostatitis; kidney disorder; C-C chemokine receptor type 5; CCR5; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying a compound, capable of treating urological disorder e.g., benign prostatic hyperplasia, by assaying the ability of the compound to modulate 313, 333, 5464, 188717 or 33524 nucleic acid expression or polypeptide activity.
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100.0%; Pred. No. 8.9e-07;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                        Human C-C chemokine receptor type 5 (333) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 81; 87pp; English.
                                                                                                                                                                                                     AA029514 standard; protein; 352 AA
Tue Sep 28 15:49:56 2004
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                                                                                                                                                                                                                                                                        (first entry)
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N-PSDB; AAL59912.
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es 18; Conserv
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Matches
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The invention relates to a method of producing an antibody, involving immunising an animal with a human G-protein chemokine receptor (HDGNR10) polypeptide (also referred to as a human 7-transmembrane receptor) and recovering an antibody which binds the polypeptide. The method is useful for producing an antibody which binds specifically to the human G-protein chemokine receptor polypeptide. This sequence represents the HDGNR10 polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                       Producing an antibody, involves immunizing an animal with a polypeptide or with a polypeptide encoded by the human G-protein chemokine receptor clone in ATCC 97183, and recovering the antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, chemokine receptor, CCR5, viral infection, surface protein, respiratory virus infection, respiratory syncytial virus infection, RSV infection, bronchiolitis, bronchitis, pneumonia, asthma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of human chemokine receptor CCR5.
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98US-00195662.
99US-00339912.
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                                                                                                                                                              03-SEP-2002; 2002US-00232686.
                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
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Best Local Similarity 100.
Matches 18, Conservative
                                                      1-transmembrane receptor
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N-PSDB; ACA61721.
                                                                                                                                                                                                                                                                           Li Y, Ruben SM;
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18-NOV-1998;
25-JUN-1999;
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                                                                                Homo sapiens
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ABP97728
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10-AUG-2001; 2001US-0311088P.

ABUG1654 ID ABU61654 standard; protein; 352 AA. AC ABU61654; XX OR-AUG-2003 (first entry)

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G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; of protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; alloss cancer; immunological-related cell proliferation related disease; AlDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; aherosclerosis; infection; ostcoarthritis; allergy; ostcoprorsis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity, nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma; Modulating viral infection of a cell, for treating or preventing respiratory virus infections, bronchitis, pneumonia or asthma, by modulating a binding interaction between a cell chemokine-receptor and a The present sequence represents human chemokine receptor CCR5. The specification describes a method for modulating viral infection of a cell. the method comprises modulating a binding interaction between a cell chemokine-receptor and a surface protein of the virus. The provise is that the cell chemokine-receptor is not CX3CR1 and that the virus in the tire receptor is not cx3CR1 and that the virus is not HIV. The method is useful for treating or preventing respiratory virus infection in vertebrates, more particularly respiratory syncytial virus (RSV) infections, and related diseases, e.g. bronchiolitis, bronchitis, pneumonia or asthma 100.0%; Score 96; DB 6; Length 352; 100.0%; Pred. No. 8.9e-07; ive 0; Mismatches 0; Indels Human C-C chemokine receptor 5 protein SEQ ID NO:352. Disclosure; Page 96-98; 120pp; English. ABP81933 standard; protein; 352 AA. SQYQFWKNFQTLKIVILG 202 SOYOFWENFOTLKIVILG 18 surface protein of the virus. 19-DEC-2001; 2001WO-US050107 (first entry) (TOPI-) TOPIGEN PHARM INC. Query Match Best Local Similarity 100. Matches 18; Conservative Zemzoumi K; WPI; 2003-256541/25. N-PSDB; ABZ68881. Sequence 352 AA; WO200261087-A2 Homo sapiens. 04-MAR-2003 08-AUG-2002. Renzi P, 185 ABP81933; ulcer. RESULT 36 셤 à

Gaps . 0

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The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino caids. Also described: (I) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (i) an isolated antibody having high specificity and high affinity or anticly for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs and in the production of specific antibody against a particular GPCR. (I) can be useful in detecting an entibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, immunological-related diseases, cell regeneration-related diseases, growth-related diseases, cell corresponding GPCRs. The antigenic peptides for treating immune-related diseases, immunological-related cell proliferative diseases, or autoimmune diseases, eg. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, atherosclerosis, bacterial, fungal, protozoan or viral infections, atherosclerosis, bacterial, fungal, protozoan or viral infections, cellialmmation, allergies, Crohn's disease, graft versus host disease, parkinson's disease, multiple sclerosis, pain, psoriasis, cancer, cellialmmation, allergies, cancer, cardiomyopathy, chronic and acute cinflammation, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis, ABZ42289 encode GPCR proteins given in ABP81675 to ABZ42869 encode GPCR proteins given in ABP81675 to ABZ42869 encode cemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                 New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                        Disclosure; Fig 1; 523pp; English.
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tive 0;
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                      autoimmune diseases.
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N-PSDB; ABZ42781

ADC03341 standard; protein; 352 AA. Human chemokine receptor 88-C. (first entry) 18-DEC-2003

receptor; human, anti-HIV; virucide; HIV; SIV; 88-C; 88-2B; chemokine receptor; envelope protein; atherosclerosis; rheumatoid arthritis; tumour growth suppression; asthma; viral infection; AIDS; inflammatory condition. 26-MAR-2002; 2002US-00106623. US2002150888-A1. Homo sapiens. 17-0CT-2002

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95US-00575967. 96US-00661393. 96US-00771276.

20-DEC-1995; 07-JUN-1996; 20-DEC-1996;

(LIFE-) LIFESPAN BIOSCIENCES INC

19-DEC-2000; 2000US-0257144P.

Brown JP;

占

WPI; 2003-046718/04 Burmer GC, Roush

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This protein sequence comprises an Ala127Leu variant of a novel human macrophage-selective CC chemokine receptor (see also AAW23835) that has been designated CCR5. The sequence was deduced from an isolated cDNA clone (see AAT76919). The conservative variation should not affect the activity of CCR5. The susceptibility of human macrophages to HIV confection depends on cell surface expression of CD4 and CCR5. CCR5 is a member of the 7-transmembrane superfamily of G-protein coupled cell surface molecules. It plays an essential role in the membrane fusion step of infection by some HIV isolates. The establishment of stable, non-human CC infection by some HIV isolates. The establishment of stable, non-human CCR and CCR5 provides valuable tools for research of HIV infection.

Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding agents capable of blocking membrane fusion between HIV and target cells of HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prostaglandin; PG; B2BP3 receptor; B2BP2 receptor; CCR-5; human; chemokine receptor; ss2 adrenergic receptor; small G-protein rho; renal outer medullary potassium ion channel protein; ion-channel protein; lambda phage repressor protein; G-protein coupled receptor; bacteria; biochemical; vaccine; immunohistochemical; orphan receptor; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion between HIV and a target cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Berger EA, Alkhatib G, Murphy PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusion protein containing human chemokine receptor CCR-5.
                                                   //10/257..277
//label= VI
//note= "transmembrane domain"
296..319
//label= VII
                                                                                                                                                                 'note= "transmembrane domain"
                                      note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY41280 standard; protein; 439 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 1B; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 SQYQFWKNFQTLKIVILG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SOYOFWINFOTLKIVILG 18
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                                                                                                                                                                                                                                                                                             97WO-US009586
213. .238
/label= V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
Les 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        Combadiere C, Feng Y,
Broder CC, Kennedy PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-032650/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT76919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 371 AA;
                                                                                                                                                                                                                                                                                             38-MAY-1997;
                                                                                                                                                                                                            W09745543-A2
                                                                                                                                                                                                                                                                                                                                       28-MAY-1996;
                                                                                                                                                                                                                                                         04-DEC-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY41280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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    Domain
                                                              Domain
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DP
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                                                                                                                                                                                                                                                                                                                                   The invention relates to screening for a modulator of human immunodeficiency virus (HIV) or simian immunodeficiency virus (SIV) or infection, comprising contacting a first composition having an HIV or simian immunodeficiency virus (SIV) as forced composition having an HIV or SIV envelope protein in the a second composition having an HIV or SIV envelope protein in the presence or absence of a compound. Also included are screening for a modulator of HIV infection, detecting HIV infection of cells (comprising contacting a cell that has been recombinantly modified to express at least one of human chemokine receptors 86C and 88-2B with HIV, and detecting HIV infection of cells (comprising contacting cells with an antibody to at least one of human chemokine receptors 86C and 88-2B with HIV, and detecting HIV infection of the cell after the contacting step). The methods and compositions of the present invention are useful for the diagnosis and treatment of disorders associated with the aberrant expression or activity of 88C or 88-2B chemokine receptors, such as atherosclerosis, rheumatoid arthritis, tumour growth suppression, asthma, viral infection, AIDS and other inflammatory conditions. The genes for human 88-C and 88-C B are located on chromosome 3921. The present sequence represents human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                     Screening for a modulator of HIV and SIV infection utilizing polynucleotides that encode the 88C or 88-2B chemokine receptors, useful for diagnosing and treating disorders such as atherosclerosis, arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC chemokine receptor 5; CCR5; G-protein coupled receptor; human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human CC chemokine receptor 5 (CCR5) A127V variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23. .145
|label= III
/note= "transmembrane domain"
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                                                                                     Raport CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                 Claim 2, Page 17-18; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW23834 standard; protein; 371 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOYOFWKNFOTLKIVILG 18
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/label= IV
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/label= I
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                                                                                     Gray PW, Schweickart VL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 18; Conservative
(GRAY/) GRAY P W.
(SCHW/) SCHWEICKART V L.
(RAPO/) RAPORT C J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chemokine receptor 88-C.
                                                                                                                             WPI; 2003-182491/18.
                                                                                                                                                    N-PSDB; ADC03340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 352 AA;
                                                                                                                                                                                                                                                           AIDS and asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW23834;
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Domain
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AAW23834
ID AAW23834
XX
XX
AC AAW23
DT 08-JUI
XX
XX
DD Human
XX
XX
CC chi
KW CC chi
KW CC chi
KW CC chi
ET Domain
FT Domain
FT FT
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WO9722698-A2

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The invention provides isolated nucleic acid sequences that encode rabbit prostaglandin (PG) E2EP3 receptor, human PG E2EP2 receptor, rat renal outer chemokine receptor CRF-5, human se2 adrenergic receptor, rat renal outer medullary potassium ion channel protein or human small G-protein rho, together with deduced protein sequences. Also provided is a method for the production of enkaryotic proteins by culturing bacteria transformed with vectors containing the above nucleic acid sequences or a nucleic acid (I) that comprises: (i) first sequence that encodes either a DNA-binding protein, or a lambda phage repressor protein, placed upstream of, and in frame with, (ii) a sequence encoding a protein, placed upstream of, and in frame with, (ii) a sequence encoding a protein, (I) are used for recombinant production of eukaryotic proteins, particularly membrane proteins groteins are useful for biochemical or structural studies; and in the protein are useful for biochemical or structural studies; and indignostic and screening assays and as antigens for use in vaccines, and for raising antibodies that are useful cannels. Antibodies raised against the chemokine receptors or ion channels. Antibodies raised against the chemokine receptors or ion channels. Antibodies raised against the chemokine receptor CCR-5 can be used (when administered as antiserum or generated in vivo) to prevent control of the party of human immune deficiency virus (HIV) into cells
                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid constructs for high level expression of eukaryotic proteins in bacteria, for producing e.g. chemokine receptor CCR-5 for preventing HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 49-53; 81pp; English
                                                                                                                                                                                                                                                                                                               Breyer RM, Ma L, Kennedy C;
                                                                                                                                                                          99WO-US008214.
                                                                                                                                                                                                                       98US-0081989P.
                                                                                                                                                                                                                                                                (UYVA-) UNIV VANDERBILT
                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-620416/53.
                                                                                                                                                                                                                                                                                                                                                                               N-PSDB: AAZ24738
                                          Homo sapiens.
                                                                                     WO9953033-A1
                                                                                                                                                                             16-APR-1999;
                                                                                                                                                                                                                       16-APR-1998;
                                                                                                                                21-OCT-1999
                  Synthetic.
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100.0%; Score 96; DB 2; Length 439; 100.0%; Pred. No. 1.1e-06; cive 0; Mismatches 0; Indels 1 SOYOFWKNFOTLKIVILG 18 Query Match 100. Best Local Similarity 100. Matches 18; Conservative ð В

Sequence 439 AA;

Search completed: September 28, 2004, 09:03:38
Job time : 43.975 secs

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Gaps .; 0

263 SQYQFWKNFQTLKIVILG 280

AAW27125 standard; protein; 352 AA Macaque chemokine receptor 88C. 14-DEC-1997 (first entry) AAW27125; 40 AAN27125
ID AAN27125
ID AAN27125
XX
XX
XX
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DT 14-D
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Chen
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Che

Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour; asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy; diagnosis; leukocyte trafficking; G protein coupled receptor; ligand; modulator; antibody.

ab Macaca

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This polypeptide sequence comprises macaque chemokine receptor 88C, a G protein coupled receptor that is involved in leukocyte trafficking. Its amino sequence was deduced from a 88C DNA (AAR85163) isolated by PCR amplification. It shows 97% identity to human 88C (AAM27123). 88C receptors and their polypeptide fragments can be produced in transformed host cells. The receptors, peptides comprising one or more of the extracellular or intracellular domains, and anti-receptor antibodies can be used to modulate receptor activities, particularly ligand and G protein binding, and are potentially potentially useful in the treatment of atheroslerosis, rheumatoid arthritis, tumours, asthma, viral infection, AIDS, inflammatory conditions, pathological immune response, abnormal haematopoietic processes etc. A hybridoma that produces an antibody that specifically binds to macaque 88C is claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                New nucleic acid encoding chemokine receptors 88-2B and 88C - used modulate leukocyte trafficking, e.g. for treatment of inflammation, tumours, viral infections, auto-immune diseases, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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Pred. No. 2.6e-06;
1; Mismatches 0; Indels
                                                                                                                                                                                               Gray PW, Schweickart VL, Raport CJ;
                                                                                                                                                                                                                                                                                                                                                       Claim 36; Page 57-58; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.9%; Scor.
94.4%; Pred
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                                                                             96WO-US020759
                                                                                                              95US-00575967.
96US-00661393.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-341689/31.
N-PSDB; AAT85163.
                                                                                                                                                                (ICOS-) ICOS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 352 AA;
                                                                                 20-DEC-1996;
                                                                                                               20-DEC-1995;
07-JUN-1996;
                                              26-JUN-1997.
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US-09-734-221A-14
US-09-826-509-477
US-01-0151-45
US-10-151-45
US-10-151-45
US-10-066-80-2
US-10-066-8014-1
US-10-067-8014-1
US-10-057-801-1
US-10-225-567A-352
US-10-225-567A-352
US-10-235-314-1
US-10-125-311-1
US-09-796-202-1
US-09-139-562A-2
US-09-339-51ZA-2
US-09-938-719-5
US-09-938-703-5
US-09-502-783A-2
 September 28, 2004, 09:06:23; Search time 59.625 Seconds (without alignments) 97.074 Million cell updates/sec
                                                                                                                                                        1349238
        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                         1349238 seqs, 321558718 residues
                                      OM protein - protein search, using sw model
                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                  1 SQYQFWKNFQTLKIVILG 18
                                                                                                                                                                                              Post-processing: |Minimum Match 0% Maximum Match 100%
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Maximum DB seq length: 200000000
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96
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Title: Perfect score:

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Sequence:

Scoring table:

2, Appli 5, Appli 6, 14, Appli 6 14, Appli 6 2, Appli 6 2, Appli 6 1, Appli 7 Appli 8 1, Appli 8 2, Appli 9 2, Appli 9 2, Appli 1, Appli 2, Appli 1, Appli 2, Appli 3, Appli 4, App

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Sequence 5, Sequence 5, Sequence 5, Sequence 2, Sequence 1

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ALIGNMENTS

Published Applications AA:

Database :

Listing first 45 summaries

Sequence Sequence Sequence S

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Publication No. US20030068615A1

Publication No. US20030068615A1

Publication No. US20030068615A1

GENERAL INRORMATION:

APPLICANT: SAXINGER.

TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC

TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE

TITLE OF INVENTION: 2002-02-27

CURRENT APPLICATION NUMBER: US/10/084,813

CURRENT APPLICATION NUMBER: PCT/US00/23505

PRIOR FILING DATE: 1000-08-25

PRIOR FILING DATE: 1999-08-27

NUMBER OF SEQ ID NOS: 1242

SEQ ID NO 13

LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 96; DB 14; Length 1
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
US-10-084-813-77
Sequence 77, Application US/10084813
Publication No. US20030068615A1
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ORGANISM: Artificial Sequence
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Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 21, Appl
Sequence 2, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 15, Appli
Sequence 15, Appli
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Logn2_6/ptodata/1/pubpaa/US07_PUBCOMB.ppp:*

(gn2_6/ptodata/1/pubpaa/US07_NEW_PUB.ppp:*

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US-09-938-719-11

US-09-938-719-11

US-09-938-719-11

US-09-725-285-2

US-09-725-811-2

US-09-779-879A-2

US-09-779-879A-2

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US-09-779-880A-2
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Result õ **୰୰୰୰୰୰୰୰୰୰୰୰୰୰୰୰** ୵୵୵୵୷୵୷

4697887654

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Gaps

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Length 18;

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PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOXINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,719
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 96; DB 16; Length 49; 100.0%; Pred. No. 7.9e-08;
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ADDRESSE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Samson, Michael
APPLICANT: Parmentier, Marc
APPLICANT: Passart, Gilbert
TITLE OF INVENTION: HIV Diagnostic Methods
FILE REFERENCE: 9409/2028
CURRENT APPLICATION NUMBER: 08/938,703
PRIOR FILING DATE: 2003-07-02
PRIOR FILING DATE: 2000-07-27
PRIOR FILING DATE: 2000-07-27
PRIOR FILING DATE: 1997-04-09
PRIOR FILING DATE: 1997-04-09
PRIOR FILING DATE: 1997-03-03
PRIOR FILING DATE: 1997-03-03
PRIOR FILING DATE: 1997-03-03
PRIOR FILING DATE: 1996-03-01
PRIOR FILING DATE: 1996-03-01
PRIOR FILING DATE: 1996-03-01
PRIOR FILING DATE: 1996-03-01
SPRIOR FILING DATE: 1996-03-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/09938719
Patent No. US20020106742A1
GENERAL INFORMATION:
                                                                Sequence 11, Application US/10612791 Publication No. US20040161739A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Conservative
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; ORGANISM: Homo sapiens
US-10-612-791-11
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Best Local Similarity
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Sequence 11, Application US/10661798

Sequence 11, Application US/10661798

Sequence 11, Application No. US20040110127A1

GENERAL INFORMATION:

APPLICANT: Sameon, Michael

APPLICANT: Parmentier, Marc

APPLICANT: Varmentier, Marc

CURRENT APPLICANTION NUMBER: US/203-09-12

PRIOR PILING DATE: 2000-07-27

PRIOR PILING DATE: 1997-03-03

PRIOR PILING DATE: 1997-03-03

PRIOR PILING DATE: 1997-03-03

PRIOR PILING DATE: 1996-03-01

PRIOR PILING DATE: 1996-03-03
GENERAL INFORMATION:

APPLICANT: SAXINGER, CARL
TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
TITLE OF INVENTION: POLYPEPTIDES, COMPOSITIONS, AND METHODS OF USE
FILE REFERENCE: 218875
CURRENT APPLICATION NUMBER: US/10/084,813
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: PCT/US00/23505
PRIOR APPLICATION NUMBER: PCT/US00/23505
PRIOR FILING DATE: 1999-08-25
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 1242
SOFTWARE: Patentin version 3.1
SEQ ID NO 77
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 96; DB 14; Length 18; 100.0%; Pred. No. 3e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.(
Matches 18; Conservative
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Best Local Similarity 100.
Matches 18; Conservative
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CORGANISM: Homo sapiens
US-10-661-798-11
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US-09-938-703-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/09939226
Patent No. US20020110805A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TILLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                           Gaps
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MEDUIN TYPE: Floppy disk
CONFUTER: IBM PC compatible
CONFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRINT APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                            Query Match 100.0%; Score 96; DB 9; Length 54; Best Local Similarity 100.0%; Pred. No. 8.7e-08; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

Query Match

Best Local Similarity 100.0%; Pred. No. 8.7e-08;

Matches 18; Conservative 0; Mismatches 0; Indels
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ADDRESSE: KNODDe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
              REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: «Unknown»
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
TYPE: amino acid
STRANDEDNESS: single
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REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
                                                                                                                                                                        TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-939-226-11
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APPLICATION WUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INPORMATION:
NAME: Altman, Daniel E
                                                                                                                                                                                                                                                                                                                                                                            SQYQFWKNFQTLKIVILG 26
                                                                                                                                                                                                                                                                                                                                                   1 SOYOFWKNFOTLKIVILG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
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US-09-939-226-11
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Sequence 2, Application US/09725285;
Patent No. US2001000241A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Li, Yi
APPLICANT: Li, Y
APPLICANT:
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                                                                                                                                             APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOXINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 92660
COMPUTER READABLE FORM:
DIDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSER: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 96; DB 9; I
100.0%; Pred. No. 8.7e-08;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION WUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
Sequence 11, Application US/09938703
Patent No. US20020110870A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SOYOFWKNFOTLKIVILG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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Best Local Similarity 100.
Matches 18; Conservative
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Sequence 22. Application US/09779879A

| Sequence 22. Application US/09779879A
| Patent No. US20020048786A1
| GENERAL INFORMATION:
| APPLICANT: Rosen, Craig A.
| APPLICANT: Rosen, Steven, M.
| APPLICANT: Ruben, Steven, M.
| APPLICANT: Li, Yi
| APPLICANT: Li, Yi
| APPLICANT: Li, Yi
| APPLICANT: Ruben, Steven, M.
| TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
| FILE REFERENCE: 1488.115000A
| CURRENT APPLICATION NUMBER: US 60/181,258
| PRIOR FILING DATE: 2000-02-09
| PRIOR FILING DATE: 2000-03-09
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APPLICANT: Rosen, Craig A.
APPLICANT: Boschke, Viktor
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
FILE REFERENCE: 1488.115000C
FURRENT APPLICATION NUMBER: US 60/181,258
FRIOR PILING DATE: 2000-02-09
FRIOR APPLICATION NUMBER: US 60/181,258
FRIOR APPLICATION NUMBER: US 60/187,999
FRIOR PILING DATE: 2000-03-09
FRIOR FILING DATE: 2000-03-09
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
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100.0%; Score 96; DB 9; I
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0;
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; CRGANIEM: Homo sapiens
US-09-779-879A-2
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; ORGANISM: Homo sapiens
US-09-779-879A-22
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US-09-779-879A-22
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LENGTH: 352
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APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Rosenke, Viktor
APPLICANT: Ruben, Steven, M.
ITILE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
FILE REFERENCE: 1468-11500A
CURRENT PILION DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2000-03-09
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                                                                                                                                                                                                                                                                ; FEATURE:
, OTHER HPORMATION: Deduced Amino Acid Sequence
US-09-725-285-2
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Sequence 2. Application US/09759841

Patent No. US20010039026A1

GENERAL INFORMATION:

APPLICANT: Rickett, Graham A

APPLICANT: Rickett, Graham A

APPLICANT: Perros, Manoussos

TITLE OF INVENTION: Assay Method

FILE REFERENCE: PC10348APME

CURRENT APPLICATION NUMBER: US/09/759,841

CURRENT FILING DATE: 2001-01-12

PRIOR PILING DATE: 2000-01-12

PRIOR PILING DATE: 2000-01-12

PRIOR PELICATION NUMBER: GB 0000661.9

PRIOR PILING DATE: 2000-01-12

PRIOR PILING DATE: 2000-01-12

PRIOR PILING DATE: 2000-01-12

PRIOR PILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-01-12

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NOS: 6

SED ID N
                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence: Genomic
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                         PatentIn version 3.0
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US-09-759-841-2
          SOFTWARE: Page SEQ ID NO 2 LENGTH: 352
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US-09-779-879A-2
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US-09-759-841-2
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Gaps

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Sequence 17, Application US/09813653

Sequence 17, Application US/09813653

Benefor No. US2020064770A1

GENERAL INFORMATION:
APPLICANT: Wilson, Carol
APPLICANT: Wilson, Carol
APPLICANT: See, Raymond
APPLICANT: Tan Hehir, Christina
FILE OF INVENTION: Blinding Compounds and Methods For Identifying Binding Compounds
FILE REFERENCE: CNS-005
CURRENT FILING DATE: 2001-03-20
FRIOR PRILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PRIOR APPLICATION NUMBER: US 60/191,299
PRIOR PRIOR DATE: 2000-03-21
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100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
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; LENCTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-653-15
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CRGANISM: Homo sapiens
US-09-813-653-17
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; ORGANISM: human
US-09-796-202-1
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US-09-813-653-17
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US-09-796-202-1
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Patent No. US20020064770A1
GENERAL INFORMATION:
APPLICANT: Watson, Carol
APPLICANT: Watson, Carol
APPLICANT: Watson, Carol
APPLICANT: See, Raymond
APPLICANT: Watson, Carol
APPLICANT: See, Raymond
APPLICANT: See, Raymond
APPLICANT: See, Raymond
APPLICANT: Tan Hehir, Christina
TITLE OF INVENTION: Binding Compounds
CURRENT APPLICATION NUMBER: US/09/813,653
CURRENT FILING DATE: 2001-03-20
PRIOR FILING DATE: 2000-03-21
PRIOR PAPLICATION NUMBER: US 60/190,96
PRIOR APPLICATION NUMBER: US 60/190,96
PRIOR APPLICATION NUMBER: US 60/191,299
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
SPIOR SEQ ID NOS: 44
SSCTWARRE: Patentin version 3.0
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Sequence 22, Application US/09779880A

Patent No. US20020066834A1

GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Rosenke, Viktor
APPLICANT: Rosenke, Viktor
APPLICANT: I. William General Chemokine Receptor (CCR5) HDGNR10
FILE REFERENCE: 1488.115000C
CURRENT APPLICATION NUMBER: US/09/779,880A
CURRENT FILING DATE: 2001-02-09
FRIOR APPLICATION NUMBER: US 60/181,258
FRIOR APPLICATION NUMBER: US 60/181,258
FRIOR APPLICATION NUMBER: US 60/187,999
FRIOR FILING DATE: 2000-03-09
FRIOR APPLICATION NUMBER: US 60/234,336
FRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 58
SEQ ID NO 22
LENGTH: 352
LENGTH: 352
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100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
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; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANIEM: Homo sapiens
US-09-779-880A-2
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GORGANISM: Homo sapiens
US-09-779-880A-22
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APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,719
FILING DATE: 24-Aug-2001
CLASSIFICATION: _Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 352;
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                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSES: Karbobe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 96; DB 9; 1
100.0%; Pred. No. 5.5e-07;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
PRIOR APPLICATION WIMBER: 09/626,939
PILING DATE: 27-UULY-2000
ATTOANEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: JUBER

MOLECTLE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-938-719-5
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COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READDALE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
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; Sequence 5. Application US/09939226
; Patent No. US20020110805A1
; GENERAL INFORMATION:
                Sequence 5, Application US/09938719 Patent No. US20020106742A1 GENERAL INFORMATION:
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Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
US-09-938-719-5
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Sequence 2, Application US/09339912A;
Fatent No. US20020099176A1
GENERAL INFORMATION:
APPLICANT: Li, Yi, APPLICANT: Li, Yi, APPLICANT: Li, Yi, APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10;
TITLE OF INVENTION: (CCRS Receptor);
TITLE OF INVENTION NUMBER: US/09/339,912A;
CURRENT PAPLICATION NUMBER: 09/195,662;
PRIOR FILING DATE: 1999-06-5;
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0;
SEQ ID NO 2
LENGTH: 352
                                                                                                                                                                                                                                             APPLICANT: Li, Yi
APPLICANT: Ruben, Steven, M.
APPLICANT: Ruben, Steven, M.
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGNRIO (CCRS Receptor)
FILE REFERENCE: 1488.1150002
CURRENT APPLICATION NUMBER: US/09/195,662A
CURRENT APPLICATION NUMBER: US/09/195,662A
CURRENT APPLICATION NUMBER: US/08/195,662A
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR PILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 352
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100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 5.5e-07;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Deduced Amino Acid Sequence US-09-195-662A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Deduced Amino Acid Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence: Genomic
FEATURE:
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                                                                                                                                                                               Sequence 2, Application US/09195662A Patent No. US20020076745A1 GENERAL INFORMATION:
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                                   SQYQFWKNFQTLKIVILG 202
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  1 SQYQFWKNFQTLKIVILG 18
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Matches 18; Conserv
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Gaps

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RESULT 19

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Gaps

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Query Match
100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
    ; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-703-5
                                                                                                                                                                                                                                                                                                                                                                        185 SQYQFWKNFQTLKIVILG 202
                                                                                                                                                                                                                                                                                                                  1 SOYOFWKNFOTLKIVILG 18
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US-09-502-783A-2
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Patent No. US20020110870A1
GENERAL INFORMATION:
MICHEL
APPLICANT: SAMSON, MICHEL
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RE
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INVERMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REGISTRATION NUMBER: 34,115
REGISTRATION NUMBER: 34,115
REPERMENCE/CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION: ADATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 34,115
REGISTRATION PONIBER: 34,115
REGISTRATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERICATICS:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERICATICS:

SEQUENCE CHARACTERICATICS:
AUGUST CHARAC
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100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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US-09-938-703-5
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Sequence 2, Application US/09502783A

Patent No. US20020132269A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TO SEQUENCE 1, Yi

APPLICANT: Li, Yi

APPLICANT: No Wide Encoding Human G-Protein Chemokine Receptor (CCR5)

FILE REFERENCE: 1488.115006

CURRENT APPLICATION NUMBER: US/09/502,783A

CURRENT PILING DATE: 1995-06-06

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.0

SEQ ID NO 2

LENGTH: 352
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ELLMETER, WILFRIED
LANDAU, NATHANIEL R.
LIU, RONG
TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
NACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
USES THEREOF
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CORRESPONDENCE ADDRESS:
ADDRESSE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 352;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PILING DATE: 11-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 96; DB 9; I
100.0%; Pred. No. 5.5e-07;
tive 0; Mismatches 0;
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US-09-734-221A-14
Sequence 14, Application US/09734221A
Publication No. US20030096221A1
CENERAL INFORMATION:
APPLICANT: LITTMAN, DAN R.
DENG, HONGKUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 SQYQFWKNFQTLKIVILG 202
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COUNTRY: USA
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Best Local Similarity 100.
Matches 18; Conservative
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CNGANISM: Homo sapiens
US-09-502-783A-2
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                      APPLICANT: Littman, Dan R.
APPLICANT: Littman, Dan R.
APPLICANT: Kwon, Douglas S.
APPLICANT: Kwon, Douglas S.
APPLICANT: Wan Kooyk, Yvette
APPLICANT: Wan Kooyk, Yvette
APPLICANT: Geijeenbeck, Theo
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY
TITLE OF INVENTION: INTO
TITLE OF INVENTION: CELLS
FILE REFERENCE: 1049-1-017
CURRENT APPLICATION NUMBER: US/10/151,274
CURRENT FILING DATE: 2000-05-20
RIOR APPLICATION NUMBER: US/09/517,605
RRIOR APPLICATION NUMBER: US/09/517,605
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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MEDLUM TYPER FLORM:

MEDLUM TYPER FLORY disk

COMPUTER: 1987 Compatible

COMPUTER: 1987 PC compatible

TILING DATE: 40 MAN-

FILING DATE: 40 MRNATION:

ATTORNEY AGENT INFORMATION:

NAME: NO. US200201508884and, Greta E.
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REFERENCE/DOCKET NUMBER: 27866/33670
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/10106623 Publication No. US20020150888A1 GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS
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STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-151-274-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 5
LENGTH: 352
TYPE: PRT
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| Publication No. US20030204073A1
| GENERAL INFORMATION:
| APPLICANT: Liaw, Chen W. APPLICANT: Liaw, Chen W. TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G TITLE OF INVENTION: Protein-Coupled Receptors
| TITLE OF INVENTION: Protein-Coupled Re
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                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/666,020
APPLICATION NUMBER: US 08/227,319
FILING DATE: 19-4UN-1996
ATTORNEY/AGENT INFORMATION:
NAME: JACKSON ESQ., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-004 NZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 96; DB 10;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) ORGANISM: Homo sapiens
) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-734-221A-14
                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 5, Application US/10151274
; Publication No. US20030064071A1
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; ORGANISM: Homo sapiens
US-09-826-509-477
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US-09-826-509-477
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US-10-151-274-5
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185 SQYQFWKNFQTLKIVILG 202
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US-10-067-800-2
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APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven M.
TILE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10
FILE REFERENCE: 1488-115000M
CURRENT FILING DATE: 1002-09-03
FUCRENT FILING DATE: 1999-06-25
PRIOR PELICATION NUMBER: 09/339,912
PRIOR FILING DATE: 1999-06-25
PRIOR PELICATION NUMBER: 09/466,343
PRIOR FILING DATE: 1998-11-18
PRIOR PLING DATE: 1998-10-60
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PREENTIN VERSION 3.0
SOFTWARE: PREENTIN VERSION 3.0
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10086814
; Sequence 1, Application US/10086814
; Publication No. US20030092632A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Dragic, Millan C.
; TITLE OF INVENTION; WILLAND CRS PEPTIDES FOR HIV-1 INFECTION
; FILE REPERENCE: 61010-AB-1
; CURRENT APPLICATION NUMBER: US/10/086,814
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 38
; SOFTHARE: PatentIn version 3.1
; SEQ ID NO 1
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100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 5.5e-07;
tive 0; Mismatches 0; Indels
                                                                                                                 Length 352;
NAME/KEY: misc feature
OTHER INFORMATION: /= "88C amino acid sequence"
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                0; Indels
                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 2, Application US/10232686
; Publication No. US20030023044A1
; GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 18; Conservative
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CORGANISM: Homo sapiens
US-10-232-686-2
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US-10-086-814-1
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US-10-106-623-2
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RESULT 30

US-10-667-800-22

Sequence 22, Application US/10067800

Publication No. US20030100058A1

GENERAL INFORMATION:

APPLICANT: Rosen, Craig A.

APPLICANT: Rosen, Craig A.

TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGWR10

FILE REFERENCE: 1488-115001

CURRENT FILING DATE: 2002-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-03

PRIOR FILING DATE: 2001-02-03

PRIOR FILING DATE: 2001-02-03

PRIOR FILING DATE: 2001-10-12

PRIOR FILING DATE: 2001-12-21

NUMBER OF SEQ ID NOS: 70

SOFTWARE: PRECENTING VARIETS

LENGTH: 352

LENGTH: 352

LENGTH: 352
RESULT 29
US-10-067-800-2
| Sequence 2, Application US/10067800
| Publication No. US20030100058A1
| GENERAL INFORMATION:
| APPLICANT: Roseinke, Viktor
| TILE OF INVENTION: Human G-rotein Chemokine Receptor (CCR5) HDGNR10
| TILE REFERENCE: 1488.115001
| CURRENT APPLICATION NUMBER: US/10/67,800
| PRIOR FILING DATE: 2001-02-09
| PRIOR FILING DATE: 2001-02-09
| PRIOR PELICATION NUMBER: 60/297,257
| PRIOR APPLICATION NUMBER: 60/297,257
| PRIOR FILING DATE: 2001-06-12
| PRIOR PILING DATE: 2001-06-12
| PRIOR APPLICATION NUMBER: 60/328,447
| PRIOR APPLICATION NUMBER: 60/328,447
| PRIOR APPLICATION NUMBER: 60/328,447
| PRIOR PILING DATE: 2001-12-21
| NUMBER OF SEQ ID NOS: 70
| SOFTWARE: Patentin Version 3.1
| SEQ ID NO 2
| TABLENTH: 2001-12-21
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Sequence 1, Application US/10072301
Publication No. US20030152913A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hua, Shao-bing
APPLICANT: Pauling, Michelle H.
APPLICANT: Zhu, Li
TILLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNOBER)
TILLE OF INVENTION: VIRUS
FILE REFERENCE: 25636-718
CURRENT FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.1
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Publication No. US20030162943A1
GENERAL INFORMATION:
TILLE OF INVENTION: O. US20030162943A1e1 Molecules of the G Protein-Coupled NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 28 State Street
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100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                   Sequence 1, Application US/10323314

Publication No. US20030139571A1

GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES F
FILE REPERBENCE: 2046/61010-1/JPW/MAF/DJK
CURRENT APPLICATION NUMBER: US/10/323,314
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SOFTWARE: PatentIn version 3.0
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STATE: Massachusetts
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: human
US-10-323-314-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 1
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US-10-072-301-1
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| Sequence 352, Application US/10225567A
| Publication No. US20030113798A1
| GENERAL INFORMATION:
| APPLICANT: LifeSpan Biosciences
| APPLICANT: Brown, Joseph P. |
| APPLICANT: Brown, Joseph P. |
| APPLICANT: Roush, Christine L. |
| TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS |
| TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS |
| TILE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS |
| FILE PERRENCE: 1920-4-4 |
| CURRENT FILING DATE: 2000-12-19 |
| PRIOR FILING DATE: 2000-12-19 |
| NUMBER OF SEQ ID NOS: 2292 |
| SEQ ID NO 352 |
| LENGTH: 352 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Urological Disorders Using 313, 333, 5464, 18817 or 33524
TITLE OF INVENTION: Urological Disorders Using 313, 333, 5464, 18817 or 33524
FILE REFERENCE: MPIO1-28981RM
CURRENT APPLICATION NUMBER: US/10/290,058A
CURRENT FILING DATE: 2002-11-07
PRIOR APPLICATION WUMBER: 60/344,552
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                               Query Match 100.0%; Score 96; DB 14; Length 352; Best Local Similarity 100.0%; Pred. No. 5.5e-07; Matches 18; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/10290058A Publication No. US20030104455A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                  185 SÓYÓFWKNFÓTLKÍVÍLG 202
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Best Local Similarity 100.
Matches 18; Conservative
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; ORGANISM: Homo sapiens
US-10-225-567A-352
; ORGANISM: Homo sapiens
US-10-067-800-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT

CORGANISM: Homo Sapien

US-10-290-058A-6
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                                  APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Steven, M.
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
FILE REPREBRE: 1488.11500A
CURRENT APPLICATION NUMBER: US/10/135,839
CURRENT FILING DATE: 2002-05-01
FRIOR PAPLICATION NUMBER: US 60/187,999
FRIOR PAPLICATION NUMBER: US 60/187,999
FRIOR PAPLICATION NUMBER: US 60/234,336
FRIOR PAPLICATION NUMBER: US 60/234,336
FRIOR PLING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LINGTH 352
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US-10-135-939-22
i Sequence 22, Application US/10135839
i Publication No. US20030166024A1
i GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Viktor
APPLICANT: Ruben, M.
TILE REFRENCE: 1488.115000A
CURRENT APPLICATION NUMBER: US/09/10/135,839
CURRENT FILING DATE: 2002-05-01
PRIOR FILING DATE: 2002-05-01
PRIOR APPLICATION NUMBER: US 60/187,999
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
SEQ ID NO 22
TABGGTH: 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 96; DB 14; Length 352; Best Local Similarity 100.0%; Pred. No. 5.5e-07; Matches 18; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 SOYOFWKNFOTLKIVILG 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-135-839-22
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US-10-239-423-67
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Publication No. US20030165988A1
GENERAL INFORMATION
APPLICANT: Hua, Shao-bing
APPLICANT: Hua, Shao-bing
APPLICANT: Builing, Michelle H.
APPLICANT: Bin, in
TITLE OF INVENTION: FRAGMENTS DERIVED FROM MEMBRANE PROTEINS
FILLE REPERBENCE: 25636-717
CURRENT APPLICATION NUMBER: US/10/071,866
CURRENT APPLICATION NUMBER: US/10/071,866
CURRENT APPLICATION DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 54
SEQ ID NO 1
SEQ ID NO 1
LENGTH: 352
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0
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COMPUTER READABLE FORM:

MEDIUM TYPE: Flopgy disk

COMPUTER: IEM PC compatible

COMPUTER: IEM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/164,649

FILING DATE: 07-Jun-2002

CLASSIFICATION DATA:

APPLICATION NUMBER: US/990/045,583

FILING DATE: 07-Jun-2004

MAME: MADATA:

APPLICATION NUMBER: WIN-044

FILING DATE: CAMPANION:

NAME: MANGENATION:

TELEFRATION NUMBER: 36,207

TELEFRATION NUMBER: MNI-044

TELEFRAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 52:

SEQUENCE CAMPANTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acids

TOPPOLOGY: 14-acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 96; DB 14; Length 352; Best Local Similarity 100.0%; Pred. No. 5.5e-07; Matches 18; Conservative 0; Mismatches 0; Indels
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100.0%; Score 96, DB 14;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGWENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 37
US-10-135-839-2
Sequence 2, Application US/10135839
; Publication No. US20030166024A1
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-164-649-52
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US-10-071-866-1
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8
APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERMANN, Knut;
APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikolaj
TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells and
TITLE OF INVENTION: For Treating Tumor Diseases and Inflammatory Diseases,
TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine
TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction
FILE REPERENCE: 02221/us
CURRENT PILING DATE: 2002-09-23
PRIOR PILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 67
ILBNGTH: 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Sequence 2, Application US/10439845
Publication No. US20030195348A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
TITLE OF INVENTION: AND THERAPEUTIC AGENTS FOR HIV INFECTION
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/439,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/864,458
FILING DATE: May 28, 1997
APPLICATION NUMBER: Provisional 60/018,508
CLASSIFICATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTECS:
LENGTH: 352 anino acids
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NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SOYOFWKNFOTLKIVILG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 18; Conservative
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US-10-439-845-2
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

6; Search time 9.675 Seconds (without alignments)
178.961 Million cell updates/sec 2004, 08:57:36 September 28, Run on:

US-10-084-813-13 96 Title: Perfect score: Sequence:

1 SQYQFWKNFQTLKIVILG 18

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ļŸ	macrophage inflamm	μ		cerat		hypothetical prote	cal	probable 2-phospho	probable integral	secretion protein	nitroreductase fam	NADPH-flavin oxido	oxidoreductase yhd	chemokine receptor	periplasmic sorbit	surfactin syntheta	UTR4 protein - yea	probable branched-	hypothetical prote	FAD-dependent mono	Ω	ical		nterobact	erric enterobact		ADH2 dehydrogena	hypothetical prote
SUMMARIES	QI	m	933	\sim	449		557	G90724		m	In	10	Th.	10	_		m	I40486		-	\sim 1	_	m	~		•		$\overline{}$	137047	H83734
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	Length	352	355	196	177	302	314	31	1289	301	467	616	237	237	242	344	47	3587	241	350	383	421	421	496	159	334	334	334	46	118
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	Score	O)	47	4.6	45	45	4.5	45	4.5	44.5	44	44	43	43	43	43	43	43	42	42	42	42	42	42	ä	Ξ.		ä	41	
	Result No.	н	2	e	4	ιΩ	φ	7	ထ	Q	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59

hypothetical prote envelope-like prot	oligopeptide ABC t hypothetical prote NaDH2 debydrogense	hypothetical prote hypothetical prote	pre-mRNA splicing probable zinc-fing	related to TOM1 pr DNA-damage-inducib	DNA-damage-inducib hypothetical prote	hypothetical prote	alcohol sulfotrans
S03215 A84494	I40547 T22197 T11833	D83385 E42594	S47920 T48016	T49799 H91193	A86041 G97365	G70827 T15673	I38548
01 01	0 0 0	2 -1	0 0	~ ~	01 CJ	0 0	
244 285	303 316 318	359 456	629 812	3839 278	278 89	163 248	285
42.7	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	42.7	42.7	42.7	42.2	41.7	41.7
41	4 4 4 1 1 1	4141	44 4	41	40.5	4 4 0 0	40
30	დ	3 3 9 2	37 38	6. 4. 0. 0.	4 4 2 2	4 4 6 4	45

ALIGNMENTS

RESULT 1

	A LUCIONA L
	chemokine (C-C) receptor 5 - human
	NyAlternate names: C-C CKR-5; CCR5
	C;Species: Homo sapiens (man)
	C.Date: 12-041-1996 #sequence revision 12-041-1996 #text_change 20-04n-2000
	. C.Accession: A42.113; 5./18018; A58.844; A58.8423; G02.853; A58.8333. R.Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier. M.
	Biochemistry 35, 3362-3367, 1996
	A.Title: Molecular cloning and functional expression of a new human CC-chemokine receptor A.Title: Molecular cloning and functional expression of a new human CC-chemokine receptor
	A, Accession: A43113 A, Accession: A43113
	A; Molecule type: mRNA
	A; Restdues: 1-352 <ami)< th=""></ami)<>
	A)-CLOSF-IELELELICS: DELANIAS; NILIGIACARIO; PIDN:CAMAZ/95.1; PIDS:GIZECELICS: R. SRIGHTI S. S. SERBOD, M.; Dibert, F.: Doranz, B.J.: Rucker, J.: Liesnard, C.: Rarber, C.
	M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collinan, R.G.; Doms, R.W.; Vassart, G.; Par
_	A; ILLE: KEBLEMINGE OF HIV-I INTECTION IN CAUCABLAN INDIVIDUALS DEARING MUTANT ALLELES OF A: REFERENCE NUMBER: S71808: MITD: 962454570. PMTD: A5751424
	A; Accession: S71808
	A;Status: nucleic acid sequence not shown; not compared with conceptual translation
	A; Wolecule type: DNA
	Afterious: 1822-200;20/-230 <samz></samz>
	Astronomerous account of semience not shown, not commared with concentual translation.
	A; Molecule type: DNA
_	A;Residues: 1-184,'IKDSHLGAGPAAACHGHLLLGNPKNSASVSK' <sam3></sam3>
	A;Cross-references: GB:X99393; NID:91524062; PIDN:CAA67767.1; PID:91524063
	A,NOVE: TILS TRAMBENIE MUTABLION TESSILES IN A NON-functional receptor but conferent and may have had a selective advantage by conference to versing a degree
	Ricombaddere, C.; Abula, S.K.; Tiffanv, H.L.; Murchy, P.M.
	J. Leukoc. Biol. 60, 147-152, 1996
_	A; Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine rece
	A; Reference number: A58832; MUID:96295970; PMID:8699119
	A; Accession: AS832
	A MODECULE UPPER MICHA A POSSÍALOS TO A COMATA
	A; restances: 1-32 C-071. A; restances: GB: U57840: NID: G1502408: PIDN: AAB17071.1: PID: G1502409
	A; Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
	R;Combadiere, C.
	submitted to the EMBL Data Library, May 1996
	A;karerance number: hulb41 A;Accession: G72653
-	A; Status: translated from GB/EMBL/DDBJ
	A; Molecule type: mRNA
	A;Residues: 1-89,'L',91-352 <com2></com2>
	A;Cross-references: EMBL:U57840
	R;Raport, C.J.; Gosling, J.; Schwelckart, V.L.; Gray, P.W.; Charo, I.F.
	or billion Million of a morrol by man on definitional characterization of a morrol by mon or chomobine
	A; Reference number: A58833; MID:96291862; PMID:8663314

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C;Species: Fyrococcus abyssi
C;Date: D0-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: A75203
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
submitted to the EMBL at a Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB49072.1; PID:g5457581
A;Experimental source: strain Orsay
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: chloroplast Euglena gracilis
C;Species: chloroplast Euglena gracilis
C;Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 11-Apr-1995
C;Accession: 534499, 534867
R;Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.; Monfort, A.; Orsat, B.; Spielmann, Submitted to the EmBL Data Library, January 1993
A;Description: The complete sequence of the Euglena gracilis chloroplast genome (tentating A;Reference number: 534494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-177 cHAL1>
A; Cross-references: 18mBL: X70810
B; Hallick, R.B.; Horg, L.; Drager, R.G.; Favreau, M.R.; Monfort, A.; Orsat, B.; Spielmanr
Nucleic Acids Res. 21, 3537-3544, 1993
Nucleic Acids Res. 21, 3537-3544, 1993
A; Title: Complete sequence of Euglena gracilis chloroplast DNA.
A; Reference number: $34862; MUID: 93447989; PMID: 8346031
A; Accession: $34867
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A.Cross-references: EMBL:X70810
C.Genetics:
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                      A; Residues: 1-196 <WIL>
A; Cross-references: EMBL:270208; PIDN:CAA94143.1; GSPDB:GN00028; CESP:F54B11.8
A; Cross-references: EMBL:270208; PIDN:CAA94143.1; GSPDB:GN00028; CESP:F54B11.8
A; Experimental source: clone F54B11
C; Genetics:
A; G
                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein 177 (psbC 3' region) - Euglena gracilis chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.phosphoglycerate kinase. PAB2253 - Pyrococcus abyssi (strain Orsay)
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                                                                                                                                                                                                                                                                                             47.9%; Score 46; DB 2;
66.7%; Pred. No. 4.5;
tive 1; Mismatches
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Pred. No.
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55.6%;
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Best Local Similarity 55.6
Matches 10; Conservative
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Best Local Similarity 66.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Genome: chloroplast
C;Keywords: chloroplast
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A, Molecule type: DNA
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C;Comment: This is a receptor for chemokines MIP-lalpha (see PIR:A30574), MIP-lbeta (see
C;Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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T22609
T12609
T22609
T22609
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T22609
R;Swinburne, J.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19588
A;Accession: T22609
A;Accession: T22609
A;Status: preliminary, translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                            A;Gene: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CKR5; ChemR13
A;Cross-references: GDB:1230510; OMIM:601373
A;Map position: 3p21-3p21
C;Function:
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195 WKRFQALKLNLLG 207
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Matches 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                      A; Molecule type: mRNA
A; Residues: 1-352 <RAP>
                A; Accession: A58833
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Matches
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probable 2-phosphoglycerate kinase - Pyrococcus horikoshii

grobable 2-phosphoglycerate kinase - Pyrococcus horikoshii

C; Date: 14-Mug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000

C; Accession: C71236

R; Kawarabayasi, Y; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine

R; Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine

M; Obfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,

DNA Res. S, 55-76, 1998

A; Reference number: A71000; MUID:98344137; PMID:9679194

A; Residues: Drellminary, nucleic acid sequence not shown; translation not shown

A; Residues: 1-301 «KAW»

A; Residues: 1-301 
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                                                                                               Cypace: Lateratory meducate revision is our 1990 mean_consider 1974, 2002
Cypace: Lateratory meducate revision is our 1990 mean_consider to the protein Sequence Database, Unly 1996
A;Reference number: S67194
A;Recession: S67200
A;Molecule type: DNA
A;Residues: 1-1289 <CZI>A;Cross-references: EMBL:275204; NID:g1420655; PID:g1420656; GSPDB:GN00015; MIPS:YOR296w
A;Gene: MIPS:YOR296w
A;Gene: MIPS:YOR296w
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   Alternate names: hypothetical protein 05623
Species: Saccharomyces cerevisiae
Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
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A;Map position: 15R
C;Superfamily: Saccharomyces cerevisiae hypothetical protein YOR296w
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Pred. No. 12;
6; Mismatches 3; Indels
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C;Superfamily: 2-phosphoglycerate kinase
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77 RYIFWRRFRKMKVPLIILG 96
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Best Local Similarity 40.0%;
Matches 8; Conservative 6
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nes 7; Conserve
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
G85575
hypothetical protein Z0898 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: G85575
R;Perote Numket III, G; Burland, V; Mau, B; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L; Grocheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85575
A;Accession: G85575
A;Aclecule type: DNA
A;Residues: 1-314 <STO>
A;Cross_references: GB:AE005174; NID:912513664; PIDN:AAG55067.1; GSPDB:GN00145; UMGP:Z08
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z0898
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics: CGBnetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: CGB0767
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                                                                                                          Length 302;
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56.2%; Pred. No. 11;
iive 3; Mismatches 4; Indels
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867200
hypothetical protein YOR296w - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                  46.9%; Score 45; DB 2;
37.5%; Pred. No. 10;
cive 6; Mismatches
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56.2%; Pred. No. 11;
tive 3; Mismatches
A,Gene: PAB2253
C,Superfamily: 2-phosphoglycerate kinase
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289 SQYRFFKMFTNLALVI 304
                                                                                                                                                                                                                                                                            2 QYQFWKNFQTLKIVIL 17
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Best Local Similarity 56.21
Best Local 9; Conservative
                                                                                                                                  Best Local Similarity 37.5 Matches 6; Conservative
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Length 237;

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Genome Res. 11, 731-753, 2001
A,Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssg. A,Reference number: A86625; MUID:21235186; PMID:11337471
A,Accession: A86719
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Genome Res. 11, 731-753, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C,Accession: A99066
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Es R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Es R;LeBlanc, D.J.; Leefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; McAhren, S.; McAhren, S.; McAhren, S.; McAhren, S.; McAhren, S.; McAhrens, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Accession: A)Ascession: Ay90666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NADPH-flavin oxidoreductase (EC 1.6.99.-) homolog [imported] - Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oxidoreductase yhgA [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
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A,Molecule type: DNA
A,Residues: 1-242 <SID-424 SADA
A,Cross-references: GB:Ab005176; PID:g12723669; PIDN:AAK04851.1; GSPDB:GN00146
A,Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-237 <KUR>
A;Cross-references: GB:AE007317; PIDN:AAL00358.1; PID:g15459219; GSPDB:GN00174
C;Genetics:
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C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
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41.7%; Pred. No. 17;
Live 5; Mismatches
                                                                    Score 43; DB 2;
Pred. No. 17;
5; Mismatches
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A;Gene: yhgA
C;Superfamily: NADPH-flavin oxidoreductase homolog
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C;Superfamily: NADPH-flavin oxidoreductase homolog
C;Keywords: oxidoreductase
    C; Superfamily: NADPH-flavin oxidoreductase homolog
                                                                            44.8%;
ilarity 41.7%;
Conservative
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
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C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C;Accession: C95199
R;Tettelin, H; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 203-504, 208-506, 203-504, 203-506, 203-504, 203-506, 203-504, 203-506, 203-504, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-506, 203-5
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A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1710
A;Cross-references: GB:AL139079; GB:AL111168; NID:g6968971; PIDN:CAB73647.1; PID:g696907
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: Cj1660
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A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MuID:95350630; PMID:7542800
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C;Species: Haemophilus influenzae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2000
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                                                                                                                                                                                                        DB 2; Length 467
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C;Superfamily: protein export membrane protein secD
                                                                                                                                                                                                            45.8%; Score 44; DB 37.5%; Pred. No. 23; tive 4; Mismatches
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NRYPLWKNLMVIFIVAIG 20
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77 FYFWKKIBILNFILLG 92
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Best Local Similarity
7, Conserva
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A,Molecule type: DNA
A,Residues: 1-237 <KUR>
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Best Local Similarity
Matches 6; Conserv
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Length 242;

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Ajacession: S60866
Ajmolecule type: DNA
Ajression: S60866
Ajmolecule type: DNA
Ajression: S60866
Ajmolecule type: DNA
Ajressidues: 977-1104 cHMA>
Ajressidues: 977-1104 chmarch, N.; Albertington, J.; Puma, S.; Brouilet, S.; Bruschi, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Puma, S.; Galizzi, A.; Galler, Settler, S.D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, Settler, J.; Hamauch, A.; Hilbert, H.; Holasppel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueell, Y.; Ogiwara, A.; Oddega, B.; Park, S.H.; Parko, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Saton, A; Seror, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Oddiyama, T.; Winters, P.; Wipak, H.F.; Zumstein, B.; Yoshikawa, H.; Danchin, A.
Ajritle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
Ajritle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
Ajritle: The complete genome sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AyStatus muchae and sequence not shown; translation not shown AyStatus: nucleid acid sequence not shown; translation not shown AyStatus: nucleid acid sequence not shown; translation not shown AyStatus: nucleid acid sequence not shown; AyCoss-references: GB1293105; GB:AL009126; NID:g2632457; PIDN:CAB12143.1; PID:g2632635 A; Experimental source: strain 168

RyRabrer; C: Questin, Y: Guisseppi, A.; Busuttil, J.; Haiech, J.; Denizot, F. submitted to the EMBL Data Library, March 1993

A; Reference number: $46967

A; Accession: $46968

A; Molecule type: DNA

A; Reference muber: $134,787,2142, DSLM',2146-2444, Q',2446-2712, H',2714-2722, H',2724, 1756-1914, PR',1917-2138, VRD:G516360

R; Funa, S: Fulishima, Y: Corpell, N: D'Souza, C.; Nakano, M.; Zuber, P.; Yamane, K. Mucleic Acids Res. 21, 93-97, 1993

A; Title Nucleotide sequence of E's portion of srfA that contains the region required for A; Reference number: $35517; MUID:3181166; PMID:844623

A; Accession: $35518

A; Status: significant sequence differences

A; Status: significant sequence diff
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                A,Title: A small gene, designated comS, located within the coding region of the fourth an A,Reference number: S60866; MUID:95272393; PMID:7752896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3587;
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Pred. No. 2.7e+02;
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33.3%;
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Best Local Similarity
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G99183
periplasmic sorbitol-binding protein, smoE (AF018073) [imported] - Agrobacterium tunmefact
C; Species: Agrobacterium tunmefaciens
C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C; Accession: G98183
R; Goodner, Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A; Reference number: A97359; MUID:21608551; PMID:11743194
A; Scatus: pre-liminary
A; Molecule type: DNA
A; Residues: 1-475 <KUR>
A; Control of C; Genetics:
C; Genetics:
C; Genetics:
A; Map position: linear chromosome
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140486
surfactin synthetase component II - Bacillus subtilis
NiAlternate names: surfactin synthetase srfA2; surfactin synthetase/competence protein s
NiAlternate names: surfactin synthetase srfA2; surfactin synthetase/competence protein s
NiAlternate names: surfactin synthetase (EC 6.3.2.-)
C; Species: Bacillus subtilis
C; Date: 12-Aug-1996 #sequence revision 12-Aug-1996 #text_change 03-Nov-2000
C; Accession: 140486; S60866; C69718; S46968; S35518; S25688; S34986
R; Cosmina, P.; Rodriguez, F.; de Ferra, F.; Grandi, G.; Perego, M.; Venema, G.; van Sind Mol. Microbiol. 8, 821-831, 1993
A; Title: Sequence and analysis of the genetic locus responsible for surfactin synthesis A; Reference number: 140486
A; Reference number: 140486
A; Recession: 140486
A; Accession: 140486
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-3587 RRES>
A; Cross-references: EMBL:X70356; NID: 9396480; PIDN: CAA49817.1; PID: 9396482
A; Experimental source: strain W168 derivative of JH642
R; Hamoen, L.W.; Eshuis, H.; Jongbloed, J.; Venema, G.; van Sinderen, D.
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chemokine receptor - human
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: JC5942
R;Fan, P: Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.
Biochem: Biophys. Res. Commun. 243, 264-268, 1998
Biochem: Biophys. Res. Commun. 243, 264-269, 1998
A;Title: Cloning and characterization of a novel human chemokine receptor.
A;Reference number: JC5942, MuID:98139902; PMID:9473515
A;Accession: JC5942
A;Actus: preliminary
A;Acleule type: DNA
A;Residues: 1-344 c;AN>
A;Ross-references: GB:107123; NID:g2897070; PIDN:AAC39595.1; PID:g2897071
C;Superfamily: vertebrate rhodopsin
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Pred. No. 24;
2; Mismatches
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ilarity 50.0%;
Conservative 3
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34 FWEEDMTLKTILLG 47
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FWKHFLTLKMNI 206
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Best Local Similarity 66.7
Matches 8; Conservative
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Best Local Similarity
Matches 7; Conserv
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hypothetical protein MYPU_1320 [imported] - Mycoplasma pulmonis (strain UAB CTIF)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Date: 124-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Reference number: A99512; MUD::21267165; PMID::11353084
A;Accession: D99528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClella, Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - Agrobacterium tumefaciens (strain C58, Dupont)
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AB2315

A;Status: preliminary

A;Nolecule type: DNA

A;Residues: 1-421 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL43736.1; PID:g17741269; GSPDB:GN00186

A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-383 «KUR»
A, Cross-references: GB: AL445566, PID: g14089545; PIDN: CAC13305.1; GSPDB: GN00153
A, Experimental source: strain UAB CTIP
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C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
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                              Indels
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40;
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46.2%; Pred. No. 44;
iive 4; Mismatches
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Pred. No. 40;
3; Mismatches
      44.4%; Pred. No. 36; tive 4; Mismatches
                                                                                                                           246 TQFDFLLTFQLLIIIVLG 263
                                                                                    1 SOYOFWKNFOTLKIVILG 18
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349 RYQSWRRFDTLRM 361
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                              8; Conservative
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Matches 7; Conservative
Best Local Similarity
Matches 8; Conserva
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Matches 6, Conserv
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E97689
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C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: E8133
R;Parchill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-350 cPAR>
A, Experimental source: 8:AL139077, GB:AL111168, NID:g6968444; PIDN:CAB73272.1, PID:g696845
A, Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ribietrich, F.S.

Submitted to the EMBL Data Library, December 1994
A; Description: The sequence of S. cerevisiae cosmids 8199, 8334, and 9871.
A; Reference number: $50491
A; Recession: $50506
A; Roccession: $50506
A; Roccession: $1241 * DNB
A; Roccession: $1233 * 372-386; $1993
A; Title: The gene clusters ARC and COR on chromosomes 5 and 10, respectively, of Sacchar A; Reference number: $38543; MUID: 94016558; PMID: 8411151
                                                                                                                                                                                                                                                         UTR4 protein - yeast (Saccharomyces cerevisiae)
N/Alternate names: protein YEL038w
C/Species: Saccharomyces cerevisiae
C/Species: Saccharomyces cerevisiae
C/Bate: 28-May-1993 #sequence revision 28-May-1993 #text_change 18-Aug-2000
C/Accession: 830843; S50506; S38544
R/Mulligan, J.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor, Submitted to the EMBL Data Library, February 1993
A/Accession: S30843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: GB:U18779; EMBL:L10830; NID:g603625; PIDN:AAB65004.1; PID:g603641
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A;Residues: 1-69, MH',72-152,'GMIRMI' <MEL>
A;Cross-references: EMBL:866121, NID:9430827; PIDN:AAB28443.1; PID:9430828
            Gaps
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C;Superfamily: Klebsiella oxytoca methionine salvage pathway enzyme
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            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 2;
Pred. No. 25;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: SGD:S0000764; MIPS:YEL038w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 42;
                                                                                                      :: | | |::|:::| | | 1751 ASFAFDANFESLRLIVLG 1768
               9
                                                                  1 SOYOFWKNFOTLKIVILG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.8%;
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               Conservative
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KYQVYKNFETL 241
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecule type: DNA
Residues: 1-241 <MUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Gene: livM; Cj1016c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Accession: S38544
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               . 9
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               Matches
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A;Cross-references: GB:AL139074; GB:AL111168; NID:g6967505; PIDN:CAB72717.1; PID:g6967726 A;Experimental source: serotype O2, strain NCTC 11168 C;Genetical Source: Serotype O2, strain NCTC 11168 C;Genetical O20249 C;Superfamily: Campylobacter jejuni hypothetical protein Cj0249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 YOFWKN-----FOILKIVIL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:||||
33 YKFWKNAEIGRYQGTRIIFL 52
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 40.0%;
Matches 8; Conservative
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hypothetical protein AGR C 4995 [imported] - Agrobacterium tumefaciens (strain C58, Cere C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Date: 30-Sep-2001 #text_change 18-Nov-2002 C; Accession: E97689 # Scassion: E97689 # Scassion: E97689 # Sidut, F:, Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2326, 2001 # Science 294, 2323-2326, 2001 # Science 294, 2323-2326, 2001 # A; Recence number: A97359; Muid: 21608551; PMID:11743194 # A; Accession: E97689 # A; Status: preliminary A; Accession: B97689 # A; Status: preliminary A; Mollam, A; Mollam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 23
C84678
hypotherical protein At2g27900 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Decies: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: 024678
A; Kaul, S:; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nibranan, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1959
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: C84678
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-496 <STO>
A;Cross-references: GB:AE002093; NID:g4510426; PIDN:AAD21512.1; GSPDB:GN00139
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H8142
H81442
H81442
C;Pate1 protein Cj0249 [imported] - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: H81442
R;Parkhill, M; Rajandream, M.A.; Katley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp. A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: H81442
A;Accession: H81442
A;Accession: L994848
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Pred. No. 44;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43.8%; Score 42; DB 2; Length 496; 52.9%; Pred. No. 52;
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100 SIHQFLKNYEDLSIFIL 116
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Best Local Similarity 52.99,
Best Local Similarity 52.99,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 OYOFWKNFOTLKI 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
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Best Local Similarity
Matches 6; Conserve
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A,Map position: 2
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A/Accession: S16296
A/Cross-references: EMBL:X57471; NID:g41429; PIDN:CAA40707.1; PID:g41430
B/Cross-references: EMBL:X57471; NID:g41429; PIDN:CAA40707.1; PID:g41430
B/Title: Organization of genes encoding membrane proteins of the Escherichia coli ferrier A/Accession: S16305
A/Accession: D4792
A/Accession: D64792
A/Accession: D64792
A/Accession: D64792
A/Accession: D64792
A/Accession: D64792
A/Accession: D64792
A/Accession: D64
A/Accession: D64792
A/Accession: D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Escherichia coli
C;Date: 04-Dec-1992 #sequence revision 04-Dec-1992 #text_change 01-Mar-2002
C;Accession: S16396; S16305; D64792; S14841
R;Shea, C.M.; McIntosh, M.A.
Mol. Microbiol. 5, 1415-1428, 1991
A;Title: Nucleotide sequence and genetic organization of the ferric enterobactin transpon
A;Reference number: S16295; MUID:92157868; PMID:1838574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ferric enterobactin transport protein fepD - Escherichia coli (strain K-12)
N;Alternate names: ferrienterobactin permease fepD
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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     DB 2; Length 159;
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                                                                                                                3; Indels
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C;Superfamily: vitamin B12 transport protein btuC
C;Superfamily: vitamin B12 transport protein btuC
C;Superfamily: transmembrane #status predicted <TM1>
F;65-81/Domain: transmembrane #status predicted <TM2>
F;94-110/Domain: transmembrane #status predicted <TM3>
F;121-137/Domain: transmembrane #status predicted <TM4>
F;138-114/Domain: transmembrane #status predicted <TM5>
F;188-214/Domain: transmembrane #status predicted <TM6>
F;284-306/Domain: transmembrane #status predicted <TM6>
F;284-300/Domain: transmembrane #status predicted <TM6>
F;310-326/Domain: transmembrane #status predicted <TM8>
Score 41.5; DE Pred. No. 20; 4; Mismatches
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Best Local Similarity 34.8%; Pred. No. 42;
Matches 8; Conservative 5; Mismatches
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Length 46; Indels

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hypochetical protein BH0680 (imported) - Bacillus halodurans (strain C-125)
C'Species: Bacillus halodurans
C'Species: Bacillus halodurans
C'Species: Bacillus halodurans
C'Space: Ou-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C'Spacession: H83734
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran
Nuclaic Acids Res. 28, 4317-4311, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and c
A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-118 <STO>
A;Cross-references: GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BAB04399.1; GSPDB:GN001
A;Experimental source: strain C-125
A; Residues: 1-46 <hOR>
A; Cross-references: GB:D38484; NID:g558513; PIDN:BAA07494.1; PID:g558514
C; Genetics:
A; Genome: ND1
A; Genome: mitochondrion
A; Genome: mitochondrion
C; Superfamily: NGC1
C; Superfamily: NADH dehydrogenase (ubiquinone) chain 1
C; Superfamily: membrane-associated complex; mitochondrion; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Species: Sulfolobus particle SSV1
C.Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Apr-2000
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R;Palm, P.; Grampp, B.; Zillig, W.; Yeats, S.; McWilliams, P.; Reiter, W.D.
submitted to the EMBL Data Library, March 1988
A;Reference number: S03211
A;Reference number: S03212
A;Molecule type: DNA
A;Residues: 1-244 PALL.
A;Cross-references: EMBL:X07234; NID:g46703; PIDN:CAA30214.1; PID:g46708
C;Superfamily: Sulfolobus particle SSV1 hypothetical protein D-244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein D-244 - Sulfolobus particle SSV1
                                                                                                                                                                                                                                                             Score 41; DB 2;
Pred. No. 6.7;
2; Mismatches
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Pred. No. 17;
5; Mismatches
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17;
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Best Local Similarity 40.0%;
Matches 6; Conservative 6
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Best Local Similarity 41.2%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               15 YLLWKNFLPLTLALL 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 QYEYWKHTQLIIDVVDG
                                                                                                                                                                                                                                                                                                                            7; Conservative
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 7; Conserv
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A;Gene: BH0680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ferric enterobactin (enterochelin) transport EC80629 [imported] - Escherichia coli (stra C; Species: Escherichia coli (c) Species: Escherichia coli (c) Species: Escherichia coli (stra C; Species: Escherichia coli (c) Species: ES-011-2011 #sequence_revision 18-Jul-2001 #text_change 17-May-2002 (c) Accession: E90707 R; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. A; Hayashi, T.; Makino, K.; Ohnishi, M.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2011 A; Shiba, T.; Hattori, M.; Shinagawa, H. A; Hile: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gench A; Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                             C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
C;Accession. A65558
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Mature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-334 <STO>
A;Cross-references: GB:AE005174; NID:g12513480; PIDN:AAG54925.1; GSPDB:GN00145; UWGP:Z07
A;Experimental source: strain 0157:H7, substrain EDL933
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NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain 1 - siamang mitochondrion (fragment)
C,Species: mitochondrion Hylobates syndactylus (siamang)
C,Bate: 21-Feb_1997 #sequence_revision 21-Feb-1997 #text_change 03-Jun-2002
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                                                              ferric enterobactin (enterochelin) transport [imported] - Escherichia coli (strain O157
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Thorat, S.; Satta, Y.; Hayasaka, K.; Kondo, R.; Inoue, T.; Ishida, T.; Hayashi, S.; Sattata, Y.; Hayasaka, K.; Kondo, R.; Inoue, T.; Ishida, T.; Hayashi, S. J. Mol. Evol. 35, 32-43, 1992

A,Title: Man's place in Hominoidea revealed by mitochondrial DNA genealogy.

A,Reference number: 137047; MUID:92389366; PMID:1518083

A,Accession: 137047

A,Status: preliminary; translated from GB/EMBL/DDBJ

A,Molecule type: DNA
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C;Superfamily: vitamin B12 transport protein btuC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: fepD
C;Superfamily: vitamin B12 transport protein btuC
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Best Local Similarity 34.8%;
Matches 8; Conservative 5
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Best Local Similarity
Matches 8; Conserv
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Query Match
Best Local Similarity 41.7%;
Matches 5; Conservative

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NADRIZ dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - common gibbon mitochondrion C.Species: mitochondrion Hylobates lar (common gibbon, white-handed gibbon) (C.Date: 16.701-1999 #sequence_revision 16.701-1999 #text_change 03.70n-2002 C.Accession: T1833
R.Arnason, U.; Gullberg, A.; Xu, X.
Hereditas 124, 185-189, 1996
A.Title: A complete mitochondrial DNA molecule of the white-handed gibbon, Hylobates lar, A.Reference number: Z17353
A.Accession: T1833
A.Accession
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A.; Larbig, K.; Lim,
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                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F44G3.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T22197
R;McMurray, A.
Submitted to the EMBL Data Library, November 1996
A;Reference number: Z19529
A;Reference number: Z19529
A;Accession: T22197
A;Accession: T22107
A;Accessi
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C;Superfamily: NADH dehydrogenase (ubiquinone) chain 1
C;Keywords: membrane-associated complex; mitochondrion; NAD;
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Pred. No. 48;
3; Mismatches 3
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Pred. No. 48;
2; Mismatches
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Best Local Similarity 57.1%;
Matches 8; Conservative
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Best Local Similarity 46.7%;
Matches 7; Conservative
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29 FWEKFSKNKLAILG 42
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A;Introns: 142/3; 185/3; 256/3
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INGORDENCE ABC transporter (permease) appC - Bacillus subtilis
Cipder: 12-Aug-1996 #Requence_revision 12-Aug-1996 #text_change 20-Jun-2000
Cipdocession 140647; E69566
Rivoide A.; Hoch, J.A.26, 1994
A.Title: Identification of a second oligopeptide transport system in Bacillus subtilis a A; Accession: 140647; E69566
A.Fitle: Identification of a second oligopeptide transport system in Bacillus subtilis a A; Accession: 140647; E69566
A.Fitle: Identification of a second oligopeptide transport system in Bacillus subtilis a A; Accession: 140647; E69566
A.Fitle: Identification of a second oligopeptide transport system in Bacillus subtilis a A; Accession: 140647; E69566
A.Fitle: Identification of a second oligopeptide transport system in Bacillus subtilis a A; Accession: 140647; E69566
A.Fitle: Identification of a second oligopeptide transport system in Bacillus subtilis a A; A; Accession: 140647; E696679
A.Fitle: Togasawara N; Mozer, I.; Albertini, A, M.; Alloni, G.; Accrece, N.M.; Alloni, G.; Accrece, D.A.
A.Fitlick: S.D.; Emarchi, C.Y.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch.
A.; Entick, S.D.; Emarchi, C.Y.; Entition, K.D.; Errington, J.; Pabret, C.; Ferrari, C.; Accession, J.; Accession: 140647; A.; Accession, J.; Accessi
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: A84494
C;Accession: A84494
R;iin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84494
A;Reference number: A84494
A;Accession: A84494
A;Accession: A84494
A;Accession: Lyge: DNA
A;Accession: A84494
A;Access
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Pred. No. 46;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 2; Length 285;
Pred. No. 43;
4; Mismatches 3; Indels
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42.7%;

Query Match
Best Local Similarity 50.0%

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Drobable zinc-finger protein - Arabidopsis thaliana
N.Alternate names: protein T17J13.200
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C.Accession: T48016
R.Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer, Pstreiger, C. the Protein Sequence Database, February 2000
A.Recession: T48016
A.Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                               A)Description: pre-mRNA splicing A,Note: necessary for the stable interaction of mRNA precursors with the snRNP component: C,Keywords: nucleus; pre-mRNA splicing; transmembrane protein F;429-445/Pomain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Accession: T49799
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
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C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
                                  A;Cross-references: EMBL:L29224; NID:9460045; PIDN:AAA20131.1; PID:9460046
A;Note: the authors translated the codon GAC for residue 29 as Ala
R;Odell, C.; Bowman, S.
Bubmitted to the EMBL Data Library, January 1995
A;Reference number: S50941
A;Accession: S50946
                                                                                                                                                                                                                                                              A;Cross-references: EMBL:Z47816; NID:g642303; PID:g642309; MIPS:YML046w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 812;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-812 <RIE>
A;Cross-references: EMBL:AL138651
A;Experimental source: cultivar Columbia; BAC clone T17J13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            related to TOM1 protein [imported] - Neurospora crassa N,Alternate names: protein B11B22.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 2; Le.
Pred. No. 1.2e+02;
5; Mismatches 2;
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Pred. No. 96;
4; Mismatches
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A;Introns: 56/3; 159/3; 229/2; 245/3; 275/3; 296/3
A;Note: T17J13.200
                                                                                                                                                                                                                                                                                                                          A,Gene: SGD:PRP39
A,Cross-references: SGD:S0004509; MIPS:YML046w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.7%; Scor.
37.5%; Pred
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Best Local Similarity 46.2%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 QYEYYKNYDDLEI 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 37.59
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 YOFWKNFOTLKIVILG
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A;Molecule type: DNA
A;Residues: 1-629 <LOC>
                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-629 <ODE>
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A,Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                 A, Map position: 13L
C; Function:
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                                                                                                                                                              A;Residues: 1-359 <STO>
A;Cross-references: GB:AE004636; GB:AE004091; NID:g9948093; PIDN:AAG05478.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA2090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CiSpecies: Pseudomonas sp.
CiSpecies: Pseudomonas sp.
CiDate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
CiDates: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
CiDates sion: 1842594; A41895
R;Watabe, K.; Ishikawa, T.; Mukohara, Y.; Nakamura, H.
Bacteriol. 14, 962-969, 1999
A;Title: Cloning and sequencing of the genes involved in the conversion of 5-substituted A;Reference number: A42594; MUID:92121137; PMID:1732229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pre-mRNA splicing factor PRD39 - yeast (Saccharomyces cerevisiae)

Nylternate names: protein YMB27.06; protein YML046w

C;Species accharomyces cerevisiae

C;Species accharomyces cerevisiae

C;Species: 13-Jan-1995 #sequencc_revision 13-Jan-1995 #text_change 21-Jul-2000

C;Accession: S4720; S50946

R;Lockhart, S.R.; Rymond, B.C.

Mol. Cell. Biol. 14, 3623-3633, 1994

A;Title: Commitment of yeast pre-mRNA to the splicing pathway requires a novel U1 small A;Reference number: S47920; MUID:94254621; PMID:8196608
     A;Title: Identification and sequencing of a gene encoding a hydantoin racemase from the A;Reference number: A41895; MUID:92276321; PMID:1339422 A;Accession: A41895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein ORFS hyuC 3'-region, hyuE 5'-region - Pseudomonas sp. plasmid pHN6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-245 <WA2>
A; Cross-references: GB:D10494; GB:D90469; NID:g216829; PIDN:BAA01380.1; PID:g216834
A; Notes: sequence extracted from NCBI backbone (NCBIN:77753, NCBIP:77764)
B; Natebe, K.; Ishikawa, T.; Mukohara, Y.; Nakamura, H.
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A;Residues: 244.456 <WAT>
A;Experimental source: strain NS671
A;Experimental source extracted from NCBI backbone (NCBIN:104597, NCBIP:104598)
C;Genetics:
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C,Superfamily: Escherichia coli probable transport protein b0511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB 1; Length 456;
Pred. No. 69;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                             Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                          42.7%; Score 41; DB 2; ilarity 60.0%; Pred. No. 54; Conservative 2; Mismatches (
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Best Local Similarity 42.9%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 KFWKHFQ----VILG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                382 OYKYWKNVNPAAII 395
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Best Local Similarity
9, Conserve
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S47920
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A;Residues: 1-3839 <SCH>
A;Cross-references: EMBL:AL356834; GSPDB:GN00116; NCSP:B11B22.10
B;Experimental source: BAC clone B11B22; strain OR74A
B;Genetics: A;Genetics: 0.05P:B11B22.10
B;Gene: NCSP:B11B22.10
B;Map position: 6
A;Map position: 6
A;Introns: 16/3; 2607/1; 2623/1; 2658/1; 2845/1; 2987/2; 3204/3; 3694/1; 3809/1
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0
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1219 YKNFQTLRVLL 1229
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RESULT 40
H91193
DNA-damage-inducible protein [imported] - Escherichia coli (strain O157:H7, substrain RI C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: H91193
R;Hayashi, T.; Makino, K.; Chnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA, Res. B., 11-22, 2001
A;Tile: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gench, Reference number: A99629; MUID:21156231; PMID:11258796
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Status: prelliminary
A;Molecule type: DNA
A;Residues: 1-278 cHXX>
A;Crossrion: H9119
A;Residues: 1-278 cHXX>
A;Crossrion: H9119
A;Residues: 1-278 cHXX>
A;Crossrion: By H91191 Solutce: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Genetics:

23; 42.2%; Score 40.5; DB 2; Length 278; 25.6%; Pred. No. 50; cive 4; Mismatches 2; Indels 23 Query Match 42.2 Best Local Similarity 25.6 Matches 10, Conservative

3 YOFWKNFQ-----TLKIVILG 18

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ä

Gaps

Search completed: September 28, 2004, 09:07:09 Job time : 11.925 secs

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us-10-084-813-13.rsp

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

September 28, 2004, 08:55:11; Search time 5.625 Seconds (without alignments) 166.624 Million cell updates/sec Run on:

US-10-084-813-13 96 1 SQYQFWKNFQTLKIVILG 18 Title: Perfect score: Sequence:

Scoring table:

141681 seqs, 52070155 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		Description	cer	υ	062743 cercocebus	ρ	P51681 homo sapien	097883 hylobates l	Q95nc0 hylobates m	Q95nc5 hylobates s	P56440 pan troglod	P56441 papio hamad	O97881 pongo pygma	097880 pygathrix b		097878 trachypithe			P51682 mus musculu		P51675 mus musculu	P51683 mus musculu						cercop			Q04747 bacillus su	P32626 saccharomyc		20213	4206
SUMMARIES		ID	CKR5 CERAE	CKR5_CERPY	CKR5 CERTO	CKR5 GORGO	CKR5 HUMAN				CKR5_PANTR			CKR5_PYGBI		CKR5_TRAFR	CKR5_TRAPH	CKRS_MACMU	CKR5_MOUSE	CKR5_RAT	CKR1_MOUSE	CKR2_MOUSE	CKR1_MACMU	YCX3_EUGGR	DYHB_HUMAN			CKR3_CERAE	- 1	VIOD_CHRVO	٦١	۲,	PDE	اير	APPC_BACSU
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	Result	No.	П	~	m	4	S	9	7	æ	σ	10	11	12	13	T -	15	16	17	18	19	20	21	22	23	24	52	56	27	29	29	30	31	32	33

Q96126 hylobates 1 Q9213 cavia porce Q52193 rattus norv P81910 drosophila O75072 homo sapien P39682 saccharomyc Q06820 homo sapien P44298 haemophilus P32246 homo sapien Q44298 cacharomyc Q063246 homo sapien Q44298 cacharomyc Q083246 box sapien Q97855 clostridium
NUIM HYLLA CKR3_CAVPO CKR3_CAVPO 022B_DROWE FCWD HUWAN PR39_YEAST SUIA_HUWAN YBGK_HAEIN CKR1_HUWAN YBGK_HAEIN CKR1_HUWAN ARLY_CLOAB ARLY_CLOAB
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ALIGNMENTS

RANSMEM FRANSMEM

DOMAIN DOMAIN

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SEQUENCE FROM N.A.

SETAIN=ISOJAte 079, 085, 087, and 089;

MEDLINE-93212155, PubMed-955699;

Chen Z., Gettie A., Ho D.D., Marx P.A.;

Chen Z., Gettie A., Ho D.D., Marx P.A.;

"Primary SITVS isolates use the CRS correcptor from sooty mangabeys
naturally infected in west Africa: a comparison of correceptor usage
of primary SIVSM, HIV-2, and SIVMac.";

Virology 244:113-124(1998).

-I. FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

MIP-1-beta and RANIES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or

differentiation.
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C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR5)
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOWALN
1 58 1 (POTENTIAL).

    -!- SUBCELLULAR LOCATION: Integral membrane protein.
    -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELUIAR (POTENTIAL).
7 (POTENTIAL).
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4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EF17D67CBCCCG3DB0 CRC64;
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CYTOPLASMIC (POTENTIAL).
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100.0%; Pred. No. 6.6e-08;
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nes 18; Conservative
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352 AA;
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RI AIDS Res. Hum. Retroviruses 15:931-939(1999).

- I FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, C.C. increasing the intracellular calcium ions level. May play a role intracellular calcium ions level. May play a role differentiation.

- SUBCELLULAR LOCATION: Integral membrane protein.

- SUBCELLULAR LOCATION: Integral membrane in moverne modified medities requires a license agreement (see by and for commercial medities requires a license agreement (see by and for commercial medities requires a license agreement (see by non-profit integral protein.

- SUBCELLULAR LOCATION: Integral license agreement is not removed. Usage by and for commercial membrane and an email to license@lisb-sib.ch).
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115-MAR-2004 (Rel. 43, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCRS OR CMKBRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cercopithecus pygerythrus (Vervet monkey).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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Pred. No. 6.6e-08;
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
                                                               2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                           CYTOPLASMIC
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MEDLINE=99335215; PubMed=10408730;
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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Local 18, Conservative
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352 AA;
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R EMBL; AF051902; AAC39830.1; -.
R RMBL; AF051904; AAC39831.1; -.
R RMBL; AF051905; AAC39831.1; -.
R MRL; AF051905; AAC3983.1; -.
R InterPro; IPR000276; GPCR_Rhodpsn.
R PRINTS; PR00001; 7tm 1; 1.
R PRINTS; PS00237; GPCRHODOSN.
R PROSITE; PS00237; GPROTEIN RECEP_F1_1; 1.
R PROSITE; PS00237; GPROTEIN RECEP_F1_2; 1.
R PROSITE; PS00262; GPROTEIN RECEP_F1_2; 1.
R G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
T DOMAIN 1 58 CYTOPLASHIC (POTENTIAL).
T TRANSMEM 31 59 GB CYTOPLASHIC (POTENTIAL).
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MEDLINE=97268687; PubMed=9108095;

Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
Peiper S.C., Parmentier M., Broder C.C., Doms R.W.,
"Differential utilization of CCR5 by macrophage and T cell tropic
simian immunodeficiency virus strains.",
Proc. Natl. Acad. Sci. U.S. 94:4005-401(1997).

Proc. Natl. Acad. CC type chemokine. Binds to MIP-1-alpha,
"IP-1-beta and RANTES and subsequently transduces a signal by
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15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5)
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CCRS OR CMKBRS.
CCRS OR CMKBRS.
Gorilla gorilla (Lowland gorilla).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
NCBI_TaxID=9595;
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V -> G (IN ISOLATE 087).
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100.0%; Pred. No. 6
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les 18; Conserv
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PITA: PRODOUG); 7tm 1; 1.

PRINTS; PF00001; 7tm 1; 1.

PRINTS; PF00237; GPCRHODOPSN.

PROSTITE; PS00237; GF0TENN RECEP. F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

G-protein 1 30 EXTRACELULAR (POTENTIAL).

TRANSMEM 1 59 GR CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                             100.0%; Score 96; DB 1; Length 352; 100.0%; Pred. No. 6.6e-08; ive 0; Mismatches 0; Indels
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EXTRACELLULAR (POTENTIAL)
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7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL) .

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EXTRACELLULAR (POTENTIAL)
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increasing the intracellular calcium ions level. May play a role

differentiation.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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AF011532;
                                                                                                                  CC-CKR-
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SEQUENCE FROM N.A.
MEDLINE=56291862; PubMed=86633114;
Rappir C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.;
"Molecular cloning and functional characterization of a novel human CC chemokine receptor (CCRS) for RANTES, MIP-1beta, and MIP-1alpha.";
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MEDLINE=98022612; PubMed=9359654;
Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
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Munmidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;
Munmidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;
Mine human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts
With buman CC chemokine receptor promoter usage, and evidence for
polymorphisms within the regulatory regions and noncoding exons.";
J. Biol. Chem. 272:30662-30671(1997).
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"Polymorphisms in the CCR5 genes of African green monkeys and mic implicate specific amino acids in infections by simian and human immunodeficiency viruses."

J. Virol. 71:8642-8656(1997).
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                                                                                                                                                                                                                                                                                                                    MEDLINE-96295970; PubMed-8699119;
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"Cloning and functional expression of CC CKR5, a human monocyte
chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and
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MEDLINE-96260017; PubMed-8649511;
Deng H., Liu R., Ellmeier W., Choe S., Unutmaz D., Burkhart M.,
di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B.,
Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
"Identification of a major co-receptor for primary isolates of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Magierowska M., Barre-Sinoussi F., Issafras H., Theodorou
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Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=98001387; PubMed=9343222;
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   CC-chemokine receptor gene.";
Biochemistry 35:3362-3367(1996).
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                                                                                                                                                                                                                                                                                                       MEDLINE=99189752; PubMed=10089882; Parzan M., Mizabekov T., Kolchinneky P., Wyatt R., Cayabyab M., Garzan M., Mizabekov T., Sodroski J., Choe H.; Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glycosylation.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                           Paxton W.A.; "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,
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AF011501, AAB65701.1) --
AF011502, AAB65702.1, --
AF011503, AAB65703.1, --
AF011503, AAB65703.1, --
AF011504, AAB65706.1, --
AF011509, AAB65709.1, --
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AF011510, AAB65710.1, --
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EMBL; U54994; AAC5058.1; ---
EMBL; U57640; AAB17701.1; ---
EMBL; U58626; AAB57793.1; ---
EMBL; U83326; AAC51797.1; ---
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CKR5_HYLML
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MEDLINE-99416438; PubMed=10486970;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Sequence evolution of the CRRS chemokine receptor gene in primates.";
Mol. Biol. Evol. 16:1145-1154(1999).
-! FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of gramulocytic lineage proliferation or
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FBE-2003 (Rel. 41, Last annotation update)
26-Chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR5)
CCR5 OR CMKBR5.
Hylobates leurogenys (White-cheeked gibbon).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
NCBI_TAXID=61853;
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELULAR (POTENTIAL).
3 (POTENTIAL).
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EMBL, AF011533, AAB65733.1; --
EMBL, AF011534, AAB65734.1; --
EMBL, AF011534, AAB65735.1; --
EMBL, AF011537, AAB65736.1; --
EMBL, AF011537, AAB65737.1; --
EMBL, AF031237, AAB64735.1; --
EMBL, AF031237, AAB6131.1; --
EMBL, AY221093, AAD18131.1; --
Genew, HGNC:1606; CCR5.
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DR EMBL, AF075451, AAD19863.1;

DR PRINTS, PR002077 Tum. 1;

DR PRINTS, PR002077 GGCRHODOPSN.

DR PRINTS, PR002077 GGCRHODOPSN.

DR PROSITE; PS00267 GPROTEIN RECEPEL1; 1.

DR PROSITE; PS00267 GPROTEIN RECEPEL2; 1.

KW G-Protein coupled receptor; Transembrane; Glycoprotein; Sulfation.

FT TRANSMEM 31 58 (TYDORAINE (POTENTIAL).

FT TRANSMEM 69 89 2 (POTENTIAL).

FT TRANSMEM 69 89 2 (POTENTIAL).

FT TRANSMEM 103 124 3 (POTENTIAL).

FT DOWAIN 125 141 GYTOPLASMIC (POTENTIAL).

FT DOWAIN 125 141 GYTOPLASMIC (POTENTIAL).

TRANSMEM 167 198 EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
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MEDLINE=9916439; PubMed=10486970;
MEDLINE=9916439; PubMed=10486970;
MEDLINE=9916439; PubMed=10486970;
Sequence evolution of the CRR5 chemokine receptor gene in primates.";
Mol. Biol. Evol. 16:1145-1154(1999).
I-FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
I-FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
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increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
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-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCRS )
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Hylobates moloch (Silvery gibbon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hylobatidae, Hylobates.
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Zhang Y.-W., Ryder O.A., Zhang Y.-P.;

Mol. Biol. Evol. 16:1145-1154(1999).

-!-FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or integration.

"ffrentiation. Triegral membrane protein.
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15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CC-CS) (CCRS).
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Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODDPSN.
PROSITE; PS00237; G_ROTEIN_RECEP_F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hylobatidae, Hylobates.
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Pred. No. 6.6e-08;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=98022612; Pubmed=9359654;
Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
Ho D.D.;
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P56440; 002778;
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR5).
                                                                                                                                                                                                                                                                                                 Glycoprotein; Sulfation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
NCBI_TaxID=9598;
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100.0%; Pred. No. 6.6e-08;
.ive 0; Mismatches 0; Indels
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Zimmerman P.A., Buckler-White A., Alkhatib G.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
                                                                                                                                EMBL; AF177884; AAK43367.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR000237; GFCRRHODOFSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; GPROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane;
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SEQUENCE FROM N.A.
MEDLINE=97268687; PubMed=9108095;
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R EMBL; U94329; AAB5446.1;

R EMBL; U94329; AAB5442.1;

R EMBL; U970166; AAC51670.1;

R EMBL; U89797; AAC31670.1;

R EMBL; AF011840; AAR65740.1;

R EMBL; AF017894; AAK43377.1;

R INCEPPO; IFR000276; GPCR HODOSN.

R PRINTS; PR00027; GPCRHODOSN.

R PROSITE; PS00237; GPCRHODOSN.

R PROSITE; PS00237; GPCRHODOSN.

R PROSITE; PS00237; GPCRHODOSN.

R PROSITE; PS00237; GPCRENCEDFF1.2; 1.

CW G-POTCHAIN COUPLED FOR TEXTRACELLULAR (POTENTIAL).

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CYTCHANNEM 1 59 68 CYTCHIALLIAR.

T DOMAIN S CYTCHANNEM 1 59 68 CYTCHIALLIAR.
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Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
                                      SEQUENCE FROM N.A.
MEDLINE=97426118; PubMed=9282822;
Zacharova V., Zachar V., Goustin A.S.;
"Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
"HIV type 1 subtypes, coreceptor usage, and CCRS polymorphism.", AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=88090115; PubMed=9430250;
Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.,
"Chimpanzee CKR4 and CKR5 act as coreceptors for HIV type 1.";
AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
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                                                                                                                                                                                                               SEQUENCE FROM N.A. Shang Y.; Shang Y.; Sequence comparison of the CCR5 gene in primates and primate
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SULFATION (BY SIMILARITY).
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EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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4A33E698B80FE34C CRC64;
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                             HIV type 1 host.";
AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
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-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lal R.B.;
Asian
                               Gaps
                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
CCR5 OR CKKRRS.
Papio hamadryas (Hamadryas baboon), and
Papio anubis (Olive baboon),
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                  SPECIES=P.hamadryas;
MEDLINE=97268687; PubMed=9108095;
Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
Pipfferential utilization of CORS by macrophage and T cell tropic simian immunodeficiency virus strains.";
Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
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MEDLIKE=99210133; PubMed=10195758;
Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., I Species-specific changes in the CCR5 gene from African and inonhuman primates.";
AIDS Res. Hum. Retroviruses 15:479-483(1999).
Score 96; DB 1; Length 352;
Pred. No. 6.6e-08;
Mismatches 0; Indels
                                                                                                                                                                352 AA
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EMBL; AF105287; AAD20556.1; --
EMBL; AF105288; AAD20557.1; --
EMBL; AF105289; AAD20558.1; --
EMBL; AF105290; AAD20558.1; --
EMBL; AF024529; AAC63830.1; --
InterPro; IPR000276; GPCR_Rhodpsn.
Query Match
Best Local Similarity 100.0%; Boatches 18; Conservative 0;
                                                                                      185 SQYQFWKNFQTLKIVILG 202
                                                          1 SOYOFWKNFOTLKIVILG 18
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NCBL_TaxID=9557, 9555;
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EMBL; AF075445; AAD19857.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
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NCBI_TaxID=61621;
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CKR5_PYGBI
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28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          differentiation.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
PROTEIN RECEP F1 1; 1.
PROTEIN_RECEP_F1_2; 1.
sceptor; Transmembrane; Glycoprotein; Sulfation.
30
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pongo pygmaeus (Orangutan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 96; DB 1; Length 352;
Pred. No. 6.6e-08;
                                                                                                                    3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                             SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
N-LINYED (GLONAC. ) (POT.
N; 551504A9BA1FE8B2 CRC64;
                                                                                                                                                                                                                                           6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
                                                                       1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             352 AA.
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                                                                                                       2 (POTENTIAL)
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 SQYQFWKNFQTLKIVILG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SOYOFWKNFOTLKIVILG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CKRS PONPY STANDARD; 1
0978\; 1;
30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                      40489 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                  G-protein coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      352 AA;
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       PROSITE; | PROSITE; |
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                                                                                                                                                                                                                                                                               TRANSMEM
DOMAIN
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CARBOHYD
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CKR5_PONPY
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Matches
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MEDLINE=99416418; PubMed=10486970;
Mang Y.-P.;
Mang Y.-
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Pygathix bleti (Black snub-nosed monkey) (Rhinopithecus bieti).
Pygathix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CRR-5) (CC-CKR-5) (CCR-5)
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-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS0237; G PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50262; G PROTEIN_RECEP_F1_2; 1.
DOMAIN 1 30 TERRACELLULAR (POTENTIAL).
TRANSMEM 31 58 1 (POTENTIAL).
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SULFAITON (BY SIMILARITY).
SULFAITON (BY SIMILARITY).
SULFAITON (BY SIMILARITY).
x, F4E2F47135AF658A CRC64;
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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SULFATION (BY SIMILARITY)
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CYTOPLASMIC (POTENTIAL).
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Best Local Similarity luv...
Loca 18; Conservative
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InterPro; IPR000276; GPCR_Rhodpsn.
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097878;
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TRANSMEM
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CKRS TRAFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99416438; PubMed=10486970; Zhang Y.-F.; Zhang Y.-W., Ryder O.A., Zhang Y.-F.; Zhang Y.-P.; Zhang Y.-W., Ryder O.A., Zhang Y.-P.; Sequence evolution of the CCR5 chemokine receptor gene in primates."; Mol. Biol. Bvol. 16:1145-1154(1999).
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordatā; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C.C chemokine receptor type 5 (C-C CKR-5) (CC-CK) (CCRS).
PFAM, PF00001, 7tm 1, 1.

PRINTS, PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein cdupled receptor; Transmembrane; Glycoprotein; Sulfation.

BXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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0
                                                                                                                                                                                                                                                                                                         Length 352;
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                         SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
N; 4366F142730F938F CRC64;
                                                                           1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                           4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                     3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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Pred. No. 6.6e-08;
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CYTOPLASMIC (
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100.0%;
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Les 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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1166
1198
2318
2318
2277
2301
178
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                                                                                                                                                                                                                                                                                   352 AA;
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TRANSMEM
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SEQUENCE
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097882;
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Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Sequence evolution of the CCRs chemokine receptor gene in primates.";
Mol. Biol. Evol. 16:1145-1154(1999).
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleoscomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae, Colobinae,
Trachypithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Interro; ......
Pfam, PF00017, Thm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS50262; GPROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
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SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).

* FEAFPDD9BD131E861 CRC64,
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EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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BY SIMILARITY.
SULFATION (BY SIMILARITY
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CYTOPLASMIC (POTENTIAL).
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100.0%; Pred. No. 6.6e-08;
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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352 AA;
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es 18; Conserv
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EMBL, AF075443; AAD19855.1; ...

InterPro; IPR000276; GPCR_Rhodpsn.

Pfam, PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRHODDSN.

PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G_PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G_PROTEIN COUpled receptor; Transmembrane; Glycoprotein; Sulfation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES-W.mulatta; STRAIN=Indian macaque;
MEDLINE=97213934; PubMed=9060623;
Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
Genetically divergent strains of simian immunodeficiency virus use CCRS as a coreceptor for entry.";
J. Virol. 71:2705-2714(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCRE MACMU STANDARD, PRT, 352 AA.
P79436; 002746;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
02-NOV-1997 (Rel. 35, Last sequence update)
03-NOV-1997 (Rel. 35, Last sequence update)
03-NOV-1997 (Rel. 36, Last sequence)
03-NOV-1997 (Rel. 36, Last se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
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SPECIES=M.mulatta;
MEDLINE=97184592; PubMed=9032394;
MEDLINE=97184592; PubMed=9032394;
Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
Newman W., Gerard N., Gerard C., Sodroski J.;
Mutilization of C-C chemokine receptor 5 by the envelope
glycoproteins of a pathogenic simian immunodeficiency virus,
SIVMac239.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 352;
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6 (POTENTIAL).

7 (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

SYLFATION (BY SIMILARITY).

SULFATION (BY SIMILARITY).

SULFATION (BY SIMILARITY).

SULFATION (BY SIMILARITY).
                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
5 XTRACELLULA.
5 (POTENTIAL).
5 (POTENTIAL).
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100.0%; Pred. No. 6.6e-08;
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NCBI_TaxID=9544, 9541, 9545;
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Zhang Y.-W., Ryder O.A., Zhang Y.-P.,

"Sequence evolution of the CCR5 chemokine receptor gene in primates.";

"Nol. Biol. Bvol. 16:1145-1154(1999).

"Increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.

-! SUBCELIULAR LOCATION: Integral membrane protein.

-! SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CKR5 TRAPH STANDARD; PRT; 352 AA.
097879;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCRS).
                                                          PRINTS; PRO0237; GPCRAHODPSN.
PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
DOMAIN 1 30 1 (POTENTIAL).
TRANSMEM 31 58 1 (POTENTIAL).
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SULFATION (BY SIMILARITY).
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SULFATION (BY SIMILARITY).
4366F148C255938F CRC64;
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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    EMBL; AF075442; AAD19854.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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MEDLINE=99416438; PubMed=10486970;
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Best Local Similarity 100.
Matches 18; Conservative
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352 AA;
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                                                                                                                                      PECISES.M. mulatta, M. fascicularis, and M. nemestrina,
MEDINES-97266687; Pubde=9108095;
Sharron M., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
"Differential utilization of CCRS by macrophage and T cell tropic
simian immunodeficiency virus strains.";
"Differential utilization of CCRS by 444005-4010 (1997).
"In The Complex Section of CC type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
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EMBL; U77672; AACS1109.1; -.
EMBL; U97622; AACS1158.1; -.
EMBL; AF005660; AAB62555.1; -.
EMBL; AF005662; AAB62555.1; -.
EMBL; AF005662; AAB62556.1; -.
EMBL; AF00562; AAB62556.1; -.
EMBL; AF000001; 7tm 1; 1.
FRINTS; PR00037; GPCRRHODOPSN.
PROSITE; PS00237; GPRCPEIN RECEP F1.1; 1.
FRINTS; PS00237; GPRCPEIN RECEP F1.2; 1.
G-protein coupled receptor; Transmembrane, Glycoprotein; Sulfation.
DOWNIN 1 1 30 EXTRACELULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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SULFATION (BY SIMILARITY).
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SULFATION (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-X (IN REF. 3).
I -> M (IN REF. 3).
W, 58B96C85909FACB2 CRC64;
                                                      Margulies B.J., Hauer D.A., Clements J.E.; "Identification and comparison of eleven rhesus macaque chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)
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SULFATION (BY
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                       SPECIES=M.mulatta;
MEDLINE=21354176; PubMed=11461684;
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352 AA;
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1 SGYCGPRENTICATION 15 19

TENDENT 17

CRASS_MODES

TO COT -2003 (RRI) 16, tast sequence update)

DT 1-0CT-1936 (RRI) 16, tast sequence update uppate)

DT 1-
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Length 352;

DB 1; 2e-07;

Score 93; Pred. No.

96.9%;

Query Match Best Local Similarity

28 15:49:57 2004

Tue Sep

1 SOYOFWKNFOTLKIVIL 17

187 TQYHFWKSFQTLKMVIL 203

8 8

354 AA.

PRT;

STANDARD;

RESULT 18 CKR5_RAT ID _CKR5_RAT

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                                                                                                                                                                                             Gaps
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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N-LINKED (GLCNAC. ..) (POTENTIAL).
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                                                                                             EMBL; U47036; AAC52454.1; -
EMBL; X94131; CAA63867.1; -
EMBL; U83327; AAC533867.1; -
EMBL; U83327; AAC53389.1; -
EMBL; AF02290; AAC53389.1; -
EMBL; AF0127290; AAC53389.1; -
EMBL; AF01772; AAD71183.1; -
MGD; MGI:107182; CCr5.
GO; GO:0016493; F:C.C chemokine receptor activity; IDA.
GO; GO:000552; F:Gefense response; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77.1%; Score 74; DB 1; Length 354 76.5%; Pred. No. 0.0002; ive 3; Mismatches 1; Indels
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N -> I (IN REF. 5).
H -> Y (IN REF. 5).
P -> S (IN REF. 1).
B4A6B942E88F9CF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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STRAIN=Sprague-Dawley;
MEDLINE=98318173; PubMed=9655467;
MEDLINE=98318173; PubMed=9655467;
MEDLINE=98318173; PubMed=9655467;
MEDLINE=98318173; PubMed=9655467;
Defiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
Defiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
"Chemokine receptor expression in cultured glia and rat experimental allergic encephalomyellitis.";
J. Neuroimmunol. 86:1-12(1998).
INP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level.
INCELLULAR LOCATION: Integral membrane protein.
-:- SUBCELLULAR LOCATION: Integral membrane protein.
-:- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
             01-NOV-1997 (Rel. 35, Created)
NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last amontation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (MIP-1
                                                                                                                                                                                                                              STRAIN=Wistar; TISSUE=Brain;
BEDIINE=9834064; Pubmed=9870989;
Spleiss O., Gourmala N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,
Berger M., Gebicke-Haerter P.J.;
"Cloning of rat HIV-1-chemokine coreceptor CKR5 from microglia and
upregulation of its mRNA in ischemic and endotoxinemic rat brain.",
J. Neurosci. Res. 53:16-28(1998).
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Pred. No. 0.0002;
3; Mismatches 0; Indels
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EMBL; V17350; AAC03343.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODPSN.
PROSITE; PS00237; GPROTEIN RECEP_F1_2; 1.
PROSITE; PS00262; G_PROTEIN RECEP_F1_2; 1.
TRANSMEM 33 60 1. (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLUIAR (POTENTIAL).
7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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1 Similarity 81.2%;
13; Conservative 3
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Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                     alpha receptor).
CCR5 OR CMKBR5.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0016493; P:C-C chemokine receptor activity; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:000555; P:immune cell chemotaxis; IDA.
GO; GO:0006954; P:inflammatory response; IMP.
GO; GO:0010099; P:myeloid blood cell differentiation; IMP.
InterPro; IPR000276; GPCR_Rhodpsn.
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
M -> V (IN REF. 3).
H -> Q (IN REF. 3).
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CYTOPLASMIC (POTENTIAL).
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PROSITE; PRO0237; GFORHODOPSN.
PROSITE; PS00237; GFORHODOPSN.
PROSITE; PS00237; GFORPEIN RECEP F1 1; 1.
DODAIN 134 EXTRACELLULAR. (POTENTIAL)
TRANSMEM 35 60 I (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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FCE9FFF70E6F38B1 CRC64;
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CYTOPLASMIC (POTENTIAL).
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EMBL; U2844; AAA89153.1; -.
EMBL; BC011092; AAH11092.1; -.
PIR; 149339; 149339.
MGD; MGI:104618; Ccrl.
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CKR2_MOUSE
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**X MEDLINE=22388257; PubMed=12477932;

**A Strausberg R.L., Felingold E.A., Grouse L.H., Derge J.G.,

**A Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

**A Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

**A Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

**A Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

**A Altachul S.F., Zeeberg B., Bonaldo M.F., Carainot P., Haibeh F.,

**Brownstein M.J., Usdin T.B., Toshiyuki S., Carninot P., Prange C.,

**Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

**Robards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,

**Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,

**Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,

**Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,

**Richards S., Worley K.C., Schards S.J., I. X., Gibbs R.A.,

**A Haley J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

**A Anting M., Madan A., Young A.C., Shewchenko Y., Bouffard G.G.,

**A Rodrigues A.C., Garmwood J., Schmutz J., Myers R.M.,

**A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

**A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

**A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

**A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

**Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903[2002].

**Proc. Rawres, And Less Eprelcishur, Towns M.P.-1-BETA OR P.P.-1 BETA OR P.P. PROCIPERATION.

**PROCIPERATION RESERVENTED AND M.P.-1 BETA OR P.P.-1 BETA OR P.P.-1 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=129/SvJ;
MEDINE=95340546; PubMed=7542241;
MEDINE=95340546; PubMed=7542241;
"Cloning and differential tissue-specific expression of three mouse beta chemckine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor-";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gerard C.; "Molecular characterization of two murine eosinophil beta chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLUIAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Detected in the heart, spleen, lung,
peritoneal exudate cells and leukcytes.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse),
Verkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                          CKRI_MOUSE STANDARD; PRT; 355 AA.
P51675; O91VP9;
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2003 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
(Macrophage inflammatory protein-1 alpha receptor) (MIP-1alpha-R) (RANTES-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=129/Sv; TISSUE=Peritoneal macrophage;
MEDLINE=96072806; PubMed=7594543;
Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunol, 155:5299-5305(1995).
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QYRFWKHFQTLKMVIL 203
                                           2 OYOFWKNFOTLKIVIL 17
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TISSUE=Breast;
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                                                                                                                    CKR2 MOUSE STANDARD; PRT; 373 AA.

CKR2 MOUSE STANDARD;

01-OCT-1996 (Rel. 34, Created)

01-NOV-1997 (Rel. 35, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

CC chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2)

CJE/FIC receptor) (MCP-1 receptor).

CCR2 OR CMKBR2.
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=96205938; PubMed=8631787;
Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L.,
Charo I.F.;
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                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=97026720; PubMed=8872898;
MEDLINE=97026720; PubMed=8872898;
MEDLINE=97026720; PubMed=8872898;
Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,
Host T.W., Gerard C., Dorf M.E.;
Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse
T transcriptase-polymerase chain reaction does not detect mRNA for the
T KC or new MCP-1 receptor.";
I. J. Neurosci. Res. 45:382-391(1996).
I. J. Neurosci. Res. 45:382-391(1996).
I. J. Neurosci. Res. 45:382-391(1996).
I. SUNCTION: Receptor for the MCP-1 (UE), MCP-3 (FIC) and MCP-5
C clenium fons level.
C -1 SUBCELLULAR LOCATION: Incegral membrane protein.
II SUBCELLULAR LOCATION: Detected in monocyte/macrophage cell lines,
Dut not in nonhematopoietic cell lines.
C -1 SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REMEL; U47035; AAC52453.1; ---
REMEL; U51717; AAC52557.1; ---
REMEL; U561919; AAC52557.1; ---
REMEL; U561919; AAC52784.1; ---
REMOD; WG1.106185; CCZ.2
GC1.0019955; P:Cyclonien binding; IPI.
GC); GC1.0019957; P:Cyclonien binding; IMP.
GC); GC1.0019954; P:Infiammatory response; IMP.
GC); GC1.0016594; P:Infiammatory response; IMP.
GC); GC1.00165954; P:Infiammatory response; IMP.
GC); GC1.00165954; P:Infiammatory response; IMP.
RC); GC1.0016554; P:Infiammatory response; IMP.
GC); GC1.0016593; GCR.Rhodpsn.
RPRINTS; PR00217; GPRRHODOPSN.
RPRINTS; PR00217; GPRRHODOPSN.
RPROSITE; PS00227; GPRRHODOPSN.
GPROCHER; PS00227; GPROTEIN RECEPF1.1; 1.
RPROSITE; PS00262; GPROTEIN RECEPF1.2; 1.
WR GPROCHER; PS00262; GPROTEIN RECEPF1.2; 1.
WHICH COUNTY RECEPF1.2; 1.
            chemoattractant protein 1) and murine macrophage inflammatory protein lalpha receptors: evidence for two closely linked C-C chemokine receptors on chromosome 9.";
"Molecular cloning and functional expression of murine JB (monocyte
                                                                                                                                                  Kurihara T., Bravo R.;
Closing and functional expression of mCCR2, a murine receptor for
the C-C chemokines JB and FIC. ";
J. Biol. Chem. 271:11603-11606(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
Y -> H (IN REF. 1).
A -> G (IN REF. 1).
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1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
                                                               Biol. Chem. 271:7551-7558(1996)
                                                                                                               STRAIN=BALB/c;
MEDLINE=96216064; PubMed=8662823;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptors.";
AIDS Res. Hum. Retroviruses 17:981-986(2001).
-- PUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, --- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, RANTES, MCP-3 AND, LESS BFFICTENTLY, TO MIP-1-BETA OR MCP-1 AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                     15-UU-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
15-UUL-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type I (C-C CKR-1) (CC-CKR-1) (CCRI).
CCRI OR CMKBRI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUMILARITY; Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Margulies B.J., Hauer D.A., Clements J.E.; "Identification and comparison of eleven rhesus macaque chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordatā, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae;
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CYTOPLASMIC (FOTENTIAL).
N-LINKED (GLCNAC. ..) (FOTENTIAL).
BY SIMILARITY.
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                                                                       Length 373;
                                                                                                                   4; Indels
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CYTOPLASMIC (POTENTIAL).
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EXTRACELUIAR (POTENTIAL).
5 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
264 264 V -> G (IN REF. 1).
373 AA; 42782 MW; FA012C10F4C9325A CRC64;
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CYTOPLASMIC (POTENTIAL).
                                                                  / Match
Local Similarity 64.3%; Pred. No. 5.8;
les 9; Conservative 1; Mismatches 6
                                                                                                                                                                                                                                                                                                                               355 AA.
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MEDLINE=21354176; PubMed=11461684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macaca mulatta (Rhesus macaque).
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ciliary dynein heavy chain 11 (Axonemal beta dynein heavy chain 11).
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ARG-639; CYS-654; ALA-1023; THR-1038; GLY-1640; ASN-2641; THR-3474;
VAL-3715; PRO-3765 AND ILE-4177.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=Z / UNIEX 753;
MEDLINE=23347989; PubMed=8346031;
Hallick R.B., Hong L., Drager R.G., Favreau M.R., Monfort A., Orsat B., Spielmann A., Stutz B.;
"Complete sequence of Euglena gracilis chloroplast DNA.";
Nucleic Acids Res. 21:3537-3544(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.9%; Score 45; DB 1; Length 634; 55.6%; Pred. No. 14; 2; Indels ive 2; Indels
                                         46.9%; Score 45; DB 1; Length 355; 50.0%; Pred. No. 8;
                                                                                    5; Indels
                                                                                                                                                                                                                                                                           YCX3_EUGGR STANDARD; PRT; 634 AA.
P31916, P31917;
01-JUL-1993 (Rel. 26, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 78.0 kDa protein in PSBC intron 2 (ORF635).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z11874; -; NOT ANNOTATED_CDS.

EMBL; X70810; CAA50080.1; -.

PIR; S34499; S34499.

PIR; S34500; S34500.

Chloroplast; Hypothetical protein.

SEQUENCE 634 AA; 78049 NW; D966B8864519E334 CRC64;
355 AA; 41198 MW; 41CAEA7CC19D23D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
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                                                                                  3; Mismatches
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                  Ouery Match
Best Local Similarity 50.00
Best Local 8; Conservative
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Chloroplast.
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EMBL; AJ320497; CAC60121.1; ...

EMBL; AJ32087; CAC6012.1; ...

EMBL; AJ32087; F: axonemal motor activity; NAS.

EMBL; AJ32087; Exconemal motor activity; NAS.

Tue Sep 28 15:49:57 2004

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Science 269:496-512(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycoplasma penetrans.
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PYRB OR MYPE7890.
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15-MAR-2004
15-MAR-2004
15-MAR-2004
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PYRB_MYCPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Rd / KW20 / ATCC 51907;

STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95550630; PubNed=7542800;

RElischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fitchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Genem C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pasteurellaceae; Haemophilus.
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                              FTId=VAR_013858.
:-> Q (in PCD; not proven to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 45; DB 1; Length 4523;
Pred. No. 97;
3; Mismatches 4; Indels
                                                                                                       nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [ -> 1.
/FTId=VAR_013863.
4; 7C9A7IC95B296B89 CRC64;
COIL (POTENTIAL)
COIL (POTENTIAL)
COIL (POTENTIAL)
                                                                                                      (requires 2
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FTId=VAR_013857.
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FTId=VAR_013855.
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/FTId=VAR_013859.
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'FTIG=VAR_013862.
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FTId=VAR_013852
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FTId=VAR_013854
                                                                                                                                                                                                                                                                                     FTId=VAR_013856.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                               FTIG=VAR_013853
                                              (POTENTÍAL)
(POTENTÍAL)
                                                                         (POTENTIAL)
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substitutions)
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Matches 7; Conserv
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28-FEB-2003
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"The complete genomic sequence of Mycoplasma penetrans, an
intracellular bacterial pathogen in humans.",
Nucleic Acids Res. 30:5293-5300(2002)
-!-CATALYUTY: Carbamoyl phosphate + L-aspartate = phosphate
+ N-carbamoyl-L-aspartate.
-!- PATHWAX: Pyrimidine biosynthesis; second step.
-!- PATHWAX: Pyrimidine biosynthesis; second step.
-!- SIMILARITY: Belongs to the ATCase/OTCase family.
-!- FUNCTION: Involved in protein export (By similarity).
-!- SUBUNIT: Part of the prokaryotic protein translocation apparatus which comprise secA, secB, secB, secE, secF, secG and secY (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                  similarity).
SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
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Complete proteome.
TRANSMEM 11 31 POTENTIAL.
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                                                                                                                                                         (By similarity).
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15-MAR-2004 (Rel. 43, Last annotation update)
Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate transcarbamylase) (ATCase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
7DE1E4B085065F8F CRC64;
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STRAIN=HF-2;
MEDLINE=22354719; PubMed=12466555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR005791; SecD.
InterPro; IPR003335; SecD_SecF.
Pfam; PF02355; SecD_SecF; I.
PRINTS; PR01755; SECFTRNICASE.
TICRRAMS; TIGR00916; 2A0604801; I.
TIGRFAMS; TIGR01129; SecD; 1.
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Best Local Similarity 38.5.
The Conservative
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The sep 28 15:49:5/ 2004

Gaps ö 44.8%; Score 43; DB 1; Length 300; 50.0%; Pred. No. 14; ive 5; Mismatches 3; Indels Query Match
Best Local Similarity 50.0°
Matches 8; Conservative

|: :|:|: || |:| 143 YEKFKSFEGLKIAIVG 158 3 YOFWKNFOTLKIVILG 18 g

15-JUL-1998 (Rel. 36, Created)
30-MAY-2000 (Rel. 36, Last sequence update)
C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR-3) (CCR3) PRT; 355 AA STANDARD; CCR3 OR CMKBR3. CKR3 CERAE ID CKR3 CERAE AC P56492; C-C ch (CKR3) THE STATE OF THE S

SEQUENCE FROM N.A.

Sol N., Treboute C., Gomas E., Ferchal F., Alizon M.;

Sul N., Treboute C., Gomas E., Ferchal F., Alizon M.;

Submitted (ULL-1997) to the EMBL/GenBank/DBM databases.

-!- FUNCTION: Receptor for a C-C type chemokine. Binds to ectaxin, MCP-3, MCP-4 and RAMTES and subsequently transduces a signal by increasing the intracellular calcium ions level.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- SUMILARITY: Belongs to family 1 of G-protein coupled receptors. Cercopithecus aethiops (Green monkey) (Grivet).

Bukaryota, Metazoa, Chordata, Graniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinee, Cercopithecus.

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EMBL; Y13775; CAA74106.1; -.

InterPro; IPR000276; GPCR_Rhodpsn.

PRINTS; PR00037; GFCRHODDSN.

PROSITE; PS000237; GFRRHODDSN.

PROSITE; PS00237; GFROTEIN RECEP_F1_2; 1.

PROSITE; PS0262; GPROTEIN RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane.

DOMAIN

TRANSMEM 35 62 1 (POTENTIAL).

3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL). 6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL). BY SIMILARITY.
44F7A5EFEEB978FF CRC64; 2 (POTENTIAL). EXTRACELLULAR (POTENTIAL) (POTENTIAL) DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN DOMAIN DISULFID SEQUENCE

. 0 Score 43, DB 1; Length 355; Pred. No. 17; 3; Mismatches 2; Indels 44.8%; 58.3%; Query Match
Query Match
Best Local Similarity 58.3%,
Best Local Similarity 58.3%,

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|::| |||: || 195 WRHFHTLKMTIL 206 6 WKNFOTLKIVIL 17

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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 3 (C-C CKR-3) (CCR3) (CCR3) STANDARD; MACMU RESULT 27 CKR3_MACMU ID CKR3_MACM AC P56483;

CCR3 OR CMKBR3.

Macaca mulatta (Rhesus macaque).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Mammalia; Butheria, Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Macaca.

SEQUENCE FROM N.A. MEDLINE=21354176; PubMed=11461684; Margulies B.J., Hauer D.A., Clements J.E.; Margulies a.J., Hauer D.A., Clements J.E.; "Identification and comparison of eleven rhesus macaque chemokine receptors."; AIDS Res. Hum. Retroviruses 17:981-986(2001)

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EMBL, AF017283; AAB70527.1; -. EMBL, X13776; CAA74107.1; -. InterPro; IPR000276; GPCR_Rhodpsn. Pfam; PF00001; 7tm 1; 1. PRINTS; PR00237; GPCRRHODOPSN

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(Rel. 36, Last sequence update)
(Rel. 42, Last annotation update)
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EMBL, AB012799; BAA84785.1; -.
EMBL, AAC16921, AAC60935.1; -.
InterPro, IPR000733; Flav monooxygnse.
InterPro; IPR000133; Rlav monooxygnse.
InterPro; IPR0001042; Rng_mnoxygenase.
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15-UUL-1998 (Rel. 36, Last sequence
10-0CT-2003 (Rel. 42, Last annotatis
Surfactin synthetase subunit 2.
SRFAB OR SRFA2 OR COMI OR BSU03490.
Bacillus subtilis.
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SEQUENCE OF 1-3077 FROM N.A.
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Q04747;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=ATCC 12472 / DSM 30191;
MEDLINE-25828280. PubMed=14500782;
MEDLINE-25828280. PubMed=14500782;
Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
Alves-Gomes J.A., Andrade E.M., Araripo J., de Araujo M.F.F.,
Astodie.Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.
Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,
Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
Carvalho C.M.B., Cascado J.C.M., Cavada B.S., Chueire L.M.O.,
Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Chromobacterium.
NOSI_TaxID=536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB 1; Length 355;
Pred. No. 17;
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"Biosynthetic gene cluster for violacein pigment.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
PROSITE; PS00237; G_PROTEIN RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G_PDIOLEIN 1 34 EXTRACELLULAR (POTENTIAL)

DOMAIN 35 62 1 (POTENTIAL).

DOMAIN 63 72 CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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K -> R (IN REF. 2).
E271F1E694970D9F CRC64;
                                                                                                                 2 (POTENTIAL)
EXTRACELULAR (POTENTIAL)
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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0953708; 0950N2;
28-FBB-2003 (Rel. 41, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Probable tryptophan hydroxylase vioD (EC 1.-.-.).
VIOD OR CV3271.
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MEDLINE=20525185; PubMed=11075927;
                                                                                                                                                                                                                                                                                                                                                                                                                                        40805 MW;
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                        355 AA;
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TRANSMEM
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TRANSMEM
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TRANSMEM
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Fartinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA Grattapaglia D., Grisard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA Madeira H.M.F., Manfie G.P., Maranhao A.C., Martins W.S.,
A immuro S.M.Z., de Medeiros R.B., Meisener R.V., Moreira M.A.,
RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Pereira S.C.,
RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA Santos B.B.P., Santos F.R., Schneider M.P.C., Seuanez H.N.,
R. Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Sinces I.C.,
RA Santos B.B.P., Soares R.B.A., Souza E.M., Souza K.R.L.,
RA Since A.M. Wassem R., Zaha A.L., Singson A.J.G.;
RT "The complete genome sequence of Chromobacterium violaceum reveals
RT "The complete genome sequence of Chromobacterium violaceum reveals
RT "The complete genome sequence of Chromobacterium violaceum reveals
RT "The complete Genome sequence of Chromobacterium violaceum reveals
RT "The complete Genome sequence of Chromobacterium violaceum reveals
RT "The complete Genome sequence of Chromobacterium violaceum reveals
RT "The COMPLIAL"
C.- CATALYTIC ACTIVITY: Tryptophan + O(2) = 5-hydroxytryptophan.
C.- CATALYTIC ACTIVITY: Tryptophan + D(2) = 5-hydroxytryptophan.
C.- CAT
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PRINTS; PR00420; RNGMNOXGNASE.
Oxidoreductase; Flavoprotein; FAD; Antibiotic biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.8%; Score 43; DB 1; Length 373;
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V -> I (IN REF. 1).
V -> A (IN REF. 1).
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ij

MEDINE-98044033; PubMed-9384377; Albertini A.M., Alloni G.,

KURAINIE-98044033; PubMed-9384377; Albertini A.M., Alloni G.,

KUNDEL E., Ogasawara N., Moszer I., Bolctin A., Borchert S.,

Azevedo V., Bertero M.G., Bessieres P., Bolctin A., Borchert S.,

Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

Azevedo V., Catter N.M.,

Brouillet S., Bruschi C.V., Caldwell B., Capbano V., Catter N.M.,

A Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

Britz C., Fujita M., Fubret C., Ferrari E., Fouger D.,

A Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

Entian K.D., Errington J., Fabret C., Ferrari E., Fouger D.,

A Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Garadi G.,

A Hilbert H., Holsappel S., Haga K., Haiech J., Harwood C.R., Henaut A.,

A Hilbert H., Holsappel S., Haga K., Haiech J., Harwood C.R., Medin G.,

A Hilbert H., Holsappel S., Hosenra S., Kumano M.,

A Hilbert H., Holsappel S., Hosenra S., Kumano M.,

A Noris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

Kobayashi Y., Koetter P., Mizuno M., Mosell D., Nakai S., Noback M.,

A Medina N., Mellado R.P., Liu H., Masuda S., Mauel C., Medigue C.,

Mone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

A Persecan E., Pujic P., Purnelle B., Ropeott G., Rey M., Reynolds S.,

A Rieger M., Rivolta C., Rocha B., Rapoport G., Rey M., Ander S.,

A Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

Sato T., Scanlan E., Schleich S., Schroeter R., Takeuchi M., Tamakoshi A., Taraka T., Taraka T., Tarkaman H., Takeman K.,

Yashida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,

Whitters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,

Whitters P., Wipat A., Yamamoto G. the Gram-positive bacterium Bacillus

Mitters P., Wipat A., Yamamoto G. the Gram-positive bacterium Bacillus STRAIN=168 / JH642; MEDLINE=93360813; PubMed=8355609; Cosmina P., Redriguez F., de Ferra F., Grandi G., Perego M., Venema G., van Sinderen D.; "Sequence and analysis of the genetic locus responsible for surfactin Synthesis in Bealllus subtils."; Mol. Microbiol. 8:821-831(1993). "Nucleotide sequence of 5' portion of srfA that contains the region required for competence establishment in Bacillus subtilis."; Nucleic Acids Res. 21:93-97(1993). Yamane K., Kumano M., Kurita K.,
"The 25 degrees-36 degrees region of the Bacillus subtilis
"The 25 degrees-36 degrees region of the Sequence of a 146 kb segment and
identification of 113 genes.";
Microbiology 142:3047-3056(1996). ., Fujishima Y., Corbell N., D'Souza C., Nakano M.M., P., Yamane K.; MEDLINE=93181186; PubMed=8441623; MEDLINE=97124189; PubMed=8969502; SEQUENCE FROM N.A. SEQUENCE FROM N.A. [2] SEQUENCE FROM N.A. STRAIN=168 Fuma S. Zuber

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EMBL, D13262, BAA02523.1; -EMBL, X70356; CAA49817.1; -EMBL, D50453; BAA08983.1; -EMBL, Z99105; CAB12143.1; -EMBL, X65835; CAA46678.1; --

PATHWAY: Cyclic peptide antibiotic surfactin biosynthesis. SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme

-!- SIMILARITY: Contains 3 acyl carrier domains

EMBL, D.C.,

EMBL, D.C.,

EMBL, S6505, CAA.,

DR PILL, X6505, CAA.,

DR PUblists, 14067, 14040.

BR Subtilists, 12010673, Sarba.

DR Subtilists, 12010673, Sarba.

DR InterPro; IPR001242; Condensatin.

DR InterPro; IPR001242; Condensatin.

DR InterPro; IPR001242; Condensatin.

DR PRINS; PR00154; AMPLIALE S.

DR PRINS; PR00154; AMPLIALE S.

DR PROSITE, PR00154; AMPLIANING; 3.

DR PROSITE, PR00455; AMP ENDING; 3.

DR PROSITE; PS00455; AMP ENDING; 3.

PROSITE; PS00455; AMP ENDING; 3.

DR PROSITE; PS00455; AMP ENDING; 3.

PROSITE; PS00455; -> APSPGGLICMSRCIC . 2 a S -> F (IN REF. 1).
Q -> G (IN REF. 1).
RQA -> AQG (IN REF. 1).
L -> W (IN REF. 1).
R -> A (IN REF. 1).
TPA -> SRP (IN REF. 1).
TPA -> SRP (IN REF. 1).
RHY -> ETL (IN REF. 1).
CHY -> L (IN REF. 1).
CHY -> L (IN REF. 1).
CHY -> L (IN REF. 1).
CHY -> C (IN REF. 1).
CHY -> CHY (IN REF. K (IN REF. 1) (IN REF. 1). R -> C (IN REF. A -> V (IN REF. ARLTP -> LRDSLN 130096 130086 1300886 1300886 100886 111099 1110 11133 1310 1333 1384 1582 939 1038 1133 1310 1333 1582 2075 2079 2141 1915 CONFLICT
CONFLICT CONFLICT CONFLICT CONFLICT CONFLICT CONFLICT CONFLICT CONFLICT CONFLICT CONFLICT CONFLICT

SEQUENCE OF 514-800 FROM N.A.
STRAIN=ATCC 21332;
MEDLINE=92290255; PubMed=1601288;
Borchert S., Patil S.S., Marahiel M.A.;
"Identification of putative multifunctional peptide synthetase genes using highly conserved oligonucleotide sequences derived from known

Nature 390:249-256(1997).

synthetasee.", FEMS Microbiol. Lett. 71:175-180(1992).
-!- FUNCTION: THIS PROTEIN IS A MULTIFUNCTIONAL ENZYME ABLE TO ACTIVATE AND POLYMERIZE THE AMINO ACTIOS LEU, GLU, ASP AND VAL. ACTIVATE ON SITES FOR THESE AA CONSIST OF INDIVIDUAL DOMAINS.
-!- COFACTOR: Contains 3 covalently bound phosphopantetheines.

InterPro; IPR005834; Hydrolase.

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Pfam; PF00702; Hydrolase; 1.
CONFLICT 70 71
                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli.
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Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEPD OR B0590
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                                                      CONFLICT
SEQUENCE
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RAFFS
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  E -> Q (IN REF. 1).
ATDLF -> RQICS (IN REF. 1).
TVHQLFEETVQRHKDRPAVTY -> DGCISYSKRLSSATKT
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MEDIATE=973264; PubMed=9169868;
MEDIATE=973264; PubMed-9169868;
Araujo R., Awiles E., Berno A., Brennan T., Carpenter U., Chen E., Cherry J.M., Chung E., Duncan M., Garman B., Hartzell G.,
Hunicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.,
Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,
Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,
Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
I'the nucleotide sequence of Saccharomyces cerevisiae chromosome V.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94016558; PubMed=8411151;
Melnick L., Sherman F.;
"The gene clusters ARC and COR on chromosomes 5 and 10, respectively,
of Saccharomyces creevisiae share a common ancestry.";
J. Mol. Biol. 233:372-388(1993).
                                                                                                                                                                                                                                                                                                                               Gaps
                                                      ARLSHT (IN REF. 1).

MSAAVLGV -> KCPPRCSAS (IN REF. 1).

KL -> NV (IN REF. 1).

D -> H (IN REF. 1).

GELCA -> RALING (IN REF. 1).

GELCA -> RALING (IN REF. 1).

RF -> L (IN REF. 1).

EDR -> CDA (IN REF. 1).

EDR -> CDA (IN REF. 1).

EDR -> A (IN REF. 1).

R -> A (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                                                                   Score 43; DB 1; Length 3587;
Pred. No. 1.6e+02;
8; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1993 (Rel. 27, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) UTR4 protein (Unknown transcript 4 protein). UTR4 OR YEL038W OR SYGP-ORF20.
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1751 ASFAFDANFESLRLIVLG 1768
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EMBL; S66121; AABS8443.1; --
EMBL; U18779; AAB65004.1; --
PIR; S30843; S30843.
Germonline; 139042; --
GGT. S000754. UTR4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27, Created)
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                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 33.3%;
Matches 6; Conservative
                                                                                                                                                                                                                                                   AA; 401248
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SEQUENCE OF 1-158 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 387:78-81(1997).
                                                                                                                                                                  2881
2900
2960
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                                                                                    25608
27113
27113
27123
28876
39899
3584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 30
UTR4 YEAST

DU TR4 YEAST

DU TO-CT-1993

DT 10-OCT-1993

DT 10-OCT-2003

DT 10-OCT-2003

DT 10-OCT-2003

DT 10-OCT-2003

DT 10-OCT-2003

DT 10-OCT-2003

DE UTR4 Protein

CO Saccharomyce

CO Saccharomyce

CO CO SACCHAROMYCE

RO STRAIN=22886

RA Araujo R., A RA DIELINE=973

RA Araujo R., A RA DIELINE=973

RA Araujo R., A RADINESPERO PROTEIN RA DIELINE=973

RA DIELINE=973

RA MEDLINE=973

CC CT NA SEQUENCE OF CC CT SECHAROM CC CT SEMBL; S65954

DR EMBL; S65954

DR EMBL; S65943

DR EMBL; S65943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Federspiel N., Hyman R., Roberts D., Schramm S., Davis R.W.; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM FOR FERRIC ENTEROBACHTIN. PROBABLY RESPONSIBLE FOR THE TRANSLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE.
-!- SUBCELLIARA LOCATION: Integral membrane protein. Inner membrane.
-!- INDUCTION: Controlled in part by the amount of available irron.
-!- SIMLLARITY: Belongs to the binding-protein-dependent transport system permease family.
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chenault S.S., Earhart C.F.; "Organization of the Escherichia coli ferrienterobactin permease."; Mol. Microbiol. 5:1405-1413(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Nucleotide sequence and genetic organization of the ferric enterobactin transport system: homology to other periplasmic binding protein-dependent systems in Bscherichia coli."; Mol. Microbiol. 5:1415-1428(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
STRAIN=K12 / MG1655;
SIRDININS—19426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                  ö
                                                                                                                                                                                                                                                         RESULT 31
FEPD ECOLI STANDARD; PRT; 334 AA.

AC P23876; P77097;
DT 01.NOV-1991 (Rel. 20, Created)
DT 01.NOV-1991 (Rel. 21, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ferric enterobactin transport system permease protein fepD.
ID -> MH (IN REF. 2).
AHDSLD -> GMIRWI (IN REF. 2).
                                                                             Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997)
                                                                                                                  Indels
                                        BF6FBBC7FB14B5AD CRC64;
                                                                             43.8%; Score 42; DB 1;
63.6%; Pred. No. 16;
iive 3; Mismatches 1
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                                          241 AA; 26735 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shea C.M., McIntosh M.A.;
                                                                                                                        7; Conservative
                                                                                                                                                                                    :|| :|||:||
231 KYQVYKNFETL 241
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and for commercial
            (See http://www.isb-sib.ch/announce/
                                                     EMBL; AE000164; AAC73691.r; --
EMBL; U82598; AAB40789.1; ALT_INIT.
EMBL; U82598; EAB40789.1; ALT_INIT.
ECGENG; EG10296; fepb.
InterPro; IPR000515; BPD transp.
InterPro; IPR000522; PecD.
ProDon; PD001557; FecCD; 1.
ProDon; PD001557; FecCD; 1.
Iron transport; Transport; Inner membrane; Transmembrane;
  þ
                                                                                                                                                                                                                                       V -> AL (IN REF. 2).
BB5C5E939A96951B CRC64;
lified and this statement is not removed. It is requires a license agreement (See Fornd an email to license@isb-sib.ch).
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                                      EMBL; X57471; CAA40707.1; -. EMBL; X59402; CAA42043.1; -.
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172
262
300
326
234
                                                                                                                                                     Complete proteome.
 modified and entities requ
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179 QLRFWQAGSLDIRNLHTLKVVLI 201 OYOFW-----KNPOTLKIVIL 17 C٧ à 유

MEDLINE-92024080; PubMed=1926776; Palm P., Schleper C., Grampp B., Yeats S., McWilliam P., Reiter W.-D., Zillig W.; 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
Hypothetical 28.5 kba protein (ORF D-244).
Sulfolobus virus-like particle SSV1.
Viruses, dsDNA viruses, no RNA stage; Fuselloviridae; Fusellovirus. "Complete nucleotide sequence of the virus SSV1 of the archaebacterium Sulfolobus shibatae."; Virology 185:242-250(1991). 244 AA. STANDARD; NCBI_TaxID=244589; SEQUENCE FROM N.A. Y28K SSV1 NAME OF THE PROPERTY OF THE PR

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PIR; S03215; S03215. Hypothetical protein. SEQUENCE 244 AA; 28515 MW; 9326209BC3B9DD86 CRC64; EMBL; X07234; CAA30214.1; -.

ò Gaps . 42.7%; Score 41; DB 1; Length 244; 40.0%; Pred. No. 24; 5; Indels tive 4; Mismatches 5; Indels Conservative Query Match Best Local Similarity

216 OYWKNLTDLRVSLKG 230 OFWKNFOTLKIVILG 18

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PRT; STANDARD; BACSU RESULT 33
APPC BACSU
ID APPC BACS

01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOCT-2003 (Rel. 42, Last annotation update)
01igopeptide transport system permease protein appC.
APPC OR BSUI1400.

Bacillus subtilis. Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus. NCBI_TaxID=1423;

SEQUENCE FROM N.A. STRAIN=168;

MEDLINE=95089678; PubMed=7997159;

Koide A., Hoch J.A.;
"Identification of a second oligopeptide transport system in Bacillus
subtilis and determination of its role in sporulation.";
Mol. Microbiol. 13:417-426(1994).

ij

Gaps

7;

3; Indels

5; Mismatches

/ Match Local Similarity 34.8%; les 8; Conservative

Query Match

Score 41.5; DB 1; Length 334; Pred. No. 27;

SEQUENCE FROM N.A.

RECONTINE—588,

RECONTINE—588,

RUBLINE—58844013; PubbMed=5384377;

RA Agevedo V. Berrero M.G., Bessieres P., Bolotin A., Borchert S.,

Raveved V., Berrero M.G., Bessieres P., Bolotin A., Borchert S.,

Rorriss R., Boursier L., Brans A., Earun M., Erignell S.C., Bron S.,

RA Borriss R., Codamerton I.F., Cummings N.J., Daniel R.A.,

RA Britz C., Fujita W., Pujita Y., Furlich S.D., Emmerson P.T.,

RA Fritz C., Fujita M., Pujita Y., Farrari E., Foulger D.,

RA Fritz G., Guy B.J., Haga K., Haiech J., Grandi G.,

Gliseppi G. Guy B.J., Haga K., Haiech J., Grandi G.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

RA Kobayashi Y., Koetter P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Bessen S., Wiellly M., Portetelle D., Porwollik S., Park S.H.,

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Park S.H.,

RA Freecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

RA Berger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,

RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,

RA Freecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

RA Freecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

RA Scrokin A., Tanakoshi A., Tanaka T., Tarkahashi H., Takemaru K.,

Sorokin A., Tamakoshi A., Tanaka T., Vashaka H., Neitzenegger T.,

RA Tosato V., Uchiyama S., Vandenbol M., Vannier P., Vasta K.,

RA Tosato V., Wipat A., Yamanoto H., Yamine R., Yoshikawa H.,

RA Tosato W., Wipat A., Yamanoto H., Yamine R., Yashan H.,

RA Winters P., Wipat A., Yamanoto F., Yashan H.,

RA Winters P., Wipat A., Yamanoto F., Banchin R.,

RA Winters P., Wipat A., Yamanoto F., Yashan H.,

RA Winters P., Wipat A., Yamanoto F., Yasharerium Radilling M., Wanier P., Wipat A., Yamanoto F., Yasharerium Radilling M., Wanier P., Wipat A., Yamanoto F., Yasharerium R., Pasharerium R., Pasharerium R., Pasharerium R., Pasharerium R.

"The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";

Nature 390:484-256(1997).

-!- FUNCTION: This protein is a component of an oligopeptide permease, a binding protein-dependent transport system. This APP system can completely substitute for the OPP system in both sporulation and genetic compenence, though, unlike OPP, is incapable of transporting tripeptides. Probably responsible for the translocation of the substrate across the membrane (By Nature 390:249-256(1997)

similarity).
SUBCELLULAR LOCATION: Integral membrane protein (Potential).
SIMILARITY: Belongs to the binding-protein-dependent transport system permease family. OppBC subfamily.

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Tue Sep 28 15:49:57 2004

Query Match

42.7%; Score 41; DB 1; Length 358;

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Query Match
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   between the Swiss Institute of Bioinformatics and the EMBL outstation -
the Buropean Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not remoyed. Usage by and for commercial
                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch),
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the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                        InterPro; IPR000515; BPD_transp.
Pfam; PF06228; BPD_transp; 1.
PR05ITE; PS50228; ABC_TM1; 1.
Competence; Sporulation; Transport; Peptide transport; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arnason U., Gullberg A., Xu X.; A complete mitochondrial DNA molecule of the white-handed gibbon, Hylobates lar, and comparison among individual mitochondrial genes of all hominoid genera.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hereditas 124:185-189(1996).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-!- SIMILARITY: Belongs to the complex I subunit 1 family.
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PROSITE; PS00667; COMPLEXI_NDI_1; 1.
PROSITE; PS00668; COMPLEXI_NDI_2; 1.
Oxidoreductase; NAD; UbiquInone; Mitochondrion; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 1; Length 303;
Pred. No. 29;
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NADH-ubjquinone oxidoreductase chain 1 (EC 1.6.5.3)
MTND1 OR ND1 OR NADH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 AA.
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InterPro; IPR001694; Resp_NADH_dhl.
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                                                                                                                                                                                                     EMBL; U20909; AAA62360.1; -.
EMBL; Z99110; CAB12997.1; -.
PIR; 140647; 140547.
Subtilist; BG11089; appC.
INCEPPC; IPR000515; BPD transp.
Pfam; PF00528; BPD_transp; 1.
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TRANSMEM 39
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE=99049845; PubMed=9834099; Sabroe I., Collins P.D., Post T.W., Sabroe I., Conroy D.M., Gerard N.P., Li Y., Collins P.D., Post T.W., Jose P.J., Williams T.J., Gerard C.J., Ponath P.D.; "Cloning and characterization of the guinea pig eosinophil eotaxin receptor, C-C chemokine receptor-3: blockade using a monoclonal antibody in vivo.";
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Immunol. 161:6139-6147(1998).

-!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin, MCP-3, MCP-4 and RANTES and subsequently transduces a signal by increasing the intracellular accellulation increasing the intracellular accellular accellular accellular accellular accellular accellular coupled for similarity)
-!- SUMCELULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cavia porcellus (Guinea pig).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Cavidae, Cavia.
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                                                         Length 318;
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EXTRACELLULAR (POTENTIAL)
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318 AA; 35814 MW; 3988A4B0EFE13711 CRC64;
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                                                      42.7%; Score 41; DB 1; ilarity 46.7%; Pred. No. 31; Conservative 2; Mismatches 6
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InterPro; IPR000276; GPCR_Rhodpsn.
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Matches 7; Conser
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SEQUENCE FROM N.A.
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Length 373;

42.7%;

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Query Match
Best Local Similarity 66.7
Matches 8; Conservative
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                                                                                                                         RESULT 37
022B_DROME
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                                                                                                                                                                                                                                                                                                                 MEDLINE-98318173; PubMed=9655467;
MEDLINE-98318173; PubMed=9655467;
MEDLINE-98318173; PubMed=9655467;
MEDLINE-98318173; PubMed=9655467;
M.Y., Adhikari S., Xia Y., Feng L., Sonntag M.K., deFiebre C.M., Pennell N.A., Streat W.J., Harrison J.K., "Chemokine receptor expression in cultured glia and rat experimental allergic enceptor expression in cultured glia and rat experimental allergic enceptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5 chemokines. Transduces a signal by increasing the intracellular calcium ions level (By similarity) and similarity.
-! SUBCELLULAR LOCATION: Integral membrane protein.
-! TISSUE SPECIFICITY: Expressed in lung, spleen, kidney, thymus and
                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 2 (C-C CKR-2) (CC-CXR-2) (CCR-2).
CCR2 OR CMKBR2.
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TAXID=10116;
              Gaps

    macrophages.
    -!- INDUCTION: In animals in which experimental allergic encephalomyelitis (EAE) has been induced.
    -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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              Indels
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
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CYTOPLASMIC (POTENTIAL).
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                4.
                                                                                                                                       373 AA.
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InterPro; IPR000276; GPCR_Rhodpsn.
PETam; PF00001; 7tm 1; 12.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; P800237; GPCRRHODOPSN.
PROSITE; P850262; GPROTEIN RECEP F1 1; 1.
G-protein coupled receptor; Transmembrane.
Pred. No. 35;
2; Mismatches
                                                                                                                                        PRT;
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53.8%;
                                                         || || ||:: | |
199 WKRFQALRMNIFG 211
                                         6 WKNFQTLKIVILG 18
                Conservative
                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
92
113
1129
1171
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121
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221
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333
343,
Best Local Similarity
Matches 7; Conserv
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055193;
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REGUENCE FROM N.A.

REGUENCE FROM N.A.

REGUENCE FROM N.A.

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Adams W.D., Levis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandrews Pfannkoch C., Baldwin D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,

RA Abril J.F., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Brysaktaroglu L., Beasley E.M.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center P., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Posler C., Gabriellan A.E., Garg N.S., Gelbart W.M.,

RA Hostin D., Houston K.A., Heiman T.J., Herris M.-, Harris M.-,

RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegwam C.,

RA Liask P., Kadra C.D., Kraft C., Kravitz S., Kull D., Lai Z.,

RA Liask P., Mattei B., McIntosh T.C., McLeed M.P., Mosteron D.,

RA Liask M. Moy M., Murphy B., Murphy L., Murzhy D.M., Nelson D.L.,

RA Merkulov G., Milshina M.V., Mobarry C., Morris J., Posler M.G.,

RA Mensulov G., Milshina W.V., Mobarry C., Morris J., Wolley D.,

RA Mensulov G., Milshina W. Wirphy B., Palazzolo M., Pillard J., Puri V., Reese M.G.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
STRAIN=Oregon-R; TISSUE=Antenna;
STRAIN=99189757; PubMed=101089884.
Vosshall L.B., Amrein H., Morozov P.S., Rzhetsky A., Axel R.;
"A spatial map of olfactory receptor expression in the Drosophila
                                                                                                                                                                                                                                               DECORAGE STANDARD, PRT, 397 AA.

C PR1910; Q9UGKS, Q9VQ19;

T 16-OCT-2001 (Rel. 40, Created)
T 16-OCT-2001 (Rel. 40, Last sequence update)
T 10-OCT-2003 (Rel. 42, Last annotation update)
E Odcrant receptor 22b.
E Odcrant receptor 22b.
S Drosophila melanogaster (Fruit fly).
C Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
C Bukaryota; Medpterygota; Ditera; Brachycera; Muscomorpha;
X Neoptera; Endopterygota; Ditera; Brachycera; Muscomorpha;
X NebL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDILINE-9938973; PubMed=10458908;
MEDILINE-9938978 N.;
"Identification of candidate Drosophila olfactory receptors from
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EXUSION TO 58.
VOSSBALL L.B., Amrein H., Morozov P.S., Rzhetsky A., Axel Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                   3; Indels
Score 41; DB 1;
Pred. No. 36;
1; Mismatches
                                                                                                                         |||||||
211 WKNFQTIMRNIL 222
                                                                                            6 WKNEQTLKIVIL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genomic DNA sequence.";
Genomics 60:31-39(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AF127924; AAD26359.2; -.
EMBL, AF003586; AAF71363.1; -.
Flybase, F8003066; AAF71363.1; -.
GO, GO:0016021; C:integral to membrane; NAS.
GO, GO:0004984; F:Olfactory receptor activity; NAS.
GO; GO:0004986; P:Offactory receptor activity; NAS.
GO; GO:0007186; P:Of-protein coupled receptor protein signalin. ..; NAS.
GO; GO:0007608; P:olfaction; NAS.
                                                                                                                                                                                                                                                 TISSUE=Antenna;
MEDLINE=99166868; PubMed=10069338;
Clyne P.J., Warr C.G., Freeman M.R., Lessing D., Kim J., Carlson J.R.;
Clyne P.J., Warr C.G., Freeman M.R., Lessing D., Kim J., Carlson J.R.;
novel family of divergent seven-transmembrane proteins: candidate odorant receptors in Drosophila.";
Neuron 22:327-338(1999).
-i- FUNCTION: Probable role in the odorant response, being an odorant
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier B., Spradling A.C., Stapleton M., Strong R., Sun E., Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.-Y., Wasaarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Yelng K.-F., Zaveri J.S., Zhan M., Zhou G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu S., Smith H.O. Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane protein (Potential).
TISSUE SPECIFICITY: EXPRESSED IN 20-22 SENSORY NEURONS ON THE
MEDIAL-PROXIMAL EDGE OF THE ANTENNA. THIS EXPRESSION PATTERN
MATCHES THE DISTRIBUTION OF THE LARGE SENSTILA BASICONICA.
EXPRESSION IS FIRST SEEN AT 60 HOURS APF IN A SUBSET OF CELLS
RESTRICTED TO A SUBREGION OF THE DEVELOPING ANTENNA. EXPRESSION
CONTINUES TRROUGHOT ANTENNAL DEVELOPMENT.
SIMILARITY: Belongs to family Dr-or of G-protein coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MVKLAFTVVTIVKOFNLAEKFQ -> VSINQYEL (IN
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-> TICFDKFFYLPYFFS (IN REF. 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 1; Length 397;
Pred. No. 38;
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6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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Pfam; PF02949; 7tm_6; 1.
Transmembrane; G-protein coupled receptor; Olfaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                         "The genome sequence of Drosophila mela
Science 287:2185-2195(2000).
[5]
IDENTIFICATION, AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46387 MW;
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53.3%;
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DOMAIN 1
TRANSMEM 50
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Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Brain;
MEDLINE=983157-86; PubMed=9690476;
MEDLINE=983157-86; PubMed=9690476;
MEDLINE=983157-86; PubMed=9690476;
Momura Y., Nakahori Y., Mayake M., Saito K., Osawa M., Hamano K., Nomura Y., Nomaki I., Nakagome Y., Kanazawa I., Nakamura Y., Tubunaga K., Toda T.;
"An ancient retrotransposal insertion causes Fukuyama-type congenital
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: May interact with and reinforce a large complex encompassing the outside and inside of muscle membranes. May also be involved in brain development.
-!- SUBCELLULAR LOCATION: Secreted (Probable). May be located in the
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-21099876; PubMed=11165248;
Kobayashi K., Sasaki J., Kondo-Iida E., Fukuda Y., Kinoshita M.,
Sunada Y., Nakamura Y., Toda T.;
"Structural organization, complete genomic sequences and mutational
analyses of the Fukuyama-type congenital muscular dystrophy gene,
                                                                                                                                                                                                                                                                                 Euteleostomi;
;
                                                                                                                                          PCMD HUMAN STANDARD; PRT; 461 AA.
075072, 20961B-1, 209295.
16-OCT-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Fukutin precursor (Fukuyama-type congenital muscular dystrophy protein).
                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Babbage A.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
   .
9
   Mismatches
   ..
H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB008226; BAA32000.1; -. EMBL; AB038490; BAA94082.1; -. EMBL; AL158070; CAC22162.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEBS Lett. 489:192-196(2001).
                                 3 YQFWKNFQTLKIVIL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            muscular dystrophy.";
Nature 394:388-392(1998).
 Conservative
                                                               48 YKLWSTFVTLVIFIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genew, HGNC:3622, FCMD.
MIM, 607440, -.
MIM, 253800, -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                              PCMD HUMAN
   Matches
                                                                                                            RESULT 38
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                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A.
STRAIN-S288C / ABB72;
MEDLINE-97313268; PubMed-9169872;
MEDLINE-97313268; PubMed-9169872;
Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome
XIII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "identification of the proteins of the yeast UI small nuclear ribonucleoprotein complex by mass spectrometry.";

ribonucleoprotein complex by mass spectrometry.";

-1. FUNCTION SAL 94:385-390(1997).

UI SNRNP PARTICLE TO FACILITATE OR STABILIZE THE UI SNRNP/5'

SPLICE SITE INTERACTION, HAS A DIRECT ROLE IN THE ASSEMBLY OR FUNCTION OF A CATALYTICALLY ACTIVE SPLICEOSOME.

-1. SUBCELLULAR LOCATION: Nuclear.

-1. SIMILARITY: Contains 7 HAT repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97165029; PubMed-9012791;
Neubauer G., Gottschalk A., Fabrizio P., Seraphin B., Luehrmann R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=GRF88;
MEDLINE=94254821; PubMed=8196608;
Lockhart S.R., Rymond B.C.;
"Commitment of yeast pre-mRNA to the splicing pathway requires a novel U1 small nuclear ribonucleoprotein polypeptide, Prp39p.";
Mol. Cell. Biol. 14:3623-3633(1994).
                                                                                         . .) (POTENTIAL)
                                                                                                                                                                                        12;
                                                                                                                                                       Length 461,
                                                                                                                                                                                        3; Indels
                                                                                                            R -> Q (IN REF. 1).
2D11F28E4BCCD858 CRC64;
                                                                         FUKUTIN.
N-LINKED (GLCNAC.
                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-07-2003 (Rel. 42, Last annotation update)
Pre-mRNA processing protein PRP39.
PRP39 OR YML046W OR YM9827.06.
                                                                                                                                                         Score 41; DB 1; Pred. No. 44; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                  629 AA
GO; GO:0005615; C:extracellular space; TAS. GO; GO:0007517; P:muscle development; TAS. GO; GO:0007399; P:neurogenesis; TAS. Glycoprotein; Signal. 21 POTENTIAL.
                                                                                                                                                                                                                                               2 OYOFWKN-----FOTLKI 14
                                                                          22 461 FU
92 92 N--
203 203 R
461 AA; 53724 MW;
                                                                                                                                                         42.7%;
ilarity 40.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 387:90-93(1997).
                                                                461
92
                                                                                                                                                  Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4932;
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CARBOHYD
CONFLICT
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PR39 TEAS.

DD PR39 FEB-11
DT 01-FEB-11
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DE PR29 OR
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ON BRATANG
RN (1)
RP SEQUENCE
RX MEDLINE=
RA LOCKHART RT
RT NOVEL UIR
RY NEDLINE=
RA GORMAN REPRINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBA HUMAN STANDARD; fn., GO6520; Created)
01-NOV-1995 (Rel. 32, Created)
01-NOV-2096 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Alcohol sulfotransferase (EC 2.8.2.2) (Hydroxysteroid Alcohol sulfotransferase) (HST) (Dehydroepiandrosterone sulfotransferase)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-93143674; PubMed-7678732; Comer K.A., Falany J.L., Falany C.N.; "Cloning and expression of human liver dehydroepiandrosterone
                                                                                                                                                                                                                                                                                                                                                                                                                                       ore 41; DB 1; Length 629;
ed. No. 60;
Mismatches 6; Indels
                                                                                                                                                                                                                                  mRNA processing; mRNA splicing; Nuclear protein; Repeat.
REPEAT 68 100 HAT 1.
REPEAT 102 134 HAT 2.
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                                                                                                                                                                                                                                                                                                                                                                                                   67480ED01347B6AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41;
Pred. No. (
EMBL, L29224, AAA20131.1; -.
EMBL, 247816; CAA87828.1; -.
PIR, S47920; S47920.
GermOnline; 142575; -.
SGD, S0004509; PRP39.
GO, GO:0000243; C:Commitment complex; I
GO; GO:0000271; F:RNA binding; IPI.
GO; GO:000371; F:RNA binding; IPI.
InterPro; IPR003107; HAT.
SMART; SN00396; HAT.
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Mol. Cell. Endocrinol. 112:53-60(1995)
                                                                                                                                                                                                                                                   HAT 3.
HAT 3.
HAT 4.
HAT 5.
HAT 6.
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37.5%; Pred
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MEDLINE=92269778; PubMed=1588921;
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SULT2A1 OR STD OR HST.
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175
233
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446
629 AA;
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Best Local Similarity
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SUHA_HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED custation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kong A.-N.T., Yang L., Ma M., Tao D., Bjornsson T.D.; "Molecular cloning of the alcohol/hydroxysteroid form (hSTa) of sulfotransferase from human liver."; Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Statemer Blochem. B
                                                                                                                                                                                                                                              "Human dehydroepiandrosterone sulfotransferase gene: molecular
                                                                                                                               [5]
SEQUENCE FROM N.A.
MEDILINE=9522590; PubMed=7710689;
Otterness D.M., Her C., Aksoy S., Kimura S., Wieben E.D.,
Weinshilboum R.M.;
                                                                                                                                                                                                                                                                    cloning and structural characterization.";
DNA Cell Biol. 14:331-341(1995).
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92392364; PubMed=1520333;
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EMBL, X70222, CAA49755.1, -.
EMBL, U08024, AAA17749.1, -.
EMBL, U08025, AAA17750.1, -.
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REMBL; 913059; AAC51333.1; JOINED.

REMBL; 913059; AAC51353.1; JOINED.

REMBL; 913059; AAC51353.1; JOINED.

REMBL; 923859; AAC51353.1; JOINED.

REMBL; 153037; I38548.

REMBL;
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PAPS BINDING SITE (POTENTIAL).

A -> P (IN REF. 1; AA SEQUENCE)

I -> D (IN REF. 1).

L -> D (IN REF. 1; AA SEQUENCE)

L -> V (IN REF. 6).
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2; Mismatches
                                                                                                                                     123(194) AAA75491.1) JOINED.
123(194) AAA75491.1) JOINED.
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123(194) AAC51353.1) JOINED.
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284 AA; 33648 MW;
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L36193; 1
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SEQUENCE FROM N.A.
MEDLINE=95322029; PubMed=7598806;
Luu-The V., Dufort I., Paquet N., Reimnitz G., Labrie F.;
"Structural characterization and expression of the human dehydroepiandrosterone sulfotransferase gene.";
DNA Cell Biol. 14:511-518(1995).
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Search completed: September 28, 2004, 09:04:06 Job time : 6.625 secs

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Gaps

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4; Indels

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September 28, 2004, 08:56:16; Search time 28:8 Seconds (without alignments) 197.199 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                       OM protein - protein search, using sw model
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BLOSUM62 Gapop 10.0 , Gapext 0.5 1 SQYQFWKNFQTLKIVILG 18 US-10-084-813-13 96 Title: Perfect score: Scoring table: Sequence:

1017041 Total number of hits satisfying chosen parameters:

1017041 seqs, 315518202 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL 25:*

1: Sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_nho:*
7: sp_phage:*
7: sp_prammal:*
7: sp_pramm Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Ogpits homo sapien Ogpits homo sapien Ogtug7 erythrocebu Ogtug7 erythrocebu Ogun24 homo sapien Ogun23 homo sapien Ogubj7 homo sapien Ogun25 homo sapien Ogun26 homo sapien Ogun28 homo sapien Description 099115 091694 0914694 0914694 091002 090002 090002 090002 090002 090002 090002 090002 090002 090002 090002 090002 090002 090002 090002 Length DB Query Match Score $\begin{array}{c} \mathbf{Q} \quad \mathbf{$ Result No.

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                                                                                                                                                    166 SOYOFWKNFOTLKIVILG 183
                                                                                                          1 SOYOFWKNFOTLKIVILG 18
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                                                           Conservative
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Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,

Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,

HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";

AIDS Res. Hum. Retroviruses 0:0-0(1997).

EMBL, AR011504, AA665704.1;

GO; GO:001601; C:integral to membrane; IEA.

GO; GO:00018472; F:receptor activity; IEA.

GO; GO:0001848; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001848; P:rhodopsin-like receptor protein signalin. .; IEA.

InterPro; IPR000276; GPCR_Rhodpsn.

PFam; PP00001; Tumli.......
                                                                                                                                                                                                                                                                                                                                                   "Characterization of a third CCR5 amplicon from CCR5-delta32-
heterozygous HIV-1-infected individuals.";
heterozygous HIV-1-infected individuals.
heterozygous HIV-1-infected individuals.
heterozygous HIV-1-infected individuals. HEA.
heterozygous HIV-1-infected individuals.
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MEDLINE=99392755; PubMed=10465086;
Aikhionbare F.O., Newman C., Womack C., Roth W.W., Stringer H.G. Jr.,
Bond V.C.;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                           Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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333 AA; 38174 MW; AEFBA07A67893AEB CRC64;
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60 AA; 7156 MW; AFF4B9CAF6B80AFB CRC64;
                       Oppir4;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
Chemokine receptor CCR5 (Fragment).
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00001; 7tm 1; 1. PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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PRINTS; PR00237; GPCRRHODOPSN.
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es 18; Conservative
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  PRELIMINARY;
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GO, GO:0016021; C:integral to membrane; IEA.

GO, GO:0004872; F:receptor activity; IEA.

GO; GO:000184; F:rhodopsin-like receptor activity; IEA.

GO; GO:000186; P:rportein coupled receptor protein signalin. .; IEA.

InterPro; IPR000276; GPCR_Rhodpsn.

PRIMIS; PR00027; TML_1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
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                                                                Gabs
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Brythrocebus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCR5 genes from diverse simian and prosimian
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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100.0%; Score 96; DB 4; Length 333; 100.0%; Pred. No. 1.9e-07; tive 0; Mismatches 0; Indels
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334 AA; 38460 MW; B19D0CEC667B69F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                          334 AA.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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339 339
339 AA, 39115 MW, 3C6369F922C91AA7 CRC64;
                                 178 SQYQFWKNFQTLKIVILG 195
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                               Homo sapiens (Human)
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species.";
Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF161919; AAD47676.1;
GO; GO:0016201; C:integral to membrane; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor protein signalin. .; IEA.
InterPro; IPR000276; GPCR_Rhodopsn.
FRAM; PR00037; GPCR_RHODOPSN.
PROSITE; PS00037; GPRRHODOPSN.
PROSITE; PS50262; GPROTEIN_RECEP_FI_1; 1.
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A KUDSTEAR K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

KUDSTEAR K., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;

T. Sequences of the CCR5 genes from diverse simian and prosimian

T. Sequences of the CCR5 genes from diverse simian and prosimian

T. Submitted (JUL-199) to the EMBL/GenBank/DDBJ databases.

EMBL; AR161316; AAD47673.1; -.

EMBL; AR161316; AAD47673.1; -.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001586; P:rhodopsin-like receptor activity; IEA.

GO; GO:0001586; P:rhodopsin-like receptor protein signalin. .; II

RO; GO:0001186; P:G-protein coupled receptor protein signalin. .; II

PROSITE; PS00023; GPCRHODOPSN.

PROSITE; PS00023; GPROTEIN_RECEP_F1_1; 1.

RECEPTOR:

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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
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339 339
339 AA; 39162 MW; AS6369FE0529F4AB CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 SQYQFWKNFQTLKIVILG 195
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ID Q9UN23
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sequence of the Corp Senes from Corporation of the Embly GenBank/DDBU databases.
Submitted (UIL-1999) to the EmBL/GenBank/DDBU databases.
EMBL; AF161921; AAD47674.1; -.
EMBL; AF161917; AAD47674.1; -.
EMBL; AF161917; AAD47674.1; -.
EMBL; AF161917; AAD47674.1; -.
EMBL; AF161917; AAD47674.1; -.
GO; GO:0001631; F:receptor activity; IEA.
GO; GO:000184; F:receptor activity; IEA.
GO; GO:000186; F:receptor activity; IEA.
GO; GO:000186; F:receptor activity; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PP00001; 7tm 1; 1.
PRINTS; PR00237; GPRRHODPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.
Receptor. Homo sapiens (Human), Sukaryota, Metazoa, Chordata, Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; SEQUENCE FROM N.A.
Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M
Kunstman K., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
"Sequences of the CCRS genes from diverse simian and prosimian OgubJ7 PRELIMINARY; PRT; 339 AA.
OgubJ7;
Ol-MAY-2000 (TrEMBLrel. 13, Created)
Ol-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Ol-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).

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EMBL; AFIG1914; AAD47671.11.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:000184; F:rhodopsin-like receptor activity; IEA.

GO; GO:0007186; F:rhodopsin-like receptor protein signalin. . .; IEA.

InterPro; IPR000276; GPCR_Rhodpsn.

PRINTS; PR00027; GPCRRHODPSN.

PROSITE; PS00237; GFRRHODPSN.

PROSITE; PS00237; GFRRHODPSN.

PROSITE; PS00237; GFRRHODPSN.
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EMBL; AF161910; AAD47661.1; --
EMBL; AF161910; AAD47661.1; --
EMBL; AF161911; AAD47669.1; --
EMBL; AF161911; AAD47669.1; --
EMBL; AF161912; AAD47669.1; --
GO, GO:0016872; F:receptor activity; IEA.
GO, GO:0001884; F:rhodopsin-like receptor activity; IEA.
GO, GO:0001886; P:G-Protein coupled receptor protein signalin. ..; IEA.
InterPro; IPR000276; GFCR_Rhodpsin.
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCR5 genes from diverse simian and prosimian
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K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kulken C., Marx P., Wolinksy S.,
"Sequences of the CCRS genes from diverse simian and prosimian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                       species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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339 AA; 39086 MW; 88AD8B44E2CB4ECZ CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
02-C chemokine receptor 5 (Fragment).
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1es 18, Conservative
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004812; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. ..; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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339 339
339 AA, 39128 MW, 9C3369FFF1F2F27A CRC64;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemckine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-UMY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
C-C Chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339 AA.
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                                                                                                                                                                                                                                                     Mismatches
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Thrwis, PR00237; GPCRADODSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                                                                                                                                                                                                                                                                                                                                1 SQYQFWKNFQTLKIVILG 18
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                                                                                                                                                                                                            ilarity 100.0%;
Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                            Local Similarity
les 18; Conser
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Matches
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ô Gaps . 0 Query Match
100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 339 339 339 AA; 39114 MW; 3C6369F92C29F4A7 CRC64;

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submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161887; AAD47644.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:001584; F:receptor activity; IEA.
GO; GO:0001584; F:receptor activity; IEA.
GO; GO:0001586; F:receptor activity; IEA.
GO; GO:0007186; F:receptor activity; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
FRAM; PR00037; GPCRRHODPSN.
PROSITE; PS00237; GPRRHODPSN.
PROSITE; PS50262; GPROTEIN_RECEP_F1_1; 1.
                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hylobates concolor (crested gibbon).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Mammalia, Eutheria, Primates, Catarrhini, Hylobatidae, Hylobates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCR5 genes from diverse simian and prosimian
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                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                    Receptor.

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SEQUENCE 339 AA, 39036 WW, 5555FEAF2614D35C CRC64;
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NON_TER 1 1 1 1 SEQUENCE 339 AA; 39075 MW; 09257FBFB834C4AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OJTUX1,
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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09TUU9;
01TUU9;
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
CC chemokine receptor 5 (Fragment).
CCRS.
Cercopithecus diana (Diana monkey).
                                                                                                                                                                                                                                                              100.0%; Score 96; DB 6;
100.0%; Pred. No. 2e-07;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          339 AA
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRNITS; PR00237; GPCRHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP F1 1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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Best Local Similarity 100.
Matches 18; Conservative
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Best Local Similarity 100.
Matches 18; Conservative
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178 SQYQFWKNFQTLKIVILG 195
                  1 SOYOFWKNPOTLKIVILG 18
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Matches 18; Conservative
                                                                                                                                                                    PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                                                                       RESULT 17
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                                                                                                                                                                                  species.;
submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; APIG1999) to the EMBL/GenBank/DDBJ databases.
EMBL; APIG1999; To the EMBL/GenBank/DDBJ databases.

GO; GO:0001694; AND47704.1;
GO; GO:0001584; F:rhocopror activity; IEA.

GO; GO:0007186; P:rhocopromilike receptor activity; IEA.

GO; GO:0007186; P:rhocopromilike receptor protein signalin. .; IEA.

InterPro: IPR000276; GPCR_Rhocopromilike receptor protein signalin. .; IEA.

FRAM; PR00017; Trm 1; 1.

PRINTS; PR000237; GPCRHOOPSN.

PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                       Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; "Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hylobates concolor (crested gibbon).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S.; "Sequences of the CCR5 genes from diverse simian and prosimian
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 96; DB 6; Length 339; 100.0%; Pred. No. 2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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339 AA; 39015 MW; 6D1A91546270P70D CRC64;
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339 339
339 AA, 39024 MW, EC4CE48DEEEF107E CRC64;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00001, 7tm 1; 1.
PRINTS, PR00237; GPCRHDODSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQYQFWKNFQTLKIVILG 195
                                      Cercopithecinae; Cercopithecus.
NCBI_TaxID=36224;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Conservative
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Matches 18; Conserv
                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                         Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Cercopithecus.
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF161949, AAD47705.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kulken C., Marx P., Wolinksy S., "Sequences of the CCR5 genes from diverse simian and prosimian
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Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         speciee.";
Submitted (UTL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF162023; AAA1778.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004892; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
InterPro; IFR00275; GPCR_Rhodopsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339 AA; 39216 MW; 847E935FA403E52D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9TUUB PRELIMINARY; PRT; 339 AA.
Q9TUUB;
01-MAX-2000 (TrEMBLrel. 13, Created)
01-UMAY-2003 (TrEMBLrel. 13, Last sequence update)
01-UMAY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                     01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
01-C chemokine receptor 5 (Fragment).
339 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00237; G PROTEIN RECEP F1 1; 1. PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 SQYQFWKNFQTLKIVILG 195
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EQUENCE FROM N.A.

Kunstnan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

Kunstnan K., Chen Z., Fullai S., Kuiken C., Marx P., Wolinksy S.;

Whibata R., Yoder A., Pullai S., Kuiken C., Marx P., Wolinksy S.;

"Sequences of the CCRS genes from diverse simian and prosimian

"Sequences of the CRS genes from diverse simian and prosimian

"Sequences of the CRS genes from diverse simian and prosimian

"Sequences of the CRS genes from diverse simian and prosimian

"Sequences of the CRS genes from diverse simian and prosimian

"Sequences of the CRS genes from the EMBL/GenBank/DDBJ databases.

"Sequences of the CRS genes from diverse is a special signalin..., IEA.

"Sequences of the CRS genes from coupled receptor protein signalin..., IEA.

"GO, GO: 0001584; F: Frhodopsin-like receptor protein signalin...; IEA.

"RO, GO: 0001584; F: Rhodopsin-like receptor protein signalin...; IEA.

"The CRS GO: 0001584; F: Rhodopsin-like receptor protein signalin...; IEA.

"The CRS GO: 0001584; F: Rhodopsin-like receptor protein signalin...; IEA.

"The CRS GO: 0001584; F: Rhodopsin-like receptor protein signalin...; IEA.

"The CRS GO: 0001584; F: Rhodopsin-like receptor protein signalin...; IEA.

"The CRS GO: 0001584; F: Rhodopsin-like receptor protein signalin...; IEA.

"The CRS GO: 0001584; F: Rhodopsin-like receptor protein signalin...; IEA.

"The CRS GO: 0001584; F: Rhodopsin-like receptor protein signalin...; IEA.

"The CRS GO: 0001584; F: Rhodopsin-like receptor protein signalin...; IEA.

"The CRS GO: 0001584; F: Rhodopsin-like receptor protein signalin...; IEA.

"The CRS GO: 0001584; F: Rhodopsin-like receptor protein signalin...; IEA.

"The CRS GO: 0001584; F: Rhodopsin-like receptor protein signalin...; IEA.
                            01-MAY-2000 (TYEMBLrel. 13, Created)
01-MAY-2000 (TYEMBLrel. 13, Last sequence update)
01-MAY-2003 (TYEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
CCR5.
CCR5.
CR6.
End troglodytes (Chimpanzee).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
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339 339
339 AA, 39159 MW, 8E699E882EAC0E84 CRC64;
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1es 18; Conservative
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NON TER
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Matches
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Q9TQU7
          DTT DDT TTD DDT DD
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Submitted (UTL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF161901; AAD47662.1; ...

EMBL; AF161901; AAD47658.1; ...

EMBL; AF161901; AAD47658.1; ...

EMBL; AF161901; AAD47658.1; ...

EMBL; AF161901; AAD47658.1; ...

EMBL; AF161901; AAD47661.1; ...

EMBL; AF161901; AAD47658.1; ...

EMBL; AF161901; AAD47658.1; ...

EMBL; AF161901; AAD47658.1; ...

GO; GO:00016021; C:integral to membrane; IEA.

GO; GO:00016021; C:integral to membrane; IEA.

GO; GO:00016021; F:receptor activity; IEA.

GO; GO:0007186; F:receptor activity; IEA.

EQ; GO:0007186; P:G-protein coupled receptor protein signalin. ..; IEA.

InterPro; IPR000276; GPCR_Rhodpsn.

PROJITE; PR000237; GPCRRHODOPSN.

PROJITE; PS00237; GPCRRHODOPSN.

PROSITE; PS50262; G_PROTEIN_RECEP_FI_1; 1.
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R GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:00184; F:receptor activity; IEA.

GO; GO:00184; F:rhodopsin-like receptor activity; IEA.

GO; GO:000184; F:rhodopsin-like receptor protein signalin. ..;

R GO; GO:000186; P:G-protein coupled receptor protein signalin. ..;

R InterPro; IPR00027; GPCR_Rhodopsn.

R PROSITE; PR00237; GPCRHODOPSN.

R PROSITE; PS00237; GPCRHODOPSN.

R R Receptor.

R R Receptor.

I NON TER 339 339

C SEQUENCE 339 AA; 33049 MW; GDIA93F66270F3ED CRC64;
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K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;

"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan troglodytes (Chimpanzee).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
NCBI_TaxID=9598,
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Local Similarity 100.0%; Pred. No. 2e-07;
les 18; Conservative 0; Mismatches 0; Indels
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NON TER 1 1 1
NON TER 339 339 84; 4A88F8BBG01D46A4 CRC64;
SEQÜENCE 339 AA; 39129 MW; 4A88F8BBG01D46A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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Gaps

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100.0%; Score 96; DB 6; Length 339; 100.0%; Pred. No. 2e-07; tive 0; Mismatches 0; Indels

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RP KUNSTEAL ROOM N.A.

RA KUNSTMAN K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;

RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;

RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;

RE Shipting G. UIL-1999) to the EMBL/GenBank/DDBJ databases.

RE Shipting AP162047; AAD47792.1; -

DR EMBL; AF162047; AAD47792.1; -

DR EMBL; AF162042; AAD47792.1; -

DR GO; GO:0001584; Fireceptor activity; IEA.

GO; GO:0001584; Fireceptor activity; IEA.

GO; GO:0001584; Fireceptor activity; IEA.

DR GO; GO:0001584; Fireceptor activity; IEA.

GO; GO:0001584; Fireceptor activity; IEA.

DR ROSITE: PRO0021; GFCR_Rhodpsn.

DR PRINTS; PRO0227; GFCR_Rhodpsn.

DR PRINTS; PRO0237; GFCRRHODOPSN.
                                                                                                                                         Cercopithecus nictitans (white-nosed guenon).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Cararrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UMY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
PRELIMINARY;
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339 AA

PRELIMINARY;

RESULT 20 Q9TUW4 ID Q9TUW4

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Score 96;
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339 33
339 AA;
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                                                          SEQUENCE FROM N.A.
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   NCBI_TaxID=33548;
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Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF162026; AAD47781.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
InterPro; IPR000276; GPCR_Rhodopsn.
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Colbus guereza (Black-and-white colobus monkey).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
Colobus.
                                                                                                                                                                                                                                     Gaps
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinkey S.;
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Cercopithecus.
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339 339
339 AA, 39150 MW, 847D5F92BB03E6E2 CRC64;
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339 339
339 AA; 39178 MW; 9DF2A6F446C55AED CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
02-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    339 AA.
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PRINTS; PR00237; GPCRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                                                                                                                                                                                                                                                                                                                               178 SQYQFWKNFQTLKIVILG 195
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                                                                                                                                                                                                                                                                                             1 SOYOFWKNFOTLKIVILG 18
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1es 18; Conservative
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                                  Receptor.
NON TER
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SEQUENCE
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                                                                                                                                                                                                         Best Loca
Matches
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Matches
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Q9TUR6
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Q9TQV6
ID Q9TQV
AC Q9TQV
DT 01-MA
DT 01-MA
DT 01-JU
DE CCR C
GN CCR C
OC Bukar
OC Bukar
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SO FFF SO
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                                                                                                                                                             EMBL; AF162005, AAD47755.1; --

R EMBL; AF162005, AAD47755.1; --

R EMBL; AF162000, AAD47755.1; --

R EMBL; AF162001, AAD47756.1; --

R EMBL; AF162001, AAD47756.1; --

R EMBL; AF162002, AAD47758.1; --

R EMBL; AF162004; AAD47759.1; --

R GO; GO:0001681; F:receptor activity; IEA.

GO; GO:000184; F:rhodopsin-like receptor activity; IEA.

R GO; GO:000186; P:G-protein coupled receptor protein signalin. . .;

R InterPro; IPR000275; GPCR.Rhodopsn.

R Pfam; PF00001; 7tm 1, 1.

R PRINTS; PR00217; GFCRRHODOPSN.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
BMBL, AF161900, AAD47657.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
InterPro; IFR00276; GPCR_Rhodopsn.
FF00001; 7tm_1; 1.
Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
"Sequences of the CCRS genes from diverse simian and prosimian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 96; DB 6; Length 339; 100.0%; Pred. No. 2e-07; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 339;
                                                                                                            species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339 339
339 AA; 39168 MW; 6A4BF72FBBFF566F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39103 MW; 4038C132D024C5A4 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE, PS00237, G PROTEIN RECEP F1 1, 1.
PROSITE; PS50262, G PROTEIN RECEP F1 2; 1.
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PRINTS; PR00237; GPRRAHOOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN_RECEP_F1_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C-C chemokine receptor 5 (Fragment)
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DB 6;

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Gaps

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100.0%; Score 96; DB 6; Length 339; 100.0%; Pred. No. 2e-07; ive 0; Mismatches 0; Indels

us-10-084-813-13.rspt

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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF162034; AAD47789.1; -
GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:00164372; F:receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:00011584; F:rhodopsin-like receptor protein signalin.

InterPro; IPR0027; GPCR_Rhodpsn.

PRINTS; PR00237; GPCR_Rhodpsn.

PROSITE; PS00237; GPCRENDOPSN.

PROSITE; PS50262; G_PROTEIN_RECEP_F1 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339 AA; 39138 MW; AD31455EBBC69499 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor.
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Q9TQU5
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                     셤
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REQUIRENCE FROM N.A.

REQUIRENCE FROM N.A.

REQUIRENCE FROM N.A.

REQUIRENCE FROM T., Corber B., Oprondek J., Stanton J., Agy M.,

Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S.;

Togenies.";

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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

REL, AF162041; AAD47796.1; -.

REL, AF162041; AAD47796.1; -.

RO; GO:00016021; C:integral to membrane; IEA.

RO; GO:00016324; F:receptor activity; IEA.

RO; GO:000184; F:rhodopsin-like receptor activity; IEA.

RO; GO:000186; P:G-protein coupled receptor protein signalin. .; IEA.

InterPro; IPR000276; GPCR_Rhodpsn.

PROSITE; PS00237; GPCRRHODOPSN.

RRINTS: PR00237; GPCRRHODOPSN.

RRINTS: PS00237; GPRRHODOPSN.

RRINTS: PS00237; GPCRRHODOPSN.

RRINTS: PS00237; GPROTEIN_RECEP_FI_1; 1.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Cercopithecus.
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Enythrocebus patas (Red guenon) (Hussar).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Erythrocebus.
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCR5 genes from diverse simian and prosimian species.";
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             100.0%; Pred. No. 2e-07;
Live 0; Mismatches 0; Indels
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                             339 AA.
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                                                                                                                                                                                    178 SQYQFWKNFQTLKIVILG 195
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                                                                                                                               1 SOYOFWKNFOTLKIVILG 18
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                                                18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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    Best Local Similarity
Matches 18; Conserv
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097009
AC 097009
DT 01-MA
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Q9TUR2
AC Q9TUR
AC Q9TUR
DT 01-MA
DT 0
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCR5 genes from diverse simian and prosimian
species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                           Papio papio (Guinea baboon).
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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339 339
339 AA, 39113 MW, 7F9803EAOEOAF9ED CRC64;
                                                                                                                                                                           01-NAY-2000 (TrEMBLrel. 13, Created)
01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                        339 AA.
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PROSITE; PS00237; G PROTEIN RECEP_F1_2; 1.

Receptor.

NON TER

SEQUENCE 339 AA; 39113 MW; 7F9803EA0E0.
                                                                                                                                        PRT;
                     178 SQYQFWKNFQTLKIVILG 195
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1 SOYOFWKNFOTLKIVILG 18
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Query Local Similarity 100...
Best Local Similarity 100...
                                                                                                                                        PRELIMINARY;
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NCBI_TaxID=100937;
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Papio papio (Guinea baboon).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mamalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Papio.
NCBI_TaxID=100937;
PS50262; G PROTEIN RECEP_F1_2; 1.
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                                                                                                                                                                                                                                                                                                                      178 SQYQFWKNFQTLKIVILG 195
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                                                                                                                                                                                                                                                                                     1 SOYOFWINFOTLKIVILG 18
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ses 18; Conservative
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NON TER
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SEQUENCE
                              Receptor.
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SEQUENCE
   PROSITE;
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Best Local S
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Q9TUS5;
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                                                                                                                                                                                                         Best Loca
Matches
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GO, GO:0004827; F:receptor activity; IEA.

GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001886; P:G-protein coupled receptor protein signalin. . .; IEA.

InterPro; IRRO0276; GER.Rhodopsn.

Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GFCRRHODOSN.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
mamalia; Eutheria, Primates; Catarrhini, Cercopithecidae,
Cercopithecinae, Papio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                        Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; "Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF162046; AAD47801.1; EMBL; AF162046; AAD47801.1; EMBL; AF162043; AAD477801.1; EMBL; AF162043; AAD477801.1; Condocular conditions of the conditions of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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339 339
339 AA, 39178 MW, 847F8F936B00E6E2 CRC64;
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                    Q9TQU5;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                         Cercopithecus nictitans (white-nosed guenon)
         339 AA.
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C-C chemokine receptor 5 (Fragment)
                                                                                                                                                  C-C chemokine receptor 5 (Fragment)
         PRT;
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         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=36228;
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         A PACA CONTRACT OF THE PACA CO
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species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161908; AAA47665.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016822; F:receptor activity; IEA.
GO; GO:000184; F:rhodopsin-like receptor activity; IEA.
GO; GO:000186; P:G-protein coupled receptor protein signalin. ..; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
PRINTS; PR000217; GPCRRHODPSN.
PRINTS; PR00237; GPCRRHODPSN.
PROSITE; PS50262; G_PROTEIN RECEP_F1_1; 1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
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Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
"Sequences of the CCR5 genes from diverse simian and prosimian
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                                                                                                               Length 339;
                                                                                                                                                                         Indels
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339 339 WW, 84EB018085DC0A62 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UMY-2003 (TrEMBLrel. 24, Last annotation update)
C_C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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                                                                                                            100.0%; Score 96; DB 6;
100.0%; Pred. No. 2e-07;
:ive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                          339 AA
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1 SOYOFWKNFOTLKIVILG 18

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178 SQYQFWKNFQTLKIVILG 195
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Best Local Similarity 100.
Matches 18, Conservative
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                                                                                                                                                                                                                                                                                PRELIMINARY;
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Q9TQV3
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

Kunstman K., Chen Z., Korber B., Chiken C., Marx P., Wolinksy S.;

Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;

"Sequences of the CCRS genes from diverse simian and prosimian

"Sequences of the CCRS genes from diverse simian and prosimian

"Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF161993; AAD47742.1; -.

EMBL; AF161991; AAD47742.1; -.

EMBL; AF161991; AAD47745.1; -.

EMBL; AAD47746.1; -.

EMBL; AAD47745.1; -.

EMBL; 
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                           SEQUENCE FROM N.A.

K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinkay S., "Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Papio.
00151_TaxID=100937;
                                                                                                                                                                         species.";
Submitted (ULL-1999) to the EMBL/GenBank/DDBJ databases.
BMBL, AF161997; ALM-152.1;
GO, GO:0016021; Cintegral to membrane; IEA.
GO; GO:001681; F:receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001786; F:receptor activity; IEA.
InterPro; IPR000276; GPCR_Rhodops.
InterPro; IPR00237; GPCR_Rhodops.
PRINTS; PR00237; GPCRHJODSN.
PROSITE; PS00237; GPRHJODSN.
PROSITE; PS00237; GPRHJODSN.
PROSITE; PS00237; GPRHJODSN.
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100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
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339 339
339 AA; 39079 MW; 7176E3EAOEO0F3ED CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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Papio papio (Guinea baboon)
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Best Local Similarity 100.
Matches 18; Conservative
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NON_TER
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SEQUENCE
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SEQUENCE
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0910V3
AC 0910V3
AC 0910V3
DT 01-Ma
DT 01-JU
DT
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EQUIRNOE FROM N.A.

RADIORNOE FROM N.A.

RADIORNOE FROM N.A.

RADIORNOE FROM N.A.

RADIORNOE S., Korber B., Oprondek J., Stanton J., Agy M.,

Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Holinksy S.;

RT "Gequences of the CCR5 genes from diverse simian and prosimian

RT "Second RT "Second
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                 Cercopithecus mona.

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Cercopithecus.
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100.0%; Pred. No. 2e-07;
cive 0; Mismatches 0; Indels
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339 339
339 AA, 39079 MW; 7176E3EA0E00F3ED CRC64;
                                              Q9TQV3;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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The Sequences of the Construction of the Emblograph of the Emblosia of E
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GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001586; P:G-protein coupled receptor protein signalin. . .; IEA.
InterPro; IPR000276; GPCR_Rhodopsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                      Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Pongo.
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Sukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Erythrocebus.
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K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 96; DB 6; Length 339; 100.0%; Pred. No. 2e-07; ative 0; Mismatches 0; Indels
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
         01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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OPTOX2;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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EMBL; AF162035; AAD47790.1; --
EMBL; AF162036; AAD47791.1; --
EMBL; AF162048; AAD47803.1; --
EMBL; AF162050; AAD47805.1; --
EMBL; AF162052; AAD47805.1; --
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                                                                                                                                                                                                                            Pongo pygmaeus (Orangutan).
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates;
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EMBL; AF162045; AAD47800.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor protein signalin. .;
InterPro; IPR000276; GPR-Rhodpsn.
PFam; PF00001; 7tm 1; 1.
PRINTS; PR000237; GPRCRHODOPSN.
PROSITE; PS00237; GPRCRHODOPSN.
PROSITE; PS50262; G_PROTEIN RECEP_F1 1; 1.
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCR5 genes from diverse simian and prosimian
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Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Erythrocebus.
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Pred. No. 2e-07;
Mismatches 0; Indels
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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339 339
339 AA, 39148 MW; OCA289CDDEEDE831 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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nes 18; Conservative
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Matches 18; Conservative
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R PRINTS; PR000217; GPCRRHODOPSN. RECEP_FI_1; 1.

R PROSITE; PS00237; GPCRRHODOPSN. RECEP_FI_2; 1.
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01-VMY-2000 (TEBMELRel. 13, Created)

01-VMY-2000 (TEBMELRel. 13, Last sequence update)

01-JUN-2003 (TEBMELRel. 24, Last annotation update)

C-C chemokine receptor 5 (Fragment).

C-GCs.

Gorilla gorilla (Lowland gorilla).

Eukaryota, Metazoa; Chordata, Craniata; Vertebrata, Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammaliai, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Cercopithecus.
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100.0%; Pred. No. 2e-07;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      339 AA
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN RECEP_F1_1; 1.
RECEPCOT.
NOW TER 1 1 1
NOW TER 339 339
SEQÜENCE 339 AA; 39154 MW; 09715882A60
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Best Local Similarity 100.
Matches 18; Conservative
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DT 011-M
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Query Match
100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels

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Search completed: September 28, 2004, 09:06:19 Job time: 29.8 secs

us-10-084-813-14.rag

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AAB88996
                                                                                                September 28, 2004, 08:51:21 ; Search time 52.525 Seconds
(without alignments)
118.345 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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118
1 APYNIVLLINTFQEFFGLNNCS
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geneseqp1990s:*
geneseqp2001s:*
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Gapop 10.0 , Gapext
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length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	OCTUD VIH APPRAGE		z Human	Adc10144 Human NOV	Aaw26766 Human che	Aaw27407 Human CCR	Aaw27123 Human che	Aaw27125 Macaque c	Aaw07602 Human G-p	5 Human	Aaw88232 HIV-1 co-	m	9 Amino	Aae07046 Human G-p	8 Human	Human	1 Human	Aae07037 Human G-p	9 Human	Aab46858 Human HDG	Abb56342 Non-endog	Aab83354 Human CCR	Aab82948 Human HIV	Aau97150 Human G-p	Aau97152 Human G-p	Aam52829 Human CCR
SUMMARIES	ID		0.00000	ADCI0142	ADC10144	AAW26766	AAW27407	AAW27123	AAW27125	AAW07602	AAW23835	AAW88232	AAY80128	AAG79089	AAE07046	AAE07048	AAG80111	AAE04321	AAE07037	AAE07039	AAB46858	ABB56342	AAB83354	AAB82948	AAU97150	AAU97152	AAM52829
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Aam52828 Human CC	Abg70597 Human G-p	Abg92883 Human imm	Abg92880 Human G-p	Aae25808 Human G-p		Abb81054 G-protein		Abg75540 Human G-p	Abr58602 Human can	Human	Abu61654 Human G-p	Abp97728 Amino aci	Abp81933 Human C-C	Adc03341 Human che	Adc03359 Macaque c	Aaw23834 Human CC	Aay41280 Fusion pr	Aaw54037 Mouse CC-	Add44859 Rat Prote
AAM52828	ABG70597	ABG92883	ABG92880	AAE25808	AAE25811	ABB81054	ABB08343	ABG75540	ABR58602	AA029514	ABU61654	ABP97728	ABP81933	ADC03341	ADC03359	AAW23834	AAY41280	AAW54037	ADD44859
352 5							352 5			_			352 6						354 7
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	91.5	0.68
118	118	118	118	118	118	118	118	118	118	118	118	118	118	118	118	118	118	108	105
26	27		29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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                                                                                                                  Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist; replication; CCR5; CXCR4; CD4; STRL33.
                                                                                                                                                                                                                                                                                                                                                                                                               Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gpl20 under physiological conditions.
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                                                                                                                                                                                                                                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                        HIV gp120 protein binding peptide #89.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 21; Page 38; 114pp; English.
AAB88996 standard; peptide; 22 AA.
                                                                                                                                                                                                                                                                                            99US-0151270P.
                                                                                                                                                                                                                                                             25-AUG-2000; 2000WO-US023505
                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-244398/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22 AA;
                                                                                                                                                                                                  WO200116182-A2.
                                                                                                                                                                                                                                                                                            27-AUG-1999;
                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                 08-MAR-2001.
                                                          23-MAY-2001
                                                                                                                                                                                                                                                                                                                                                         Saxinger C;
                               AAB88996;
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1 APYNIVILLINTFQEFFGLNNCS 22

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cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective; antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX; pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder; inflammatory disorder; chromosome mapping; tissue typing; predictive medicine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, Kekuda F
Khramtsov NV, Li L, Liu X, Malyankar JW, Miller CE, Millet I;
Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;
Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK;
                                                                          Human NOVX polypeptide SEQ ID NO: 162.
           ADC10142 standard; protein; 268 AA
                                                                                                                                                                                                                                                                                                                                  2001US-0298285P.
2001US-0298528P.
2001US-0299133P.
2001US-0299230P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001US-0322297P.
2001US-0324669P.
2001US-0337477P.
2001US-0341562P.
2002US-0358656P.
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2002US-0358978P.
2002US-0359034P.
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2002US-0359121P.
2002US-0359964P.
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                                                     18-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CURA-) CURAGEN CORP.
                                                                                                                                                                                   WO2003000842-A2
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14-DEC-2001;
21-FEB-2002;
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26-JUN-2001;
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                                 ADC10142;
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Kekuda R;

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The invention relates to novel isolated polypeptides, mature form of the polypeptide, a sequence that is 95% identical to the polypeptide or the polypeptide comprising one or more conservative substitutions. The Novx polypeptide is useful for treating or preventing a pathology associated with the polypeptide e.g. disorders associated with aberrant expression or activity of the polypeptide, such as cancer, diabetes, obesity, and endocrine. CNS and inflammatory disorders. They can also be used in various detection and screening assays, chromosome mapping, issue typing and predictive medicine. This sequence corresponds to one of the
                                                                                        New isolated NOVX polypeptides and nucleic acid molecules useful for treating, preventing and diagnosing pathological conditions with NOVX-associated disorders, such as cancer, obesity, diabetes and inflammatory or CNS diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective; antiinflammatory; gene therapy; antisease therapy; thyrominetic; NOVX; pathology; cancer; diabetes; obseity; endocrine disorder; CNS disorder; inflammatory disorder; chromosome mapping; tissue typing;
 Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
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                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 118; DB 7; Length 268; 100.0%; Pred. No. 2.1e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                      Claim 1; SEQ ID NO 162; 772pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human NOVX polypeptide SEQ ID NO: 164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 APYNIVLLLNTFQEFFGLNNCS 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 APYNIVLLINIFOEFFGLNNCS 22
                                                                                                                                                                                                                                                                                                                                        polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001US-0295607P.
2001US-0295661P.
2001US-0296404P.
2001US-0296418P.
2001US-0296575P.
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2001US-0299133P.

2001US-0299230P.

2001US-029949P.

2001US-0300177P.
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2001US-0295573P.
2001US-0297567P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    22; Conservative
Stone DJ, \Lepley DM;
                                            WPI; 2003-210149/20.
N-PSDB; ADC10141.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                         Sequence 268 AA;
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12-JUN-2001; 2
12-JUN-2001; 2
14-JUN-2001; 2
15-JUN-2001; 2
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06-JUN-2001;
07-JUN-2001;
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21-JUN-2001;
22-JUN-2001;
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Spytek KA,
Burgess CE,
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Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
Gerlach VL, Gorman L, Guo X, Herrmann JL, Halt T, Ji W, Kekuda R;
Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;
Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;
Schenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK;
Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
Burgess CE,: Lepley DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated NOVX polypeptides and nucleic acid molecules useful for treating, preventing and diagnosing pathological conditions with NOVX-associated disorders, such as cancer, obesity, diabetes and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 164; 772pp; English.
26-JUN-2001, 2001US-0300883P.
28-JUN-2001, 2001US-0301530P.
28-JUN-2001, 2001US-0301550P.
03-JUL-2001, 2001US-0302550P.
31-JUL-2001, 2001US-0322297P.
25-SEP-2001, 2001US-0322297P.
25-SEP-2001, 2001US-0324562P.
14-DEC-2001, 2001US-03341562P.
21-FEB-2002, 2001US-0359034P.
22-FEB-2002, 2002US-0359034P.
21-FEB-2002, 2002US-0359034P.
21-FEB-2002, 2002US-0359034P.
21-FEB-2002, 2002US-0359944P.
01-MAR-2002, 2002US-0369858P.
112-MAR-2002, 2002US-0369868P.
112-MAR-2002, 2002US-0369868P.
112-MAR-2002, 2002US-0369868P.
113-MAR-2002, 2002US-0369868P.
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                                                                                                                                                                                                                                                                                                                                                                                     (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-210149/20.
N-PSDB; ADC10143.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 268 AA;
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The invention relates to novel isolated polypeptides, mature form of the polypeptide, a sequence that is 95% identical to the polypeptide or the polypeptide comprising one or more conservative substitutions. The NOVX polypeptide is useful for treating or preventing a pathology associated with the polypeptide e.g. disorders associated with aberrant expression or activity of the polypeptide, such as cancer, diabetes, obesity, and endocrine, CNS and inflammatory disorders. They can also be used in and predictive medicine and screening assays, chromosome mapping, tissue typing and predictive medicine. This sequence corresponds to one of the 100.0%; Score 118; DB 7; Length 268; 100.0%; Pred. No. 2.1e-11;

Mismatches 1 APYNIVLLINTFQEFFGLNNCS 22 ö Conservative Query Match Best Local Similarity Matches 22; Conserv

165 APYNIVLLLNTFQEFFGLNNCS 186 AAW26766 standard; protein; 332 AA RESULT 4
AAW26766
ID AAW2
XX
AC AAW2
XX 임

(first entry) 21-MAY-1998

chemokine receptor MMLR-CCR. Human

Mammalian mixed lymphocyte receptor; chemokine receptor; MMLR-CCR; human; macrophage; chemotaxis; heematopoiesis; infection; inflammation; proliferative disease; cardicovacular disease; tumour; rheumatoid arthritis; alveolitis; atherosclerosis; chorante granulomatous disease; esthma; wysthenia gravis; diabetes; inflammatory bowel disease; asthma; wysthenia gravis; diabetes; chediak-Higashi syndrome; therapy; diagnosis.

Homo sapiens

107. .128 /note= "conserved peptide" Location/Qualifiers Peptide

/note= "a claimed polypeptide has isoleucine at residue 121° Misc-difference

06-NOV-1997.

97WO-US006993. 25-APR-1997; 96US-00638081. 26-APR-1996;

(INCY-) INCYTE PHARM INC.

Wilde CG; Coleman R, Bandman O, Au-Young J,

1997-549729/50. N-PSDB; AAT99542. Polynucleotide encoding MMLR-CCR or MPHG-CCR chemokine receptor - useful to study, diagnose and treat, e.g. infection, inflammation, solid tumour and proliferative and cardiovascular disease.

Claim 8; Page 37-38; 59pp; English.

This protein comprises human MMLR-CCR, a novel C-C chemokine receptor associated with monocyte/macrophage infiltration and chemotaxis and haematopoiesis. The amino acid sequence was deduced from a cDNA clone (see AAT99542) obtained from a cDNA library made from monouclear cells collected on day 2 of a mixed lymphocyte culture, i.e. cells associated with inflammation and immunomodulation. Another novel chemokine receptor, MPHG-CCR (see AAM36767), is also claimed. MMLR-CCR contains 7 transmembrane spanning segments connected by a serives of intracellular and extracellular loops. MMLR-CCR and be used to study, diagnose and treat disease states in which normal leukocyte function is perturbed by normal leukopoiesis or inappropriate activation via chemokine agonists or antagonists, such as infection, inflammation, proliferative disease, tumourigenesis, autoimmune disease, abnormal cell proliferation, solid tumours, cardiovascular disease, rheumatoid arthuring, allocalities, atherosclerosis, chronic granulomatous disease, asthma, myasthenia gravis, diabetes, inflammatory bowel disease, toxic shock syndrome, septic shock and Chediak-Higashi syndrome

Sequence 332 AA;

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Gaps

. 0

Indels

0

Gaps ö Length 332; Indels 100.0%; Score 118; DB 2; 100.0%; Pred. No. 2.7e-11; iive 0; Mismatches 0; Local Similarity 100. nes 22; Conservative Query Match Matches

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RESULT 5 AAW27407 ID AAW27407 standard; protein; 352 AA.

Human CCR5.

AAW27407;

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This polypeptide sequence comprises novel human chemokine receptor 88C, a G protein coupled receptor that is involved in leukocyte trafficking. Its amino sequence was deduced from a cDNA clone (AATS161) isolated from a marcophage library. It shows 62* identity to CCCRR1. Chemokine receptor 88-28 (see AAW27124) has also been identified. 88C and 88-2B receptors and their polypeptide fragments can be produced in transformed host cells. The receptors, peptides comprising occ more of the extracellular or intracellular domains, and anti-receptor antibodies can be used to modulate receptor activities, particularly ligand and G brotein binding, and are potentially potentially useful in the treatment of atheroslerosis, theumatoid arthritis, tumours, asthma, viral infection, AIDS, inflammatory conditions, pathological immune response, abnormal haematopoietic processes etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding chemokine receptors 88-2B and 88C - used modulate leukocyte trafficking, e.g. for treatment of inflammation, tumours, viral infections, auto-immune diseases, etc.
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100.0%; Pred. No. 2.9e-11;
iive 0; Mismatches 0;
                                                                              1. .32
/label= Extracellular_domain
56. .67
/label= Intracellular_domain
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/label= Intracellular_domain
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                                                                                                                                                                                             125. .145
/label= Intracellular_domain
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/label= Extracellular_domain
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/label= Intracellular_domain
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                                                      Location/Qualifiers
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96US-00661393.
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                                                                                                                                                                                                                                                                                                                  259. .280
/label= Ex
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Matches 22; Conservative
                                                                                                                                                          .112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-341689/31.
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                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5), which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES chemokines, but not by monocyte chemoattractant protein 1 (MCP-1), MCP-2, MCP-3, interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha) chemokines. Active CCR-5 is also a receptor of human immunodeficiency virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can used to diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriaals, viral infections, especially HIV-1 or HIV-2 infection, cancer, atherosclerosis and autoimmune disorders
                                                                                                                        ruman Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus;
type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention;
inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
atherosclerosis; autoimmune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Active and inactive forms of human CC chemokine receptor CCR-5 - useful to diagnose, prevent and/or treat inflammatory disorders, autoimmune disease and viral infection.
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96EP-00870102.
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                                                               (first entry)
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N-PSDB; AAT90117.
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Best Local Similarity
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Gaps

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AAW27123;

RESULT

Matches

8 d Length 352; Indels

Macaca sp.

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Novel human mature G-protein chemokine receptor HDGNRIC (AAW07602) is a 7-transmembrane protein involved in signal transduction. Its amino acid sequence was deduced from a cDNA clone (AAY44042) isolated from a human monocyte library. Isolation of the cDNA allows prodn. of recombinant HDGNRIC in host, e.g. E. coli, COS or Sf9, cells. The recombinant receptor can be used to identify agonists or antegonists of the receptor; such cpds. can be used to identify agonists or antegonists of the receptor; expression of G-protein chemokine receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC chemokine receptor 5; CCR5; G-protein coupled receptor; buman immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.
                                                                                                                                                                                                                                                                                                                                    Human G-protein chemokine receptor, HDGNR10 - useful to identify (ant)agonists, for treatment of haematopoiesis, leukaemia, chronic and acute inflammation, rheumatoid arthritis, etc.
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/note= "extracellular loop-1 (Claim 19)"
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194. .219
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|label= III
|note= "transmembrane domain"
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|label= I
|note= "transmembrane domain"
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/label= IV
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Best Local Similarity 100.
Matches 22; Conservative
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N-PSDB; AAT44042.
                                                                                                                                                                                                                                       Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 352 AA;
  Homo sapiens.
                                     WO9639437-A1
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AAW2383
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                                                                                      Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour; asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy; disgnosis; leukocyte trafficking; G protein coupled receptor; ligand; modulator; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This polypeptide sequence comprises macaque chemokine receptor 88C, a G mino sequence that is involved in leukocyte trafficking. Its amino sequence was deduced from a 88C DAM (AATS153) isolated by PCR amplification. It shows 97% identity to human 88C (AAM77123). 88C receptors and their polypeptide fragments can be produced in transformed host cells. The receptors, peptides comprising one or more of the extracellular or intracellular domains, and anti-receptor antibodies can be used to modulate receptor activities, particularly ligand and G ratheroslerosis, rheumatoid activities, particularly ligand and G protein binding, and are potentially potentially useful in the treatment of atheroslerosis, rheumatoid arthritis, tumours, asthma, viral infection, AIDS, inflammatory conditions, pathological immune response, abnormal haematopoietic processes etc. A hybridoma that produces an antibody that specifically binds to macaque 88C is claimed
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                                                    Macaque chemokine receptor 88C.
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              (first entry)
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Local Sim.
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RESULT

Query Match

Matches

AAW07602;

AAW07602
ID AAW07602
IXX AC AAW
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Gaps

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Length 352; Indels Location/Qualifiers

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protein sequence comprises of a novel human macrophage-selective CC
                                                                                                                                                                                                                            CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion between HIV and a target cell.
                                      261. .276
/note= "extracellular loop-3 (Claim 19)"
277. .300
/label= VII
/note= "transmembrane domain"
       /note= "transmembrane domain"
238. .258
1.251 /hole "transmembrane domain"
/note= "transmembrane domain"
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Broder CC, Kennedy PE;
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Berger EA, Alkhatib G, Murphy PM;

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chemokine receptor that has been designated CCRS. The sequence was deduced from an isolated CDNA clone (see AAT76920). An Ala12Tleu variant (see W181810 of CCRS was also identified. The susceptibility of human macrophages to HIV infection depends on cell surface expression of CD4 and CCRS. CCRS is a member of the 7-transmembrane superfamily of G-protein coupled cell surface molecules. It plays an essential role in the membrane fusion step of infection by some HIV isolates. The establishment of stable, non-human coll innes and transgenic mammals having cells that infection. Antibodies that bind to CCRS, cCRS variants, and CCRS-binding agents capable of blocking membrane fusion between HIV and target cells represent potential anti-HIV therapeutics for macrophage tropic strains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 118; DB 2; Length 352;
Pred. No. 2.9e-11;
Mismatches 0; Indels
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Best Local Similarity 100.
Matches 22; Conservative
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APYNIVLLINTFQEFFGLNNCS 270
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AAW88232;
RESULT 10
AAM8823
ID AAM883
XX AAW883
XX XX AAW883
XX XX BDT 15-MAL
XX BD HIV-1
XX HIV-1
XX Gene
XX HOWO
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(first entry) HIV-1 co-receptor CCR5 15-MAR-1999

HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS; gene therapy; human.

AAY80128;

Homo sapiens

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And are the interaction by macrophage-tropic (N-tropic) strains of a co-receptor for infection by macrophage-tropic (N-tropic) strains of HIV-1. The invention relates to the identification of a CCR5 variant (see AAW88211), designated CCR5, but lacking transmembrane domains 3-7. The commains of wild-type CCR5, but lacking transmembrane domains 3-7. The positive correlation with resistance to infection with M-tropic HIV-1 consists, and may indicate slower progression of the disease. The detection of CCR5 variants may be used to identify individuals at lower correlation with relative to the general population who, if infected, is any exhibit slower progression to AIDS. Probes and primers (see AAV84127-CC may exhibit slower progression to AIDS. Probes and primers (see AAV84127-CC slow variants. A method is provided for inhibiting the presence of such variants. A method is provided for inhibiting HIV-1 infection of a cell expressing the CCR5 receptor. This involves introducing a nucleic acid encoding a CCR5 variant into the cell, thereby reducing the number correctional CCR5 molecules present on the cell surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New CCRS variant protein of the HIV-1 co-receptor - useful in developing resistance of CCRS-expressing cells to {\rm HIV}-1 infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is the amino acid sequence of wild-type human CCR5, which serves as
                                                                                           in wild-type CCR5, TGA
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                                                                                      /note= "corresponds to TGT (Cys) (Stop) in CCr5m303"
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100.0%; Pred. No. 2.9e-11;
tive 0; Mismatches 0;
                                                                                                                         103. . . 124
/note= "transmembrane domain 3"
142. . 167
/note= "transmembrane domain 4"
200. . 223
                                                                                                                                                                                                                        236. .260
/note= "transmembrane domain 6"
                                                                                                                                                                                                                                                         275. .301
/note= "transmembrane domain 7"
                                           57. .87
/note= "transmembrane domain 2"
                                                                                                                                                                                                        "transmembrane domain 5"
                           "transmembrane domain 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
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                             'note=
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 352 AA;
                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                             W09854317-A1
                                                                                                                                                                                                                                                                                                                                                                           29-MAY-1998;
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ID AAY8
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AC AAY8
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Human, receptor, DC-SIGN, dendritic cell, T lymphocyte, HIV, gpl20,
C-type lectin, ICAM3, HIV entry, T cell, macrophage, HIV infection, CCR5.
                                                                                                                                                                                                                                                                                                                                                          An antibody for the treatment or prevention of HIV-infection comprises gpl20 portion which binds to DC-SIGN or is exposed upon gpl20 binding o DC-SIGN due to concomitant conformational change.
Amino acid sequence of human CCR5 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 118-119; 131pp; English.
                                                                                                                                                                             28-FEB-2001; 2001WO-US006322.
                                                                                                                                                                                                              02-MAR-2000; 2000US-00517605.
                                                                                                                                                                                                                                          (UYNY ) UNIV NEW YORK (UYNI-) UNIV NIJMEGEN.
                                                                                                                                                                                                                                                                                                                             WPI; 2001-602565/68.
                                                                                                              WO200164752-A2
                                                                                 Homo sapiens.
                                                                                                                                              07-SEP-2001.
                                                                                                                                                                                                                                                                                              Littman DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE07046;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a human G-protein chemokine receptor designated HDGNR10 polymucleotides are useful in methods of screening the compounds which bind to and either: (1) activate the HDGNR10 polypeptides causing stimulation of haematopoiesis, wound healing, coagulation, and angiogenesis; treatment of solid tumours, chronic infections, leukaemia, T-cell mediated autoimmune diseases, parasitic infections, psoriasis, and to stimulate growth factor activity; or (2) inhibit activation of the HDGNR10 polypeptides which is useful for preventing and/or treating allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histamine and immunoglobulin B-mediated allergic reactions, prostaglandin-independent fever, bone marrow failure, silicosis, sarcoidosis, theumatoid arthritis shock and hyper-eosinophilia syndrome. The polymucleotides are also useful for diagnostic assays for detecting the polymetocides are also useful for allered level of the soluble form of the receptor polypeptides. The polymucleotides are also useful for in vitro purposes related to mutations in the polymucleotides are also useful for in vitro purposes related to constitute of DNA vectors
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                                                          Human, G-protein coupled receptor, G-protein chemokine receptor, HDGNR10, diagnosis, haematopoiesis, wound healing; coagulation, angiogenesis, throur; infection, leukaemia, psoriasis; allergy; T-cell mediated autoimmune disease, atherogenesis; anaphylaxis; inflammation, allergic reaction, silicosis; sarcoidosis; rheumatoid arthritis; hyper-eosinophilia syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acid encoding human G-protein chemokine receptor useful for diagnostic assays, scientific research and screening for compounds which bind to and activate or inhibit activation of the receptor
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                             Human G-protein chemokine receptor HDGNR10 SEQ ID NO:2.
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                                                                                                                                                                                                                                                                            95US-00466343.
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entry)
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N-PSDB; AAZ91481.
(first
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                                                                                                                                                                                                                                                                                                                                                                          Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptides.
                                                                                                                                                                                                                                                                           06-JUN-1995;
                                                                                                                                                                             Homo sapiens
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19-MAY-2000
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Best Local 9
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Geijtenbeek T;

Van Kooyk Y,

Kwon D,

NEW YORK STATE.

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The specification describes an antibody which is specific for an antigenic fragment of gpl20. This antigenic fragment binds to DC-SIGN or is exposed upon gpl20 binding of DC-SIGN due to concomitant conformational change. DC-SIGN is a receptor that is specifically expressed on dendritic cells and facilitates infection of T lymphocytes with HIV. DC-SIGN is identical to a HIV-1 gpl20-binding C-type lectin. DC-SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes) with high affinity. The antibody of the invention inhibits the trans enhancement of HIV entry into a T cell or macrophage facilitated by infection. The present sequence represents a human CCRS protein, which is a translocation promoting agent that interacts with CD4. This receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, G-protein chemokine receptor, CCR5, HDGNR10; inflammation, HIV, human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostatic; immunosuppressive, noctropic, neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 352;
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100.0%; Pred. No. 2.9e-11;
Nismatches 0;
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                                                                                                                                                                                                                                                                                                                                                functions in HIV-1 entry into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
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Best Local Similarity
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249 APYNIVILINTFQEFFGINNCS 270

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AAG79089 standard; protein; 352 AA

RESULT 12

(first entry)

10-DEC-2001

AAG79089;

AAG79089 ID AAG7 XX AC AAG7 XX DT 10-D

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Gaps

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Length 352; Indels

100.0%; Score 118; DB 4; 100.0%; Pred. No. 2.9e-11; Mismatches

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Conservative

Local Similarity nes 22; Conserv

Sequence 352 AA;

249 APYNIVLLINTFQEFFGLNNCS 270

22

1 APYNIVLLLNTFOEFFGLNNCS

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AAE07048 standard; protein; 352

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interaction. The disease or disorder may also be an infectious disease (e.g. a viral infection such as an early stage HIV infection, a cycomegalovirus infection, an autoimmune disease (e.g. rheumatoid arthritis) or a neurodesenerative disorder. The disease or disorder may be associated with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand expression, or lack of CCR5 ligand expression, or lack of CCR5 ligand concrease or decrease storage capabilities. CCR5 HGGMLO DNA are useful to increase or decrease storage capabilities. CCR5 HGGMLO DNA, or protein, antibodies, agonists and antagonists are also useful in the concretion, antibodies, agonists and antagonists are also useful in the diagnosis, treatment and prevention of cancer (breast, ovary, adrenal curagenital); immune disorders (Adabson's disease, allergies, autoimmune curagenital); immune disorders (Adabson's disease, allergies, autoimmune thyroiditis, diabetes mellitus, crohm's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular disorders (myocardial ischaemias) and wound healing. The present sequence is human CCR5 HDGNRIO protein
                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated nucleic acid encoding a human G-protein chemokine receptor (CCRS) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.
                                                                                                                                                                                                                           18. .88
| Jabel = Transmembrane_domain
| Jabel = "Segment 2"
                                                                                                                                                                                                                                                                                                                                                                                                      1abel= Transmembrane_domain
note= "Segment 4"
                                                                                      Extracellular domain
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|abel= Transmembrane_domain
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label= Intracellular_loop_1
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                                                  location/Qualifiers
                                                                                                                                                                         "Segment 1"
                                                                                                                                                                                                                                                                                                                                                      note= "Segment 3"
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/label= Transmemb
/note= "Segment 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-FEB-2000; 2000US-0181258P.
09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
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/label= Ex
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/label= Ex
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                                                                       l. .36
/label= 1
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N-PSDB; AAD13282.
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                    Homo sapiens
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                                                      Key
Domain
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Isolated nucleic acid encoding a human G-protein chemokine receptor (CCRS) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.
                                                                                                                                                                                                             Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostatic; immunosuppressive; noctrobic, neuroprotective; gene therapy; reurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.
                                                                                                                                       Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.
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09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
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                                                                              16-OCT-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488966/53.
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AAE07048;
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The invention relates to human G-protein chemokine receptor (CCR5)

HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are
useful for treating, preventing or ameliorating a disease or disorder
associated with inflammation, defective or aberrant chemotraxis of immune
cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's
cells, HIV infection such as Pneumocystis carinii pneumonia or Kaposi's
interaction. The disease or disorder may also be an infection, a
cytomegalovirus infection such as an early stage HIV infection, a
cytomegalovirus infection, or a poxyitus infection, a autoimmune
cisase (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
disease or disorder may be associated with aberrant CCR5 expression, lack
of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand
function. CCR5 HDGNR10 protein is used as a food additive or preservative
cof CCR5 function, and in gene therapy. CCR5 HDGNR10 DNA,
cof ccR6 function and in gene therapy. CCR5 HDGNR10 DNA,
cof cornomosome identification and in gene therapy. CCR5 HDGNR10 DNA,
protein, antibodies, agonists and antegonists are also useful in the
cornomosome identification and in gene therapy. CCR5 HDGNR10 DNA,
cof diagnosis, treatment and prevention of cancer (breast, overy, adrenal
cornomosome identification and in gene therapy. CCR5 HDGNR10 DNA,
cornomosome is numanne thyroiditis, diabetes mellitus, Crohn's
curogenital); immune disorders (Mocandial ischaemias) and wound healing. The
cordivosacular disorders (Mycoardial ischaemias) and wound healing. The
cornomosome is humann CCR5 HDGNR10 proteinias) and wound healing. The
cornomosome is humann CCR5 HDGNR10 proteinians
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 118; DB 4; Length 352; 100.0%; Pred. No. 2.9e-11; ive 0; Mismatches 0; Indels 0
    Example 40; Page 504-505; 518pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 APYNIVLLLNTFQEFFGLNNCS 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 22, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human CCR5 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 352 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JAN-2002
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Diagnostic agent containing two or more receptor-specific ligands, useful for detecting tumors, inflammation etc., also therapeutic use of ligand inhibitors.

Spodsberg N;

WPI; 2001-626256/72.

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Gaps

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This invention describes a novel diagnostic agent (A) comprising at least two different ligands (I) for receptors (II) that are implicated in disease. (A) are used for the diagnosis of tumors (especially colorectal or prostatio), organ rejection, inflammation and autoimmune diseases. Also inhibitors of (I) are used therapeutically against tumors (and their metastases), inflammation (particularly bronchial asthma or chronic bowel inflammation), or autoimmune diseases (theumatoid arthritis or lupus), where the (cardio) wascular, lymphatic, respiratory, nervous, diseasive, endocrine, motor or urogenital systems or skin are affected, and bone marrow diseases. The products of the invention are chemokine derivatives immunosuppressive, dermatclogical, antirheumatic, antiarthritic. Chemokines act on specific tumor and inflammatory cells through a conscellation of chemokine and inflammatory cells through a proliferation of these cells. Adag0045-AAG80128 represent human chemokine fragments used to illustrate the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; transformed mammalian cell; CD4; reporter gene; translocation;
human immuno deficiancy virus; HIV; long terminal repeat; LTR; therapy;
chemokine receptor; CKR; cellular dysfunction; HIV infection; cofactor;
CC-CKR-5; envelope glycoprotein; anti-HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transformed mammalian cell (I) that contains a CD4 gene, reporter gene and HIV LTR for identification of drugs and antibodies for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 118; DB 4; Length 352; 100.0%; Pred. No. 2.9e-11; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human chemokine receptor (CKR), CC-CKR-5 related protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Col 47-50; 37pp; English.
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(UYNY ) UNIV NEW YORK STATE.
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                                    Disclosure; Page 10; 26pp; German.
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96US-0020043P.
97US-00858660.
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Best Local Similarity 100.
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-417127/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 352 AA;
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contains a gene encoding CD4, a construct encoding a reporter gene under the regulation of an human immuno deficiency virus (HIV) long terminal repeat (LTR) and that has been transduced with a vector encoding a human chemokine receptor (CTR) where the CD4 and the CMR are present on the cell surface of transformed mammalian cell. The invention is useful for identifying drugs or antibodies that interfere with the translocation of receptor that facilitates the infection of a particular HIV strain into the transformed mammalian cell. Compounds identified can be used to treat sequence is a human chemokine receptor (CKR), CC-CKR-5 related protein. CC-CKR-5 is the principal cofactor for entry mediated by the envelope glycoproteins of primary macrophage-tropic strains of HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostatic; immunosuppressive; noctropic; neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic aneemis; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.
                                                                                                                                                                                                                                                           Query Match
100.0%; Score 118; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cardiovascular disorder; myocardial ischaemia.
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label= Transmembrane_domain
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/label= Extracellular_loop_2
196. .223
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label= Transmembrane_domain
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| label = Transmembrane_domain
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| label= Transmembrane_domain
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'label= Extracellular_domain
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/label= Tr
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                                                                                                                                                                                                                                  Sequence 352 AA;
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The present sequence is human G-protein chemokine receptor (CCR5) HDGNRIO protein. CCR5 HDGNRIO cDNA is included in ATCC Deposit No: 97183. CCR5 HDGNRIO antibodies are useful for treating, preventing or ameliorating a disease or disorder associated with inflammation, defective or aberrant chemotaxis of immune cells. HTV infection (such as Pneumocystis carini presenting cell interaction. HTV infection (such as Pneumocystis carini presenting cell interaction. The disease or disorder may also be an infection, a cytomegalovirus infection such as an early stage HIV infection, a cytomegalovirus infection, or a poxvirus infection, an infection, a cytomegalovirus infection, or a poxvirus infection, or a cutoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative context infection, aberrant CCR5 ligand expression, or lack of CCR5 function. Aberrant CCR5 ligand expression, or lack of CCR5 ingent in the disease or decrease storage capabilities. CCR5 HDGNRIO DNA are useful for chromosome identification and in gene cherapy. CCR5 HDGNRIO DNA, protein, antibodies, agonists and antagonists are also useful in the diagnosis, treatment and prevention of cancer contemporation and in gene conformune hammolytic anaemia, autoimmune thyroiditis, diabetes mellitus, colling, cardiovascular disorders (Madison's disease, allergies, colling); cardiovascular disorders (myocardial ischaemias) and wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acid encoding a human G-protein chemokine receptor (CCRS) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
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                                                                                                                    236. 260
/label= Transmembrane_domain
/note= "Segment 6"
'label= Transmembrane_domain
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                            /note= "Segment
224. .235
/label= Intracel
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09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
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N-PSDB; AAD13181.
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Gaps

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Length 352; Indels

Match 100.0%; Score 118; DB 4; Local Similarity 100.0%; Pred. No. 2.9e-11; les 22; Conservative 0; Mismatches 0;

Sequence 352 AA;

Query Match

Best Loca Matches

249 APYNIVLLINTFOEFFGLANCS 270

22

1 APYNIVLLINTFOEFFGLNNCS

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ine sep 25 Lo:49:5/ 2004

UB-TO-O84-8T3-T4.F8D

Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation, HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; vyfostatic; immunosuppressive; noctropic; neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative collitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia. Isolated nucleic acid encoding a human G-protein chemokine receptor (CRES) HubGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders. Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2. Example 40; Page 486-487; 495pp; English. Li Y, Ruben SM; AAE07039 standard; protein; 352 AA. 09-FEB-2000; 2000US-0181258P. 09-MAR-2000; 2000US-0187999P. 22-SEP-2000; 2000US-0234336P. 09-FEB-2001; 2001WO-US004152. (HUMA-) HUMAN GENOME SCI INC 16-OCT-2001 (first entry) Roschke V, WPI; 2001-488965/53. N-PSDB; AAD13198. WO200158915-A2. Homo sapiens. 16-AUG-2001. Rosen CA, AAE07039;

The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10 protein. CCR5 HDGNR10 antibodies are useful for treating, preventing or ameliorating a disease or disorder associated with inflammation, ameliorating a disease or disorder associated with inflammation, or defective or aberrant chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen presenting cell interaction. The disease or disorder may also be an infectious disease (e.g. a viral infection such as an early stage HIV infection, a cytomegalovirus infection, or a poxvirus infection), an autoimmune disease or disorder may be associated with aberrant CCRS expression, lack of CCRS function, aberrant CCRS or lack of CCRS function. CCRS HDGNR10 protein is used as a food additive or preservative to increase or decrease storage capabilities. CCRS HDGNR10 DNA are useful for chromosome identification and in gene therapy. CCRS HDGNR10 DNA, protein, and prevention of cancer (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract, liver, lung, urogenital); immune disorders (Addison's disease, multiple sclerosis, rheumatcid arthritis and ulcerative colitis); cardiovascular culcimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatcid arthritis and ulcerative colitis); cardiovascular culcimmune thyroiditis and more wound healing

Sequence 352 AA;

Query Match

100.0%; Score 118; DB 4; Length 352;

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Gaps
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           Indels
Pred. No. 2.9e-11;
Mismatches 0;
Local Similarity 100.0%; P. les 22; Conservative 0;
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Matches
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AAB46858 standard; protein; 352

AAB46858;

16-AUG-2001 (revised) 02-AUG-2001 (revised) 04-MAY-2001 (first entry)

Human HDGNR10 protein.

HDGNR10; human; G-protein chemokine receptor; antiinflammatory; inticoagulant; antialregic; immunosuppressive; cytostatic; antiparasitic; antialregic; immunosuppressive; cytostatic; antiparasitic; antiparasitic; antiparatic; antirheumatic; antiarthritic; vasotropic; gene therapy; haematopoiesis; wound healing; coagulation; anglogenesis; solid tumnour; infection; leukemia; growth factor activity; T-cell mediated autoimmune disease; pooriasis; allergy; atherogenesis; anaphylaxis; malignancy; inflammation, histamine; IgE; silicosis; shock; immunoglobulin E-mediated allergic reaction; rheumatoid arthritis; prostaglandin-independent fever; bone marrow failure; sarcoidosis; hyper-eosinophilic syndrome; vulnerary.

Homo sapiens.

US2001000241-A1.

12-APR-2001

29-NOV-2000; 2000US-00725285

95US-00466343. 98US-00195662. 99US-00339912. 06-JUN-1995;

18-NOV-1998; 25-JUN-1999;

(LIYY/) LI Y. (RUBE/) RUBEN S M.

Li Y, Ruben SM;

WPI; 2001-226317/23.

N-PSDB; AAF26390.

New human G-protein chemokine receptor polypeptides and polynucleotides, useful for identifying (ant)agonists to the G-protein chemokine receptor

Claim 1a; Page 15; 22pp; English.

This invention describes a novel receptor polypeptide (I) selected from (I) a fully defined 329 amino acid sequence (II) fully disclosed in the specification; and (ii) a polypeptide encoded by the cDNA contained in a plasmid, and fragments, analogs and derivatives of the polypeptide. The products of the invention have antiinflammatory, immunomodulatory, anticoagulant, antiallergic, immunosuppressive, vulnerary, cytostatic, antiparasitic, antiparatic, antiphoratic, antiarchritic and vasotropic activity and can be used for gene therapy. The G-products of the invention activate or inhibit activation of (I). The products of the invention can also be used for stimulating nematopoiesis, wound healing, coagulation, also be used for stimulating hematopoiesis, wound healing, coagulation, also be used for stimulating activation. HDGNRIO is useful for treating stimulating growth factor activity, HDGNRIO is useful for treating stimulating growth factor activity, HDGNRIO is useful for treating allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histamine and immunoglobulin E (IgB) -mediated allergic reactions, prostaglandin-independent fever, bone marrow failure.

Matches

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RESULT 20

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This sequence represents the human CCR5 protein sequence. The invention relates to a method for determining whether an agent is capable of modulating the interaction of chemotractic chemokine receptor 5 (CCR5) with gp120, comprising incubating the agent with CCR5 and gp120 and determining whether the agent modulates the interaction, where gp120 is associated with CDP4, and where the interaction is a low affilmity binding. The method is used to identify an agent capable of modulating the interaction of CCR5 with gp120. An agent identified by the method is used to prepare a pharmaceutical composition for the treatment of a disease or condition associated with CCR5 and gp120 interaction, to treat a subject with a disease or condition associated with CCR5 and gp120 interaction, to prepare a pharmaceutical for treating human immunodeficiency virus (HIV). It can also be treat anti-inflammatory diseases. The method is commercially useful, amenable to high throughput screening, and cetects interaction of gp120 with cells expressing only CCR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Determining if an agent can modulate CCRS-gp120 interaction, comprises incubating the agent with CCRS and gp120 and determining if the agent
                                                                                                                                                     Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5; human immunodeficiency virus; anti-inflammatory disease; human.
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100.0%; Pred. No. 2.9e-11;
ive 0; Mismatches 0;
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standard; protein; 352 AA.
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12-JAN-2000; 2000GB-0000661.
12-JAN-2000; 2000GB-0000663.
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                                                                                                                   Human CCR5 protein sequence.
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modulates the interaction.
                                                                             (first entry)
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N-PSDB; AAF87099.
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ses 22; Conserv
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                                                                             09-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to G protein-coupled receptors (GPCRs) for which the endogenous ligand has been identified. Non-endogenous constitutively activated versions of known GPCRs are used in the invention for the direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists. Such agonists are useful as therapeutic agents for diseases or disorders associated with GPCRs. The present sequence is a non-endogenous version of a known human GPCR
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silicosis, sarcoidosis, rheumatoid arthritis, shock and hypereosinophilic syndrome. (N.B. This record was resubmitted to correct errors in the keyword formatting)
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Matches 22
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Gaps

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Human HIV-1 co-receptor CCR5

RESULT 21 AAB83354

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Length 352; Indels

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us-10-084-813-14.rag

CCR5; chemokine; co-receptor; human immunodeficiency virus type 1; HIV-1; infection; therapy; vaccine; anti-HIV-1. Novel compounds comprising specific amino acids within CCR5 (HIV 1 crreceptor) amino terminal domain including negatively charged and two sulfated tyrosine residues is useful for treating HIV infection in Location/Qualifiers 2. .18 /note= "binds to HIV-1 gp120" (PROG-) PROGENICS PHARM INC. (AARO-) AARON DIAMOND AIDS RES CENT. 29-FEB-2000; 2000US-0185667P. 19-MAY-2000; 2000US-0205839P. 07-FEB-2001; 2001US-0267231P. 28-FEB-2001; 2001WO-US006699. Dragic T, Olson WC; WPI; 2001-611273/70. N-PSDB; AAH26903. WO200164710-A2 Key Binding-sitè Homo sapiens 07-SEP-2001

Claim 1; Page 30; 163pp; English.

The present sequence is that of human HIV-1 co-receptor CCR5. Amino acids cashe in the N-terminal region of CCR5 comprise an HIV-1 gpl20-binding set that determines the specificity of the interaction between CCR5 and HIV-1 gpl20. Post-translational sulfation of the tyrosine residues in the CCR5 N-terminus is required for gpl20 binding and may critically modulate the susceptibility of target calls to HIV-1 infection in vivo. The invention provides claimed sulfated peptides (see AAB82947) that are based on the CCR5 N-terminal region and which are effective for inhibiting HIV-1 binding to CCR5. These peptides are used in claimed methods of inhibiting HIV infection of CO4+ cells, of preventing CD4+ cells are infected with HIV, of treating a subject whose CD4+ cells are infected with HIV, and of identifying an agent which inhibits binding of a CCR5 isopeially a human, infected (therapeutic method), not infected with HIV (prophylactic method), or in a subject who is not infected with, but has been exposed to, HIV

Sequence 352 AA;

Gaps ö Length 352; Indels Query Match
100.0%; Score 118; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0;

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RESULT 23 AAU97150

¥. AAU97150 standard; protein; 352

AAU97150,

(first entry) 13-AUG-2002 Human G-protein chemokine receptor (CCRS) HDGNR10 #1.

Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; fimune cell chemotaxis; autoimmune disease; rheumatoid arthritis; neurodegeneration; viral infection; Kaposi sarcoma; cancer; hyperproliferative disease; neurological disease; receptor. 09-FEB-2000; 2000US-0181258P. 09-MAR-2000; 2000US-0187999P. 22-SEP-2000; 2000US-0234336P. 09-FEB-2001; 2001US-00779879 (ROSC/) ROSEN C A. (ROSC/) ROSCHKE V. (LIYY/) LI Y. (RUBE/) RUBEN S M. US2002048786-A1. Homo sapiens 25-APR-2002.

Ruben SM; Li Y, Rosen CA, Roschke V,

WPI; 2002-434754/46.

N-PSDB; ABK51853

New nucleic acid encoding an antibody specific for the G-protein chemokine receptor CCRS, useful for treatment and diagnosis of e.g. inflammation.

Claim 61; Fig 1; 180pp; English.

The present invention relates to the isolation of a novel human G-protein chemokine receptor (CCR5) designated HDGNR10, and polymucleotide sequences encoding it. The invention also describes antibodies that bind human G-protein chemokine receptor (CCR5) HDGNR10 and polymucleotide.

Chuman G-protein chemokine receptor (CCR5) HDGNR10 and polymucleotide.

Sequences encoding the antibodies. The antibodies are useful for treating or preventing inflammation, defective or aberrant chemotaxis of immune cells and T-cell/antigen-presenting cell interactions, infections and utoimmune diseases, rheumatoid arthritis, neurodegeneration, viral infections (sepecially early stage human immune deficiency virus (H1V), cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions associated with aberrant or deficient expression of the CCR5 receptor or its ligands. The antibodies are also useful to determine CCR5 expression, e.g. for diagnosis, prognosis and monitoring of cancer and other hyperpoliferative diseases. The polymucleotide sequences encoding human combinant receptor, and in the treatment of a wide range of diseases such as infectious diseases (e.g. influenza), neurological diseases (e.g. HDGNR10 and the receptor (CCR5) HDGNR10 and seceptor (CCR5) HDGNR10 and chemokine receptor (CCR5) HDGNR10 in the present sequence represents human G-protein chemokine receptor (CCR5) HDGNR10 in the creeptor (CCR5) HDGNR10 in the present sequence represents human G-protein chemokine receptor (CCR5) HDGNR10 in the present chemokine receptor (CCR5) H

Sequence 352 AA;

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Gaps 0 Length 352; Indels 100.0%; Score 118; DB 5; 100.0%; Pred. No. 2.9e-11; ive 0; Mismatches 0; Local Similarity 100. ses 22; Conservative Query Match Best Loc Matches

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ò d RESULT 24 AAU97152

AAU97152 standard; protein; 352 AA.

AAU97152; XXXXXX

13-AUG-2002 (first entry)

22-FEB-2002

receptor; CCR5; HDGNR10; inflammation;

Ruben SM;

The present invention relates to the isolation of a novel human G-protein chemokine receptor (CCR5) designated HDGNR10, and polymucleotide sequences encoding it. The invention also describes antibodies that bind human G-protein chemokine receptor (CCR5) HDGNR10 and polymucleotide sequences encoding the antibodies. The antibodies are useful for treating or preventing inflammation, defective or aberrant chemotaxis of immune cells and T-cell/antigen-presenting cell interactions, infections and autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral infections (especially early-stage human immune deficiency virus (HIV), cytomegalovius or pox virus infections, Kapoesi sarcoma, or conditions associated with aberrant or deficient expression of the CCR5 receptor or its ligands. The antibodies are also useful to determine CCR5 expression, e.g. for diagnosis, prognosis, and monitoring of cancer and other hyperproliferative diseases. The polymucleotide sequences encoding human G-protein chemokine receptor (CCR5) HDGNR10 can be used to produce the recombinant receptor, and in the treatment of a wide range of diseases council as infectious diseases (e.g. influenza), neurological diseases (e.g. present sequence represents human G-protein chemokine receptor (CCR5) processin sequence represents human G-protein chemokine receptor (CCR5) processing parkinson's diseases. Disclosure; Page 165-166; 180pp; English. HDGNR10 #2

Sequence 352 AA;

Gaps ö 100.0%; Score 118; DB 5; Length 352; 100.0%; Pred. No. 2.9e-11; ive 0; Mismatches 0; Indels (22; Conservative Query Match Best Local Similarity Matches

1 APYNIVILLINTFOEFFGLNNCS 22 APYNIVLLINTFQEFFGLNNCS 249

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AAM52829 standard; protein; 352 AA. AAM52829; RESULT 25 AAM52829 ID AAM

human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome; drug screening; identification; variant. /note= "Glu replaces wild-type Leu; encoded by CC chemokine receptor 5; human; HIV infection; /note= "Encoded by AGC" Location/Qualifiers 55 21-MAR-2001; 2001WO-US009155 Human CCR5 Gln 55 variant. Key Misc-difference Misc-difference WO200171346-A2 Homo sapiens. 27-SEP-2001

21-MAR-2000; 2000US-0190946P.
21-MAR-2000; 2000US-0190996P.
21-MAR-2000; 2000US-0191299P.
20-MAR-2001; 2001US-00813481.
20-MAR-2001; 2001US-00813651. CONS-) CONSENSUS PHARM INC. Tan Hehir CA; See RH, Nestor JJ, Wilson CJ, WPI; 2002-010610/01. N-PSDB; ABA02318. Identifying CC chemokine receptor 5 binding compound for treating AIDS, comprises binding a molecule from library to a molecule having binding property corresponding to CCR5 and identifying bound molecule.

Example 3; Fig 4B; 50pp; English.

The invention relates to a method for identifying a binding compound for chemokine receptor 5 (CCRS). The method involves screening a library of test molecules (particularly peptides) with immobilised CCRS, and then identifying those molecules which bind. The invention also relates to identifying those molecules which bind. The invention also relates to CCRS-binding molecules identified using the method of the invention, cc transfer vector encoding tagged CCRS, a computer-aided methods for identifying consensus motifies for CCRS-binding peptides, a transfer vector encoding tagged CCRS, a computer aided methods for ca computer aided drug screening assay that utilises the three-dimensional cs tructure of CCRS. Compounds identified using the methods of the invention are useful for treating or preventing HTV (human invention are useful for treating or preventing HTV (human cransplands) infection or AIRS (acquired immunodeficiency virus) infection are allowable of the invention may also be used to identify agonists or antagonists of the interaction of CCRS, with its cateuring and and to determine a binding motif for CCRS. The present cs equence represents a naturally occurring variant of human CCRS in which there is a glutamine, rather than a leucine, at position 55

Sequence 352 AA;

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Gaps ô Length 352; Indels ô 100.0%; Score 118; DB 5; 100.0%; Pred. No. 2.9e-11; Mismatches ó 22; Conservative Query Match Best Local Similarity Matches

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RESULT 26 AAM52828

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us-10-084-813-14.rag
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The invention relates to a method for identifying a binding compound for C chemokine receptor 5 (CCR5). The method involves screening a library C of test molecules (particularly peptides) with immobilised CCR5, and then identifying those molecules which bind. The invention also relates to carbiding molecules identified using the method of the invention, methods for identifying consensus motifs for CCR5-binding peptides, a transfer vector encoding tagged CCR5, a computer-aided methods for determining the relative binding assay that utilises the three-dimensional a computer aided drug screening assay that utilises the three-dimensional structure of CCR5. Compounds identified using the methods of the invention are useful for treating or preventing HTV (human immunodeficiency virus) infection or AIDS (acquired immunodeficiency syndrome) in a patient. The methods of the invention may also be used to identify agonists or antagonists of the interaction of CCR5. The present structure is represent human CCR5.
                                                                                                                                                                                                                                                                                           CCR5; CC chemokine receptor 5; human; HIV infection; human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome; drug screening; identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying CC chemokine receptor 5 binding compound for treating AIDS, comprises binding a molecule from library to a molecule having binding property corresponding to CCR5 and identifying bound molecule.
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                                                                                                                                                                                                                       Human CC chemokine receptor 5 (CCR5)
AAM52828 standard; protein; 352 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2000; 2000US-019096FP.
20-MAR-2000; 2000US-019129P.
20-MAR-2001; 2001US-00813648.
20-MAR-2001; 2001US-00813653.
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                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                   22-FEB-2002
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                                                                       AAM52828
NAME OF THE PROOF OF THE PROOF
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th 100.0%; Score 118; DB 5; Length 352; Similarity 100.0%; Pred. No. 2.9e-11; 22; Conservative 0; Mismatches 0; Indels (APYNIVLLINTFOEFFGLNNCS 270 1 APYNIVLLLNTFOEFFGLNNCS 22 Query Match Best Local Matches

ABG70597 standard; protein; 352 AA ABG70597 RESULT 27 ABG70597 ID ABG70 XX AC ABG70

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(first entry) 03-DEC-2002

Human G-protein chemokine receptor, HDGNR10.

Human; G-protein chemokine receptor; HDGNR10; CCRS receptor; hadmanopoiesis; solid tumour; chronic infection; leukaemia; T-call mediated autoimmune disease; parasitic infection; leukaemia; T-call mediated autoimmune disease; parasitic infection; psoriasis; growth factor activity; allergy; atherogenesis; anaphylaxis; mallignancy; inflammation; histamine; immunoglobulin B; IgB-mediated allergic reaction; sarcoidosis; prostaglandin-independent fever; bone marrow failure; shock; rheumatoid arthritis; hyper-eosinophilic syndrome; cytostatic; antiparasitic; antiparasitic; antiparasitic; antiparasitic; antiparasitic; antiparatic; antiparatic; antiparatic; antiparatic; antiparatic; antipyretic; receptor

Homo sapiens.

US2002099176-A1.

25-JUL-2002

25-JUN-1999;

36-JUN-1995;

95US-00466343.

(LIYY/) LI Y. (RUBE/) RUBEN S M.

Li Y, Ruben SM;

WPI; 2002-690494/74. N-PSDB; ABS54272.

Novel human G-protein chemokine receptor polypeptide useful for identifying modulators for stimulating hematopoiesis, wound healing, leukemia, for treating allergy, rheumatoid arthritis, shock and as research agents. Novel

Claim 7; Fig 1; 22pp; English.

The present invention relates to the isolation of human G-protein chemokine receptor, HDGNR10 (CCR5 receptor), and the polymucleotide sequences sequence encoding it. HDGNR10 polymeptide and polymucleotide sequences can useful for diagnosing a disease or a susceptibility to a disease. The call the construction of HDGNR10. They are useful for identifying modulators for stimulating haematopoiesis, wound healing, coagulation, angiogenesis, to treat solid tumours, orbonic infections, psoriasis, or for stimulating growth factor activity. The sequences are also useful for preventing and/or treating allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histamine and immunoglobulin E (IgE)-mediated allergic reactions, prostaglandin-independent fever, bone marrow failure, sarcoidosis, rheumatoid arthitis, shock and hyperbone marrow failure. Polymucleotide sequences encoding HDGNR10 can be used in gene therapy to treat conditions related to underexpression of HDGNR10. The present sequence represents human G-protein chemokine receptor, HDGNR10

Sequence 352 AA;

Gaps . 0

Gaps ; 0 100.0%; Score 118; DB 5; Length 352; 100.0%; Pred. No. 2.9e-11; ive 0; Mismatches 0; Indels C Query Match
Best Local Similarity 100.
Matches 22, Conservative

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RESULT 28 ABG92883

Tue Sep 28 15:49:57 2004

lymphocytopenia 8XXCCCCCCCCCCCCCCCCCCCX

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Immunoglobulin, variable heavy chain, variable light chain, human, G-protein chemokine receptor; CCR5, HDGNR10; cancer; inflammation; munuclogic deficiency syndrome; blood protein disorder; nephritis; ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease; histiocytosis; chemotaxis; infectious disease; autoimmune disease; histiocytosis; chemotaxis; infectious disease; autoimmune disease; heurodegenerative disorder; viral infection; poxvirus infection; HIV; human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma; pheumocystis carnii infection; cardiovascular disorder; atherosclerosis;
                                                                                                                                                                                                                                                                                                                      Human immunoglobulin variable heavy domain #1.
ABG92883 standard; protein; 352 AA
                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                19-NOV-2002
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Homo sapiens

WO200264612-A2.

22-AUG-2002

08-FEB-2002; 2002WO-US003634

2001US-007798B0 09-FEB-2001;

09-FEB-2001; 2001WO-US004153. 12-UN-2001; 2001US-0297257P. 08-AUG-2001; 2001US-0310458P. 12-OCT-2001; 2001US-0328447P. 2001US-0341725P 21-DEC-2001; (HUMA-) HUMAN GENOME SCI INC.

Ruben SM; Rosen CA, Roschke V,

WPI; 2002-643455/69. N-PSDB; ABS68606.

New human G-protein Chemokine Receptor gene (HDGNR10) useful for treating, preventing, ameliorating or monitoring diseases or disorders associated with aberrant expression of HDGNR10 e.g. cancer.

Example 55; Fig 4; 562pp; English

The invention describes an isolated polynucleotide encoding a first antibody at least 95-100% identical to a second antibody consisting of antibody at least 95-100% identical to a second antibody consisting of a variable heavy (VH) or variable light (VL) domain of the antibody consisting of a variable heavy (VH) or variable light (VL) domain of the antibody consisting of xF3.642, XF3.1089, XF22.3C9.6, XF22.956, XF27/28.1957, XF27/28.1855, XF27/28.1856, XF27/28.36710, XF27/28.36710, XF27/28.36710, XF27/28.36710, XF27/28.3857, XF2

The invention describes an isolated polymucleotide encoding a first antibody at least 95-100% identical to a second antibody consisting of an antibody at least 95-100% identical to a second antibody consisting of an article antibody comprising at least one, two or three CDR regions of a variable heavy (VH) or variable light (VL) domain of the antibody consisted by a hybridoma cell line consisting of XF3.5F1, XF11.1F8, XF27/28.25G10, XF27/28.3E6, XF27/28.3E7, XF27/28.3E1.8E5, XF27/28.4B2.5C2, XF27/28.4B2.1B2.7C2, XF27/28.4B2.5C2, XF27/28.4B2.5C2

New human G-protein Chemokine Receptor gene (HDGNR10) useful for treating, preventing, ameliorating or monitoring diseases or disorders associated with aberrant expression of HDGNR10 e.g. cancer.

Ruben SM;

Rosen CA,

Roschke V,

WPI; 2002-643455/69. N-PSDB; ABS68553.

(HUMA-) HUMAN GENOME SCI INC.

2001WO-US004153. 2001US-0297257P. 2001US-0310458P. 2001US-0328447P.

12-JUN-2001; 08-AUG-2001; 21-DEC-2001;

2001US-0341725P

2001US-00779880

09-FEB-2001;

09-FEB-

08-FEB-2002; 2002WO-US003634

WO200264612-A2 Homo sapiens.

22-AUG-2002

Disclosure, Fig 1A-B; 562pp; English.

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                                                                                                                                                                                         Immunoglobulin, variable heavy chain, variable light chain, human, G-protein chemokine receptor; CGR5, HDGNR10; cancer; inflammation; mimunologic deficiency syndrome; blood protein disorder; nephritis; ataxia telangiectasia; endocroxin lethality; inflammatory bowel disease; histiocytosis; chemotaxis; infectious disease; autoimmune disease; hadison's disease; dermatitis; infectious darbritis; allergy, neurodegenerative disorder; viral infection; poxvirus infection; human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma; pheumocystis carnii infection; cardiovascular disorder; atherosclerosis;
                     Gaps
                    ;
0
                    0; Indels
                                                                                                                                                                        Human G-protein chemokine receptor (CCR5) HDGNR10 #1.
 Score 118; DB 5;
Pred. No. 2.9e-11;
                    Mismatches
                                                           270
                                                                                                               ABG92880 standard; protein; 352 AA.
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                                         1 APYNIVLLLNTFOEFFGLNNCS
                                                           249 APYNIVLLINTFÓEFFGLNNCS
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ch 100.0%;
1 Similarity 100.0%;
22; Conservative 0
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  Query Match
Best Local Similarity
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                      Matches
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us-10-084-813-14.rag

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Gaps

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Indels

100.0%; Score 118; DB 5; 100.0%; Pred. No. 2.9e-11; ive 0; Mismatches 0;

22; Conservative

Similarity

Best Local Matches 2

chemokine receptor (CCR5), HDGNR10 DNA

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Sequence 352

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Length 352;

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dermatitis and rheumatoid arthritis, allergies, a neurodegenerative disorder, a viral infection e.g. HV infection, cytomegalovins or poxvirus infection, a Pneumocystis carnii infection, Kaposi's sarcoma, cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a disoase or disorder associated with aberrant expression of novel human Gprotein chemokine receptor (CCRS) HDGNR10. This is an amino acid sequence of Human G-protein chemokine receptor (CCRS)
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                                                                                                                                                                                                                                                                                                                                           100.0%; Score 118; DB 5; 100.0%; Pred. No. 2.9e-11;
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09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
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Best Local Similarity 100..
Conservative
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(ROSC/) ROSCHKE V.
(LIYY/) LI Y.
(RUBE/) RUBEN S M.
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                                                                                                                                                                                                                                                                           Sequence 352 AA;
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The invention relates to human G-protein chemokine receptor (CCR5), antibodies are used for the treatment or prevention of inflammation, defective or aberrant chemotaxis of immune cells or T cell antigenpresenting cell interaction, viral infections (specifically human immune deficiency (including its early stages), cytomegalo or pox viruses), autoimmune deficiency kaposi's sarroma or any condition associated with aberrant expression of CCR5 or their ligands. They are also used for the detection, diagnosis, prognosis and monitoring of cancers or other hyperproliferative diseases. The present sequence is human G-protein chemokine receptor (CCR5), HDGNR10 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10, useful for treatment, prevention and diagnosis of e.g. cancer, also related antibodies.
                                                                                                                                                                                                                         Human, G-protein chemokine receptor; CCR5, HDCNR10 protein; cancer; inflammation; viral infection; autoimmune disease; neurodegeneration; rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma; hyperproliferative disease; receptor.
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Pred. No. 2.9e-11;
                                                                                                                                                                                               Human G-protein chemokine receptor (CCR5), HDGNR10 #2.
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                 249 APYNIVLLINTFQEFFGINNCS 270
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1 APYNIVLLINTFOEFFGLNNCS 22
                                                                                                        AAE25811 standard; protein; 352
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09-MAR-2000; 2000US-0167999P.
22-SEP-2000; 2000US-0234336P.
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                                                                                                                                                                                                                                                                                                                                                                                                  09-FEB-2001; 2001US-00779880.
                                                                                                                                                                    (first entry)
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N-PSDB; AAD42426.
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(ROSC/) ROSCHKE V.
(LIYY/) LI Y.
(RUBE/) RUBEN S M.
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Best Local Similarity
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                                                                                                                                      AAE25811;
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Matches

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RESULT 32

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The present sequence is that of a polypeptide encoded by the human chemokine (C-C motif) receptor 5 (CCR5) gene of the invention (See ABA97319). The specification describes haplotyping the CCR5 gene of an individual by determining if the individual has one of the CCR5 specification also describes an isolated polymothetoride comprising a nucleotide sequence which is polymorphic variant of the reference CCR5 gene sequence which is a nisogene defined by a haplotype described nucleotide sequence and comprises an isogene defined by a haplotype described on the specification and its encoded polypeptide. The methods of the invention are useful to diagnose and develop treatment for diseases a ssociated with abnormal expression or function of the gene. The CCR5 isogenes and the screened compounds are useful for treating human communodeficiency virus (HTV)-1 infection and the progression to acquired immunodeficiency virus (HTV)-1 infection and the progression to acquired immunodeficiency virus (HTN)-1 infection and the progression to acquired individual; predicting a haplotype pair for the CCR5 gene of an individual; predicting a haplotype pair for the CCR5 gene of an individual; predicting a passociation between a trait and a haplotype or composition comprising a genotyping oligonucleotide for detecting a CCR5 polymorphism; a recombinant non-human organism transformed with CCR5 polymorphism; a recombinant non-human organism transformed with exquence an isolated antibody specific for the CCR5 polypeptide and a method for screening drugs targeting the CCR5 polypeptide
                                                                                                    Human chemokine C-C motif receptor 5; CCR5; haplotype pair; isogene; single nucleotide polymorphism; SNP; human immundeficiancy virus 1; HIV-1 infection; acquired immunodeficiancy syndrome; AIDS; antiviral; genotype; polymorphic variant; transgenic; drug screening; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New haplotypes of the human chemokine (C-C motif) receptor 5 gene, to diagnose and treat diseases associated with its abnormal express function, including human immunodeficiency virus-1 infection.
                                                              Human chemokine (C-C motif) receptor 5 polypeptide.
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100.0%; Pred. No. 2.9e-11;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENA-) GENAISSANCE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-APR-2000; 2000US-0194361P.
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                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Arg,
                                                                                                                                                                                                                                                                                                                                                                                 'label= Phe,
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N-PSDB; ABA97318, ABA97319.
                     18-JUN-2002 (first entry)
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Best Local Similarity
Matches 22; Conserv
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                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                       chromosome 3p21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200177125-A2
                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             which has been identified as a G-protein chemokine receptor. The GPCR HDGNR10 polypeptide can be expressed by standard recombinant methodology. Compounds that activate or inhibit the receptor polypeptide, optionally expressed from DNA in gene therapy vectors; are used to treat diseases that require: (a) activation of the receptor (e.g. stimulation of haematopoiesis, treatment of solid tumours, T-cell mediated autoimmune diseases, parasitic infections, psoriasis etc.); or (b) inhibition of the receptor (e.g. allergy, inflammation, rheumatoid arthritis, silicosis etc.). The present sequence represents the human HDGNR10 receptor
                                                                                                                                                                                                                                                                                                                                                                                 7-transmembrane receptor; G-protein coupled receptor; GPCR; HDGNR10; G-protein chemokine receptor; haemacopoleric; immunosuppressant; antiparasitic; gene therapy; human; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide encoding a human G protein chemokine receptor HDGNR10, useful e.g. for treating tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel human 7-transmembrane receptor, HDGNR10,
Gaps
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Indels
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Mismatches
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                                                                                                                                                                                                                                                                                                                                        G-protein chemokine receptor, HDGNR10.
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                                             1 APYNIVLLINTFOEFFGLNNCS
                                                                          249 APYNIVLLINTFQEFFGLNNCS
                                                                                                                                                                                                       ABB81054 standard; protein; 352
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                                                                                                                                                                                                                                                                                             05-NOV-2002 (first entry)
Conservative
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N-PSDB; ABN86542.
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(RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruben SM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-NOV-1998;
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22;
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Li Y,

0;

Gaps

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Length 352; Indels

Matches

RESULT 33

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ABB08343

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Gaps

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Indels

6

Pred. No. 2.9e-11;

100.0%; Prea. ...

22; Conservative

Matches

Best Local Similarity

22

249 APYNIVLLINTFQEFFGLNNCS 270

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1 APYNIVLLLNTFQEFFGLNNCS

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The invention discloses a G-protein chemokine receptor (sometimes ceferred to as a 7-transmembrane receptor) polypeptide, HDGNR10, and the polymucleotide encoding it. G-protein chemokine receptors are involved in signal transduction pathways. The polymucleotide and polypeptide can be used to identify compounds which activate or inhibit activation of the used to identify compounds are useful for treating a patient having need to activate or inhibit a G-protein chemokine receptor. The compound is administered by providing to the patient DNA encoding the agonist or antagonist and expressing them in vivo (gene therapy). The polymucleotides and polypeptide are also useful for for diagnosing a disease or susceptibility to a disease related to an under-expression of the protein. For chromosome identification or as immunogens for producing antibodies. Agonists are useful in stimulating haematopolesis, whond halling, coagulation, angiogenesis, to treat solid tumours, chronic infections, periasis and to stimulate growth factor activity.

Antagonists are useful in the prevention and treatment of allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histendine and igE-mediated allergic reactions, protesplandini independent fever, hone marrow failure, silicosis, sarcoidosis, rhemmatoid arthritis, shock and hyper-eosinophilic syndrome. The sequence presented is the human HDGNR10 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human G-protein chemokine receptor polypeptide useful for diagnostic purposes and for identifying modulators of the polypeptide useful for treating leukemia, autoimmune diseases, psoriasis and allergic
                                                                                                                                                                                                                                                                      Human; receptor; G-protein chemokine receptor; 7-transmembrane receptor; HDGWR10; signal transduction; gene therapy; haematopolesis; wound healing; coagulation; angiogenesis; tumour; chronic infection; leukaemia; T-cell mediated auto-immune disease; parasitic infection; psoriasis; growth factor; allergy; atherogenesis; anaphylaxis; malignant, infermediate, instamine; Igg-mediated; prostaglandin-independent fever; bone marrow failure; silicosis; sarcoidosis; rheumatoid arthritis; shock; hyper-eosinophilic syndrome.
                                                                                                                                                                                                                                  Human G-protein chemokine receptor, HDGNR10, protein.
APYNIVLLINIFQEFFGLNNCS 270
                                                                                                        ABG75540 standard; protein; 352 AA
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                                                                                                                                                                                           (first entry)
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N-PSDB; ABX10635.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2002132269-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                           16-APR-2003
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                                                                                                                                                   ABG75540;
  249
                                                               RESULT 34
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The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down-cegulated in specific cancers (e.g. about 1031 genes up-regulated in a cequlated in a partial cancers (e.g. about 1031 genes up-regulated in a caute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer related gene nucleotide sequences which encode the proteins given in ABBSB8701 to ABBSB8703. Also described: (1) determining the presence or absence of a pathological cell in a patient; (2) an expression vector comprising the vector; (4) an isolated polypeptide, which is encoded by the nucleic acid, (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a patient by administering to the patient the antibody above; and (7) a cut greening a pathology, e.g. cancer (e.g. cancer of the bone marrow, charapentic targets. In particular, the nucleic acid is useful for the panceras, prostate, skin and uterum), wounds, ischaemia, heart diseases, ather serior cancer cancer for treating these control of the patient of the patient of the patient of the bone marrow, cancers, prostate, skin and uterum), wounds, ischaemia, heart diseases, and condometriosis. The nucleic acid is also useful in the control of the patient of the pati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New genes that are up-regulated or down-regulated in cancers, useful a markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.
                                                                                                                                                                                                                                                  Human, cancer; diagnosis; screening; modulator; leukaemia; ischaemia; heart disease; atherosclerosis; endometriosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
                                                                                                                                                                                                   Human cancer related protein SEQ ID NO:259.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; Page 745; 767pp; English.
                                                 ABR58602 standard; protein; 352 AA
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13-NOV-2001; 2001US-0350666F.
08-FEB-2002; 2002US-035545FP.
08-FEB-2002; 2002US-0355257P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001US-0323469P.
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                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                         WO2003025138-A2.
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                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                    09-JUL-2003
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                                                                                                   ABR58602;
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RESULT 35
ABR58602
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6; Length 352;

DB

100.0%; Score 118;

Sequence 352 AA;

Query Match

us-10-084-813-14.rag

Human G-protein chemokine receptor (HDGNR10) polypeptide. Human; G-protein chemokine receptor; receptor; HDGNR10; 7-transmembrane receptor.

08-AUG-2003

03-SEP-2002; 2002US-00232686.

06-JUN-1995;

US2003023044-A1.

30-JAN-2003

Homo sapiens

ABU61654 standard; protein; 352 AA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method for treating an urological disorder which comprises assaying the ability of the compound to modulate 313, 333, 5464, 188717 or 33524 nucleic acid expression or polypeptide activity. The method is useful for identifying a compound for treating urological disorder comprising urinary incontinence e.g., overactive/oversensitive bladder, overflow urinary incontinence, stress urinary incontinence caused by defunction of the bladder, urethra or central/peripheral nervous system, prostatitis, benign prostatic hyperplasia, prostate cancer or kidney disorders. It is also used in gene therapy. The present sequence is human C-C chemokine receptor type 5 (CCBS; 333) protein. This sequence is used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                            Human; urological disorder; stress urinary incontinence; prostate cancer; beign prostatic hyperplasia; overactive bladder; oversensitive bladder; overselve urinary incontinence; gene therapy; nephrotropic; prostatitis; kidney disorder; C-C chemokine receptor type 5; CCR5; receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying a compound, capable of treating urological disorder e.g., benign prostatic hyperplasia, by assaying the ability of the compound modulate 313, 333, 5464, 188717 or 33524 nucleic acid expression or polypeptide activity.
                                      Gaps
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Length 352;
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                                    Indels
                                                                                                                                                                                                                                                                                                           Human C-C chemokine receptor type 5 (333) protein.
100.0%; Score 118; DB 6;
ilarity 100.0%; Pred. No. 2.9e-11;
Conservative 0; Mismatches 0;
                                                                                                       249 APYNIVLLINTFOEFFGLNNCS 270
                                                                       1 APYNIVLLINTFORFFGLNNCS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 81; 87pp; English.
                                                                                                                                                                                                AAO29514 standard; protein; 352
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                                                                                                                                                                                                                                                                         (first entry)
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N-PSDB; AAL59912.
                 Best Local Similarity
Matches 22; Conserv
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les 22; Conserv
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                                                                                                                                                                                                                                                                       27-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAY-2003
                                                                                                                                                                                                                                    AA029514;
   Query Match
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Matches
                                                                                                                                                               RESULT 36
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The invention relates to a method of producing an antibody, involving immunising an animal with a human G-protein chemokine receptor (HDGNRI0) polypeptide (also referred to as a human 7-transmembrane receptor) and recovering an antibody which binds the polypeptide. The method is useful for producing an antibody which binds specifically to the human G-protein chemokine receptor polypeptide. This sequence represents the HDGNRI0 polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                     Producing an antibody, involves immunizing an animal with a polypeptide or with a polypeptide encoded by the human G-protein chemokine receptor clone in ATCC 97183, and recovering the antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, chemokine receptor, CCR5, viral infection, surface protein, respiratory virus infection, respiratory syncytial virus infection, RSV infection, bronchiolitis, bronchitis, pneumonia, asthma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of human chemokine receptor CCR5.
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100.0%; Pred. No. 2.9e-11;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                           95US-00466343.
98US-00195662.
99US-00339912.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 1; 23pp; English.
                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-456307/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
tes 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ACA61721
                                                                                                                                                                                                                                                                                                                       Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003014153-A2
                                                                                                                                                                                                                                                                      25-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP97728;
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Matches
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Gaps

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249 APYNIVLLINTFQEFFGLINICS 270

RESULT 37 ABU61654

1 APYNIVLLINTFOEFFGLINGS 22

Conservative

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                                                                                                                                                                                                                                                                                                                                    The present sequence represents human chemokine receptor CCR5. The specification describes a method for modulating viral infection of a cell. the method comprises modulating a binding interaction between a cell chemokine-receptor and a surface protein of the virus. The proviso is that the cell chemokine-receptor is not CX3CR1 and that the proviso is that the method is useful for treating or preventing respiratory virus infection in vertebrates, more particularly respiratory syncytial virus infections, and related diseases, e.g. bronchiolitis, bronchiolitis, pneumonia or asthma
                                                                                                                                                                                                                  Modulating viral infection of a cell, for treating or preventing respiratory virus infections, bronchitis, pneumonia or asthma, by modulating a binding interaction between a cell chemokine-receptor and surface protein of the virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human C-C chemokine receptor 5 protein SEQ ID NO:352
                                                                                                                                                                                                                                                                                                              Disclosure; Page 96-98; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APYNIVLLINTFQEFFGLNNCS 270
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                               12-AUG-2002; 2002WO-CA001248
                                                                 10-AUG-2001; 2001US-0311088P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry
                                                                                                TOPIGEN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22; Conservative
                                                                                                                                    Renzi P, Zemzoumi K;
                                                                                                                                                                       WPI; 2003-256541/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                          N-PSDB; ABZ68881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 352 AA;
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                                                                                                  (TOPI-)
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The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (I) an assay for the detection of a particular Gradies and assay for the detection of a particular Gradies and antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in antibody against a particular GPCR, and in the production of specific antibody against a particular GPCR, and in the production of specific antibody against a particular GPCR, and in the production of specific antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRS. The antigenic peptides for treating immune-related disease, immunological-related diseases, coll corresponding GPCRS. The antigenic peptides for treating immune-related diseases, immunological-related cell proliferative diseases or autoinmune diseases, eg. ALDS, Alzheimer's disease, contending and acute inflammation, allergies, Crohm's disease, parkinson's disease, multiple sclerosis, pain, psoriasis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohm's disease, pain, psoriasis, concernential, the schman, tuberculosis, obesity, nausea, hyperension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassaye and immunodiagnosis. ABB42252 to ABB42869 encode GPCR proteins given in ABP81675 to ABB42252 to ABB42869 encode cemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor; human; anti-HIV; virucide; HIV; SIV; 88-CB; chemokine receptor; envelope protein; atherosclerosis; rheumatoid arthritis; tumour growth suppression; asthma; viral infection; AIDS; inflammatory condition.
                                                                                                                                       v isolated antigenic peptides e.g., for G protein-coupled receptors PCR), useful for diagnosing and designing drugs for treating conditions which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                  Disclosure; Fig 1; 523pp; English
(LIFE-) LIFESPAN BIOSCIENCES INC
                                        Brown JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human chemokine receptor 88-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-2002; 2002US-00106623.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
                                        Burmer GC, Roush CL,
                                                                                                                                                                                                            autoimmune diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 352 AA;
                                                                                                      N-PSDB; ABZ42781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                              New isolated
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The invention relates to screening for a modulator of human immunodeficiency virus (HIV) or simian immunodeficiency virus (HIV) or simian immunodeficiency virus (SIV)
infection, comprising contacting a first composition having an human (ADC03341) or macaque (ADC03359) 88C chemokine receptor polypeptide with a second composition having an HIV or SIV envelope protein in the presence or absence or amound. Also included are screening for a modulator of HIV infection, detecting HIV infection of colls (comprising contacting a cell that has been recombinantly modified to express at least one of human chemokine receptors 88C and 88-28 with HIV, and detecting HIV infection of cells (comprising contacting cells with an antibody to at least one of human chemokine receptors 88C and 88-28 with HIV, and detecting HIV infection of the cell after the contacting step). The methods and compositions of the present invention are useful for the diagnosis and crivity of 88C or 88-28 chemokine receptors, such as atheroselerosis, rheumatoid arthritis, tumour growth suppression, asthma, viral infection, AIDS and other inflammatory conditions. The genes for human 88-C and 88-28 are located on chromosome 3921. The present sequence represents human chemokine receptor 88-C.
                                                                                                                                                                                                                                                                                                 Screening for a modulator of HIV and SIV infection utilizing polymucleotides that encode the 88C or 88-2B chemokine receptors, useful for diagnosing and treating disorders such as atherosclerosis, arthritis, AIDS and asthma.
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 17-18; 29pp; English.
                  95US-00575967.
96US-00661393.
96US-00771276.
                                                                                                                                                                                             Gray PW, Schweickart VL,
                                                                                                  (GRAY) GRAY P W.
(SCHW/) SCHWEICKART V L.
(RAPO/) RAPORT C J.
                                                                                                                                                                                                                                    WPI; 2003-182491/18.
N-PSDB; ADC03340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 352 AA;
                  20-DEC-1995;
07-JUN-1996;
20-DEC-1996;
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Raport CJ;

Query Match
100.0%; Score 118; DB 7; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0 249 APYNIVLLINTFQEFFGLNNCS 270 1 APYNIVLLLNTFQEFFGLNNCS 22 ò

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Search completed: September 28, 2004, 09:03:38
Job time : 52.525 secs

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September 28, 2004, 09:00:23; Search time 19:8 Seconds (without alignments) 57.362 Million cell updates/sec
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                      389414 seqs, 51625971 residues
                                                                                                                                                                                                                                          US-10-084-813-14
118
1 APYNIVLLINTFQEFFGLNNCS 22
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Maximum Match 100%
Listing first 45 summaries
                                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 2, Appli	13,	14,	'n	25	'n	equence 52,	equence 5,	Sequence 2, Appli	Sequence 1, Appli	Sequence 2, Appli	ດັ	σ	'n	4,	4,	20	2	20	21	7	'n	equence 20	equence 4,	Sequence 2, Appli		•
SUPPLYATES	ID	-466-	US-09-087-232A-13		-08-575-9	-09-045-5	-09-517-6	-60-	-08-833-7	-09-502-7	US-09-796-202-1	õ	-09-502-	-08	-08-461-2	'n	-08-446-669-	-09-045-583-	-09-045-583-	US-09-534-185-50	4	ı	US-09-131-827A-2	US-09-131-827A-20	PCT-US95-00476-4	US-08-450-393A-2	US-08-446-669-2	
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	f Query Match Length	352	352	352	352	352	352	352	352	352	352	354	329	344	347	360	360	360	360	360	360	360	360	360	360	374	374	
d	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	8	100.0	100.0	8	91.5	87.3	87.3	87.3	87.3	87.3	87.3	87.3	87.3	87.3	87.3	87.3	87.3	87.3	87.3	87.3	
	Score	118	118	118	118	118	118	118	118	118	118	108	103	103	103	103	103	103	103	103	103	103	103	103	103	103	103	
	Result No.		N	ım	4	Ŋ	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	,

2,	77	'n	Sequence 5, Appli	Sequence 5, Appli	Ä	14,	Sequence 5, Appli	Sequence 8, Appli	Sequence 9, Appli	~	Sequence 20, Appl	ď,		Ċ	Ĭ	Sequence 12, Appl	Sequence 10, Appl	
US-08-681-192-2	US-09-087-232A-22	US-08-012-988A-2	US-08-450-393A-5	US-08-446-669-5	US-09-239-938-1	US-09-886-319A-14	PCT-US95-00476-5	US-08-833-752-8	US-08-833-752-9	US-08-875-573-6	US-08-875-573-20	US-09-232-878-2	US-09-045-583-55	US-09-534-185-55	US-08-939-107-34	US-08-103-170-12	US-08-118-270-10	ALIGNMENTS
344 3	25 3	355 1	355 1	355 3	355 4	355 4	355 5	355 4	355 4	170 3	360 3	360 3	360 3	360 4	360 4	105 2	317 1	
70 59.3	7	56 47.5	Ŋ	Ŋ	6 47.5	10	6 47.5	5 46.6	54 45.8	3 44.9	3 44.9	. 61	3 44.9	3 44.9	44.9	44.1	· -:	
28	53	30	31	32	33	34	. CT	9	3.7	. ea	С	40	4.4	4 2	4.3	44	45	

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Sequence 2, Application US/08466343D
Sequence 2, Application US/08466343D
Patent No. 6025154
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CHEMOKINE RECEPTOR HDGNRIO (AS AMENDED)
NUMBER OF SEQUENCE:
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
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Best Local Similarity 100.0%; Pred. No. 4.1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER RELABBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: THEN PC comparible
COMPUTER: THEN PC comparible
COMPUTER: THEN PC comparible
COMPUTER: THEN PC comparible
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,343D
FILING DATE: 06-UUN-1995
CLASSIFICATION: 435
ATTORNEY AGENT INPORMATION:
NAME: STEPFE, ERIC X.
REGISTRATION NUMBER: 1488.1150000/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acide
TYPE: amino acid
TYPE: amino acid
TYPE: AMINO ACID
US-08-466-343D-2
RESULT 1
US-08-466-343D-2
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N RESULT

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US-08-861-105-14
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1 Sequence 14, Application US/08861105

2 Sequence 14, Application US/08861105

3 Sequence 14, Application US/08861105

4 PEDICANT: LITTMAN, DAN R.

5 APPLICANT: LITTMAN, DAN R.

5 APPLICANT: LIANDAU, NATHANIEL R.

5 APPLICANT: LANDAU, NATHANIEL R.

5 APPLICANT: LANDAU, NATHANIEL R.

6 TITLE OF INVENTION: MACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC

7 TITLE OF INVENTION: MACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC

7 TITLE OF INVENTION: USSS THEREOF

8 NUMBER OF SEQUENCES: 14

8 CORRESPONDENCE ADDRESS:

8 ADDRESSE: David A. Jackson, Esq.

8 TREET: #11 Hackensack Ave, Continental Plaza, #th
                   Sequence 13, Application US/09087232A
Patent No. 6153431
GENERAL INFORMATION:
TITLE OF INVENTION: HUMAN IMMUNOBFICIENCY VIRUS CO-RECEPTOR
TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/087,232A
FILING DATE: 28 MAY 1998
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/048,057
FILING DATE: 30 MAY 1997
ATTORNEY/AGENT INFORMATION:
NAME: KOLE, LISA B.
REGISTRATION NUMBER: 3225
FILING DATE: ATTORNEY/AGENT NUMBER: 3225
FILING DATE: ALSA B.
FRIGHT NUMBER: 3225
                                                                                                                                                                                NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEBE: Baker & Botts, L.L.P. attn. Lisa Kole
STREET: 30 Rockefeller Plaza
GTTY: New York
STARE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: AP 31115
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 APYNIVLLINTFQEFFGLINCS 270
                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 APYNIVLLINIFOEFFGLNNCS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 408-2628
TELEFAX: (212) 765-2519
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.(
Matches 22; Conservative
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STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
US-09-087-232A-13
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COMPUTER: IN PROMISE COMPACTION:
COMPUTER: IN PROMISE PLANTED: PLANTED:
COMPUTER: IN PROMISE: TO COMPACTION:
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COMPUTER: IN PROMISE: TO COMPACTION:
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CITY: Boston
STATE: Massachusetts
COUNTRY: USA
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Best Local Similarity 100.0
Matches 22; Conservative
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; ORGANISM: Homo sapiens
US-09-517-605-5
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US-09-534-185-52
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105-045-583-52
1 Sequence 52, Application US/09045583
1 Sequence 52, Application US/09045583
2 Parent No. 62878054
2 GENERAL INFORMATION: APPLICANT: Graham, Gerard J. et al.
2 TITLE OF INVENTION: No. 6287805e1 Molecules of the G Protein-Coupled
3 TITLE OF INVENTION: No. 6287805e1 Molecules of the G Protein-Coupled
3 TITLE OF INVENTION: No. 6287805e1 Molecules of the G Protein-Coupled
3 TITLE OF INVENTION: No. 6287805e1 Molecules of the G Protein-Coupled
4 TITLE OF INVENTION: No. 6287805e1 Molecules of the G Protein-Coupled
5 CORRESPONDENCE ADDRESS: 5
6 CORRESPONDENCE ADDRESS: 5
7 TITLE OF INVENTION: ADDRESS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 352;
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                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 118; DB 3; 100.0%; Pred. No. 4.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                       TELEFAX: 206-485-1662
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acids
TOPOLOGY: limit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                       NAME/KEY: misc feature;
CTHER INFORMATION: /= 'US-08-575-967A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 22; Conservative
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// FRAGMENT TYPE: internal
US-09-045-583-52
                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 22; Conserva
TELEPHONE:
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Sequence 2, Application US/08724984A;
Sequence 2, Application US/08724984A;
Sequence 2, Application US/08724984A;
Patent No. 6388055
GENERAL INFORMATION:
APPLICANT: Derk Bergema, Mary Brawner, and Usman Shabon
TITLE OF INVENTION: CRES Receptor
TITLE OF INVENTION: CRES Receptor
NUMBER OF SEQUENCES:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
STATE: PA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
INDOMS FOR WORKGROUPS
COMPUTER: IBM 486
COMPUTER: IBM 486
COMPUTER: IMM 486
COMPUTER: IMM 486
COMPUTER: MICROSOFT WARD
CURRENT APPLICATION DATA:
SPETIANT OF THE CALLOR OF THE CAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. 6548636
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                        Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 118; DB 4; Length 352; Best Local Similarity 100.0%; Pred. No. 4.1e-12; Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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CURRENT APPLICATION NUMBER: US/09/502,783A
CURRENT FILING DATE: 2001-08-23
PRIOR PILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTHARE: PATENTIN version 3.0
LENGTH: 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 APYNIVILINIFQEFFGLNNCS 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 APYNIVLLINTFQEFFGLNNCS 270
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                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-502-783A-2
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LENGTH: 352
TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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US-08-724-984A-2
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Patent No. 6511826
APPLICANT: Li, Yi
APPLICANT: Li, Yi
TITLE OF INVENTION: Polymorleotides Encoding Human G-Protein Chemokine Receptor (CCRS TITLE OF INVENTION: HDGNR10
FILE REFERENCE: 1488.1150006
                                                                                                                                                                                                                                              ö
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Patent No. 6448375
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: UASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND WULBIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                       100.0%; Score 118; DB 4; Length 352; 100.0%; Pred. No. 4.1e-12; cive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NMBER: US/08/833,752
FILING DATE: 9-APR-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Knobbe, Martens, Olson & Bear
620 Newport Center Drive 16th Floor
       MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
                                                                                                                                                                                                                                                                                                                                                                           249 APYNÍVLLINTFQEFFGLNNCS 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 APYNIVLLLNTFQEFFGLNNCS 270
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ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                               1 APYNIVLLLNTFQEFFGLNNCS 22
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ATTORNEY AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFRENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352 amino acids
nino acid
                                                                                                                                                                              Query Match
Best Local Similarity 100.(
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS: ADDRESSEE: Knobbe, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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TOPOLOGY: li
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US-09-502-783A-2
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US-09-534-185-52
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US-08-833-752-5
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APPLICANT: Yi, Li
APPLICANT: Xi, Li
APPLICANT: Ruben, Steven M.
APPLICANT: Ruben, Steven M.
APPLICANT: Ruben, Craig A.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32
NUMBER OF SEQUENCES: 7
CORRESPONDENCES: 7
CORRESPONDENCES: 7
CORRESPONDENCES: 7
CORRESPONDENCES: 7
COUNTRY: Roseland
STREET: New Jersey
COUNTRY: USA
ZIP: 07068
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MEDIUM TYPE: Floppy disk
COMPUTER: Elappy disk
COMPUTER: Elappy disk
COMPUTER: Elab PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,244
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: FERTENCY Gregory D.
REGIGTRATION NUMBER: 35.134
REFERENCE/COKET NUMBER: 325800-445
TELECHOME: 201-994-1700
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SPETATING SYSTEM: PC-DOS/MS-DOS
SUFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/466,343D
FILING DATE: O6-JUN 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEPFE, ERIC K.
REGISTRATION NUMBER: 1488.1150000/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371.2500
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: AAAACTERISTICS:
LENGTH: amino acid
STRANDEDNESS: single
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 PYNIVILLNTFQEFFGLSNC 260
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; Sequence 3. Application US/08461244
; Patent No. 5776729
; GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-466-343D-9
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Sequence 9, Application US/09502783A
Patent No. 6511826
GENERAL INFORMATION:
APPLICANT: Li. Yi
APPLICANT: APPLICANT: Li. Yi
APPLICANT: Li. Y
AP
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Sequence 9, Application US/08466343D

Patent No. 6025154

GENERAL INFORMATION:
APPLICANT: LI, Yi
TITLE OF INVENTION:
CHEMOKINE RECEPTOR HOGNRIO (AS AMENDED)
NUMBER OF SEQUENCES:
ADDRESSEE: STERNE, KESSIER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WAGSHINGTON
STATE: DC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 87.3%; Score 103; DB 4; Length 329; Best Local Similarity 90.0%; Pred. No. 1.4e-09; Matches 18; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 91.5%; Score 108; DB 4; Length 354; Best Local Similarity 95.2%; Pred. No. 2.1e-10; Matches 20; Conservative 0; Mismatches 1; Indels
                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: William T. Han
REGISTATION NUMBER: 34,344
REFERENCE DOCKET NUMBER: ATGS0023
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270 5024
TELEPHONE: 610 270 5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 PYNIVLLITFOEFFGLNNCS 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 PYNIVILINTFQEFFGLSNC 245
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                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: Amino Acid;
TOPOLOGY: Linear
US-08-724-984A-2
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US-09-502-783A-9
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LENGTH: 329
TYPE: PRT
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US-08-466-343D-9
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US-09-502-783A-9
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Sequence 50, Application US/09045583
Fatent No. 6287805
GENERAL INFORMATION:
TITLE OF INVENTION: No. 6287805e1 Molecules of the G Protein-Coupled
TITLE OF INVENTION: No. 6287805e1 Molecules of the G Protein-Coupled
TITLE OF INVENTION: No. 6287805e1 Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES:
SOCRESSPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STRIE: Massachusetts
COUNTRY: USA
ITP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE PARTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE PARTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE PARTING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 87.3%; Score 103; DB 3; Length 360; Best Local Similarity 90.0%; Pred. No. 1.5e-09; Matches 18; Conservative 2; Mismatches 0; Indels
    MAMMALIAN MONOCYTE CHEMOATTRACTANT PROTEIN RECEPTORS
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTAN
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto
CITY: Palo Alto
STARE: California
COUNTRY: USA
                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CONTUMER: BATENIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,669
FLING DATE: May 25, 1995
CLASSIFICATION: 435
ATTORNEY/AGRNT INFORMATION:
NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REGISTRATION NUMBER: 30,092
REGISTRATION NUMBER: 30,092
TELECOMMUNICATION INFORMATION:
TELEPRAK: 415-843-5000
TELEFRAK: 415-843-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-WAR-98
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258 PYNIVILLNTFQEFFGLSNC 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPAX: 415-B5/-000.
TELEX: 380816CooleyPA
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-446-669-4
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US-09-045-583-50
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                                                                                                                                        Query Match 87.3%; Score 103; DB 1; Length 347; Best Local Similarity 90.0%; Pred. No. 1.5e-09; Matches 18; Conservative 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                             US-08-450-393A-4

Sequence 4, Application US/08450393A

Sequence 4, Application US/08450393A

Settle No. 2707815

APPLICANT: Charo, Israel

APPLICANT: Coughlin, Shaun

TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT

TITLE OF INVENTION: PROTEIN RECEPTORS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEB: Cooley Godward Castro Huddleson & Tatum

STREET: 5 Palo Alto Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 PYNIVILLNTFQEFFGLSNC 264
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                                                                                                                                                                                                                                2 PYNIVLLLNTFQEFFGLNNC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 PYNIVLLINTFQEFFGLNNC 21
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LENGTH: 360 amino acids
TYPE: amino acid
  ; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-244-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
// MOLECULE TYPE: protein
US-08-450-393A-4
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STATE: California
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NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS.
ADDRESSER: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street

CITY: Boston STATE: Massachusetts

us-10-084-813-14.rai

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RESULT 19
US-09-534-185-50
Sequence 50, Application US/09534185
Sequence 50, Application US/09534185
Fatent No. 6403767
GENERAL INFORMATION:
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 18
US-09-045-583-51
Sequence 12. Application US/09045583
Sequence 13. Application US/09045583
Farent No. 6287805
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TILLE OF INVENTION: No. 628780551 Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCES. 56
CORRESPONDENCES. LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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87.3%; Score 103; DB 3; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 20 scarc CITY: Boston STREET: 20 scarc STATE: Messachusetts
CUNTRY: Boston STATE: Messachusetts
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION 0435
PRIOR APPLICATION UNDRER:
FILING DATE: 30-MAR-98
TILING DATE: ARBOLICATION NUMBER: MNI-044
TELEPHONE: (517) 722-7400
TELEPHONE: (517) 722-7400
TELEPHONE: (517) 722-7400
TELEPHONE: GO annino acids
LENGTH: 360 annino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: beptide
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMOUNICATION INFORMATION:
TELEPHONE: (617)742-4214
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258 PYNIVILLNTFQEFFGLSNC 277
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                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide FRAGMENT TYPE: internal
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FRAGMENT TYPE: internal
                                                                                                                                                                                                          TYPE: ami TOPOLOGY:
                                                                                                                                                                                                                                                                                                             US-09-045-583-50
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US-09-534-185-51
; Sequence 51, Application US/09534185
; Patent No. 6403767
; CENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
title OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
"herefor Heptahelical Receptor Superfamily and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
COUNTY: MASACHIDSTICS

IDEA STATE: MASACHIDSTICS

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/09/534,185

FILING DATE: 24 Mar-2000

CLASSIFICATION NUMBER: US/09/534,185

FILING DATE: 4 Mar-2000

PRIOR APPLICATION NUMBER: 09/045,583

FILING DATE: CURNOWN-

ATORNEY/AGENT INFORMATION:

NAME: MANDER: MAINTER: 36,207

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: MNI-044

TELEPHONE: (617)227-7400

TELEPHONE: (617)227-7400

TELEPAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.3%; Score 103; DB 4; Length 360; 90.0%; Pred. No. 1.5e-09; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
RRAGNENT TYPE: Internal
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-534-185-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258 PYNIVILLNTFQEFFGLSNC 277
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STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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258 PYNIVILLNTFQEFFGLSNC 277

2 PYNIVLLINTFQEFFGLNNC 21

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Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                     87.3%; Score 103; DB 4; Length 360; 90.0%; Pred. No. 1.5e-09;
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JGS-09-131-827A-20

JGGUENCE 20, Application US/09131827A

JGENERAL NO. 660030

JGENERAL NIPORMATION:

APPLICANT: Dean, Michael

APPLICANT: Carrington, Mary

TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A

TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A

TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A

TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A

TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A

TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A

TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A

TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A

TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A

TITLE OF INVENTION UNMERR: US/09/131,827A

CURRENT FILING DATE: 1998-08-10

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FASTSEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Dean, Michael
APPLICANT: O"Bilen, Stephen J.
APPLICANT: O"Bilen, Stephen J.
APPLICANT: O"Bilen, Stephen J.
APPLICANT: Carrington, Mary
ITILE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
ITILE OF INVENTION: DELAYED PROGRESSION TO CR2 GENE
FILE REFERENCE: 14014.0333
CURRENT FAPLICATION NUMBER: US/09/131,827A
CURRENT FILING DATE: 1998-08-10
PRIOR PLICATION NUMBER: 60/055,659
PRIOR FILING DATE: 1997-08-14
NUMBER OF SOOID NOS: 20
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-131-827A-2; Sequence 2, Application US/09131827A; Patent No. 6600030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 PYNIVILLNTFQEFFGLSNC 277
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                                                                                                                                                                                                                                                                                                                                                  2;
                                                                                                                                                             , MOLECULE TYPE: No. 6448375e
US-08-833-752-7
               LENGTH: 360 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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; ORGANISM: Homo
US-09-131-827A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 2
LENGTH: 360
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-131-827A-2
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LENGTH: 360
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Patent No. 6448375
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARABNITER, MARC
APPLICANT: PASSART GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATABLIN Release #1.0, Version #1.25
CURRANT APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-MAT-2000
CLASSIFICATION NUMBER: US/09/534,185
FILING DATE: AURKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,583
FILING DATE: AURKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: MANIE: MANIER: 36,207
RECEING DATE: (17) 722-740

TELEPRANTION NUMBER: 36,207
TELEPRANTION NUMBER: 36,207
TELEPRANTION NUMBER: 617) 742-4214

INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 mmino acids
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ZIP: 92660
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATE:
COMPUTER: DATE:
COMPUTER: DATE:
COMPUTER: DATE:
COMPATE: DATE:
COMPATE: DATE:
COMPUTER:
COMPUTER
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CORRESPONDENCE ADDRESSE: Knobbe, Martens, Olson & Bear STREBT: 620 Newport Center Drive 16th Floor CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECTLE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       258 PYNIVILLINTFQEFFGLSNC 277
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CLASSIFICATION: 536
ATTORNEY/ACENT INFORMATION:
NAME: Altman, Daniel
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 PYNIVLLINTFOEFFGLNNC 21
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US-08-833-752-7
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Tue Sep 28 15:49:57 2004

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Gaps
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87.3%; Score 103; DB 1; Length 374;
Best Local Similarity 90.0%; Pred. No. 1.6e-09;
Matches 18; Conservative 2; Mismatches 0; Indels
                    COMPUTER READABLE FORM;

MEDIUM TYPE: Ploppy disk
COMPUTER IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,393A
FILING DATE: May 25, 1995
CLASSIFICATION: 424
ATTOKNEY/AGENT INPORMATION:
NAME: CSETT Luann
REGISTRATION NUMBER: 31,822
REBERROCY-OCKET NUMBER: 31,822
RELEPHONE: 415-843-5165
TELEFAX: 415-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 PYNIVILLNTFQEFFGLSNC 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-450-393A-2
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US-08-446-669-2
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                                                                   Gaps
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Query Match 87.3%; Score 103; DB 4; Length 360; Best Local Similarity 90.0%; Pred. No. 1.5e-09; Matches 18; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                        Query Match 87.3%; Score 103; DB 5; Length 360; Best Local Similarity 90.0%; Pred. No. 1.5e-09; Matches 18; Conservative 2; Mismatches 0; Indels
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                                                                                                                             2 PYNIVLLINIFQEFFGLNNC 21
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SEQUENCE CHRACTERISTICS:

LENGTH: 360 amino acids

TYPE: amino acid

TYPE: amino acid

MOLECTLE TYPE: protein

PCT-US95-00476-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 310-977-10
TELEFAX: 310-977-1003
TELEX:
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Sequence 2, Application US/08446669

Sequence 2, Application US/08446669

Batent No. 6132987

GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Couglin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STREET: 5 Palo Alto Square
COUNTRY: USA
ZIP: 94306-2155
COMPUTER RAADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ORPHICATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 30,092
REGISTRATION NUMBER: 30,092
REGISTRATION NUMBER: 30,092
REGISTRATION NUMBER: 30,092
REGISTRATION NUMBER: 30,092
RELEPOMMUTCATION INFORMATION:
TELEPHONE: 415-843-5000
TELEPHONE: 415-843-5000
TELEPHONE: 415-843-5000 TELEFAX: 415-857-0663
TELEX: 380816CooleyPA
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids

258 PYNIVILLNTFQEFFGLSNC 277

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RESULT 25 US-08-450-393A-2

2 PYNIVLLLNTFQEFFGLNNC 21

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US-09-087-232A-22
Sequence 22, Application US/09087232A
Sequence 22, Application US/09087232A
Sequence 22, Application US/09087232A
Sequence 22, Application US/09087232A
TITLE OF INVENTION: UMAN IMMAN IMMUNOBETICIENCY VIRUS CO-RECEPTOR
TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
NUMBER OF SEQUENCE 3
CORRESPONDENCE ADDRESS:
ADDRESSES: ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
ADDRESSES: BAKE S.
ADDRESSES: BAKE S.
ADDRESSES: BAKE S.
ADDRESSES: BAKE S.
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59.3%; Score 70; DB 3; Length 344

Best Local Similarity 57.1%; Pred. No. 0.00063;

Matches 12; Conservative 4; Mismatches 5; Indels
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APPLICATION NUMBER: US/09/087.2120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
STREET: 30 Rockefeller Plaza
                          CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: SCHECK, PATTICIA A.
RECISTRATION NUMBER: 33,777
REFERENCE/DOCKET NUMBER: 33,777
TELECHONE: 610-270-5031
TELEFAX: 610-270-5031
                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRSESEQ Version 1.5
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/681,192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: US-08-681-192-2
                                                                                                                                                               ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
: New York
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                                                                                               CITY: Kir
STATE: Pi
COUNTRY:
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                                                                                                                         Length 374;
                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application PC/TUS9500476
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION:
MAMMER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           % Sequence 2, Application US/08681192

Sequence 2, Application US/08681192

Patent No. 6287801

Patent No. 6287801

APPLICANT: BERGSMA, DERK

APPLICANT: ELSHOURBAGY, NABIL

APPLICANT: SARAY, HENRY

APPLICANT: GREWY

TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR HNFDS78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00476
FILING DATE:
                                                                                                                         Query Match 87.3%; Score 103; DB 3; Best Local Similarity 90.0%; Pred. No. 1.6e-09; Matches 18; Conservative 2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSE: Robbins, Berliner & Carson
STREET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Comparible
OPERATING SYSTEM: PC-DOS/NS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
ATTORNEY/ABOUT INFORMATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-291
TELECOMMUNICATION INFORMATION:
TELECHONE: 310-977-1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 374 amino acids TYPE: amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             310-977-1003
, TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-669-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 18; Conserv
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Sequence 5, Application US/08446669
; Patent No. 6132987
; GENERAL INCRAMATION:
GENERAL INCRAMATION:
APPLICANT: Charo, Israel
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 balo Alto Square
; CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ### Sequence 2. Application US/08012988A
### Sequence 2. Application US/08012988A
### Sequence 2. Application US/08012988A
### GENERAL INFORMATION:
### SEPLICANT: MUNIPHY, Philip M.
### TITLE OF INVENTION: Cloning and Expression of Human
### TITLE OF INVENTION: Macrophage Inflammatory Protein-1 alpha (MIP-1
### TITLE OF INVENTION: alpha)/RANTES Receptor
### NUMBER OF SEQUENCES:
### CORRESPONDENCE ADDRESS:
### ADDRESSEE: Townsend and Townsend Khourie and Crew
### STRESSEE: Townsend and To
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
47.5%; Score 56; DB 1; Length 355;
Best Local Similarity 40.0%; Pred. No. 0.16;
Matches 8; Conservative 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.7%; Score 61; DB 3; Length 25; 100.0%; Pred. No. 0.00092; tive 0; Mismatches 0; Indels
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COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOSTWARE: Patentin Release #1.0, Version #1.25
SOSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/012,988A
FLING DATE: 19930128
FLASSITICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 15.280-118
REGISTRATION NUMBER: 13.677
REFERENCE/DOCKET NUMBER: 15.280-118
TELEPHONE: 415-543-5603
TELEPHONE: 415-543-5603
TELEPHONE: 155-5613
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTER.ESTICS:
TEMPORMATION FOR SEQ ID NO: 2:
TEMPORMATION FOR SEQ ID NO: 2: 3: 4 FARMATION FOR SEQ ID NO: 4 FARMATION FOR SEQ ID NO: 4 FARMATION FOR SEQ
                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 30 MAY 1997
ATTORNEY/AGENT INFORMATION:
NAME: ROLE: LISA B. 5,225
REGISTRATION NUMBER: 35,225
REGISTRATION NUMBER: 35,225
REFERENCE/DOCKET NUMBER: AP 31115
TELEPHONE: (212) 468-2619
TELEPHONE: (212) 765-2519
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-087-232A-22
28 MAY 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 12; Conservative
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      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-012-988A-2
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254 PYNLTILISVFQDFLFTHEC 273

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Gaps . 0 Query Match
Best Local Similarity 40.0%; Pred. No. 0.16;
Matches 8; Conservative 6; Mismatches 6; Indels GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TILE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TILE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: ISP PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,393A

FILING DATE: May 25, 1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: CSerr, Luann

REGISTRATION NUMBER: 31,822

REFERENCE/DOCKET NUMBER: UCAL-237/02US

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFRAX: 415-883-0165

TELERA: 380816COOleyPA

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 355 amino acids

TYPE: amino acids

TYPE: Amino acids

TYPE: Amino acids

TYPE: Amino acids US-08-450-393A-5; Sequence 5, Application US/08450393A; Patent No. 5707815 254 PYNLTILISVFQDFLFTHEC 273 2 PYNIVLLLNTFQEFFGLNNC 21 MOLECULE TYPE: protein HYPOTHETICAL: NO CITY: Palo Alto STATE: California COUNTRY: USA linear TOPOLOGY: US-08-450-393A-5 8 a

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RESULT 32 US-08-446-669-5

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Gaps .; 0 APPLICANT: Regenbogen, Johannes
APPLICANT: Regenbogen, Johannes
APPLICANT: Regenbogen, Andreas
TITLE OF INVENTION: Use of Banosis or Treatment of Skin Disorders and Wound
TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
TITLE OF INVENTION: Active Substances
TITLE OF INVENTION: Active Substances
CURRENT APPLICATION NUMBER: US/09/886,319A
CURRENT APPLICATION NUMBER: US 60/222,081
PRIOR PELING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20

Werner, Sabine Halle, Jorn-Peter

DP

0;

Gaps

Length 355;

Query Match 47.5%; Score 56; DB 4; Best Local Similarity 40.0%; Pred. No. 0.16; Matches 6; Mismatches

TYPE: PRT ORGANISM: Homo sapiens

SEQ ID NO 14 LENGTH: 355

US-09-886-319A-14

2 PYNIVLLINTFOEFFGLNNC 21

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Sequence 5, Application PC/TUS9500476
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California TPILE OF INVENTION: MARMALLAN MONOCYTE CHEMOATTRACTANT TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDERSS: ADDRESS: ADDRESS: Robbins, Berliner & Carson STREET: 201 N. Figueroa Street, 5th Floor STREET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentl N. Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00476 5555-291 254 PYNLTILISVEODFLETHEC 273 FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
REGIETRATION UNUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555
TELECOMMUNICATION:
TELEPHONE: 310-977-1001
TELEPHONE: 310-977-1003
TELEPAX: 310-977-1003 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 355 amino acida TYPE: amino acid TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein PCT-US95-00476-5 RESULT 35 g ô ö Gaps ; 0 . 0 GENERAL INFORMATION:
APPLICANT: Qin, Shixin
APPLICANT: Qin, Shixin
APPLICANT: Newman, Walter
APPLICANT: LeukoSite, Inc.
TITLE OF INVENTION: ANTI-CR1 ANTIBODIES AND METHODS OF USE
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: LKS97-13
CURRENT APPLICATION NUMBER: US/09/239,938
CURRENT APPLICATION WIMBER: US/09/239,938
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSEQ for Windows Version 3.0
| LENGTH: 355 Query Match
47.5%; Score 56; DB 4; Length 355;
Best Local Similarity 40.0%; Pred. No. 0.16;
Matches 8; Conservative 6; Mismatches 6; Indels RESULT 34 US-09-886-319A-14 ; Sequence 14, Application US/09886319A 254 PYNLTILISVFQDFLFTHEC 273 2 PYNIVLLLNTFQEFFGLNNC 21

; ORGANISM: Homo sapien US-09-239-938-1

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Tue Sep 28 15:49:57 2004

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INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR? SEQUENCES: 17
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; MOLECULE TYPE: No. 6448375e
US-08-833-752-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-875-573-6
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US-08-833-752-8

1 Sequence 8, Application US/08833752

1 Sequence 8, Application US/08833752

2 Patent No. 6448375

3 GENERAL INFORMATION:
APPLICANT: PARMENTIER, MARC
APPLICANT: PARMENTIER, MARC
APPLICANT: TIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLBIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17

CORRESPONDENCE 17

CORRESPONDENCE 17

CITY: Newport Center Drive 16th Floor
CITY: Newport Beach
STREET: CA
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-833-752-9

Sequence 9, Application US/08833752

Patent NO. 6448710N:
Patent NO. 6448710N:
APPLICANT: PARMENTIER:
APPLICANT: PARMENTIER:
APPLICANT: PARMENTIER:
APPLICANT: PARMENTIER:
APPLICANT: LIBERT, MARC
APPLICANT: APPLICAN
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COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
PFLING DATE: 9-APF-1997
FILING DATE: 9-APF-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel B
NAME: Altman, Daniel B
RECISTATION NUMBER: 34,115
REPERENCE/DOCKET NUMBER:
INFORMATION CHARACTERISITICS:
SEQUENCE CHARACTERISITICS:
FURNISHED AND ASS AMINO ACIDERISITICS:
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47.5%; Score 56; DB 5; Length 355;
Best Local Similarity 40.0%; Pred. No. 0.16;
Matches 8; Conservative 6; Mismatches 6; Indels
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TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
WOLECULE TYPE: No. 6448375e
                                                                                                  ANTI-SENSE: NO PCT-US95-00476-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-833-752-8
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Gaps
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US-08-875-573-6

US-08-875-573-6

US-08-875-573-6

US-08-875-573-6

US-08-875-873-6

US-08-875-873-6

US-08-875-873-6

US-08-875-873-6

US-08-875-873-6

US-08-875-873-8

US-08-875-873-8

US-08-875-88-8

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TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SA CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

ADDRESSE:
CORRESCE:
CITY:
CATT:
CATT:
CATT:
CATT:
CONFUTER READABLE FORM:
MEDIUM TYPE:
Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER:
MEDIUM TYPE:
Ploppy disk
COMPUTER:
MEDIUM TYPE:
MEDIUM TY
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Best Local Similarity 35.0%; Pred. No. 0.35;
Matches 7; Conservative 7; Mismatches 6; Indels
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SEQ ID NO 2
LENGTH: 360
                                                                                                                                                                                                                                  RESULT 40
US-09-232-878-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Weels, Timothy N.C.
APPLICANT: Weels, Timothy N.C.
APPLICANT: Weels, Christine A.
TITLE OF INVENTION: A CHEMOKINE RECEPTOR ABLE TO BIND TO
TITLE OF INVENTION: MCP-1, MIP-1 ALPHA AND/OR RANTES. ITS USES
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 6150132th Glebe Rd. 8th floor
CITY: Arington
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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44.9%; Score 53; DB 3; Length 170;
Best Local Similarity 52.4%; Pred. No. 0.22;
Matches 11; Conservative 2; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: VAA

ZIP: 22201-4741

COMPUTER READABLE PORM:
MEDIUM TYPE: PloEpy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,573
FILING APPLICATION: 435
PRIOR APPLICATION NUMBER: QCT/GB96/00143
FILING APPLICATION NUMBER: QCT/GB96/00143
FILING APPLICATION NUMBER: 24-JAN-1996
PRIOR APPLICATION NUMBER: GB 9501683.8
FILING DATE: 27-JAN-1995
ATPCHING APPLICATION NUMBER: 
                                                                                       1430-172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1430-172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/08875573; Patent No. 6150132; GENERAL INFORMATION:
NAME: Wilson, Mary J.

REGISTRATION NUBER: 32,955
REFERENCE/DOCKET NUMBER: 1430-
TELECOMMUNICATION INFORMATION:
TELEPRAN: 703-816-4100
TELEPRAN: 703-816-4100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHRACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
MOLECULE TYPE: protein
US-08-875-573-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Wilson, Mary J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 14:
TELECOMMUNICATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS: LENGTH: 360 aming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-875-573-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-875-573-20
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4: /cgn2_6/ptodata/1/pubpaa/USOG_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USOG_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USOG_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USOG_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USOG_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/1/pubpaa/USOG_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/1/pubpaa/USIOG_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USIOG_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
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Maximum Match 1008
Listing first 45 summaries
                                                                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 14, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Seguence 22, Appl	Sequence 2, Appli	Sequence 22, Appl	Seguence 15, Appl	17,	Sequence 1, Appli	7	Sequence 2, Appli	Sequence 5, Appli	Sequence 5, Appli
Q 1	US-10-084-813-14	US-10-095-876A-2	US-09-725-285-2	US-09-759-841-2	US-09-779-879A-2	US-09-779-879A-22	US-09-779-880A-2	US-09-779-880A-22	US-09-813-653-15	US-09-813-653-17	US-09-796-202-1	US-09-195-662A-2	US-09-339-912A-2	US-09-938-719-5	US-09-939-226-5
DB	14	14	σ	σ	σ	σ	σ	σ	σ	σ	σ	σ	σ	σ	Φ
.% Query Match Length	22	332	352	352	352	352	352	352	352	352	352	352	352	352	352
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	118	118	118	118	118	118	118	118	118	118	118	118	118	118	118
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1 APYNIVLLINTFQEFFGLNNCS 22

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RESULT 2 US-10-095-876A-2 Sequence 2, Application US/10095876A ; Publication No. US20030148294A1

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US-09-938-703-5 US-09-502-783A-703-5 US-09-512-783A-703-5 US-10-151-274-7 US-10-151-274-7 US-10-10-151-274-7 US-10-10-10-623-7 US-10-086-814-7 US-10-087-814-7 US-10-10-10-10-10-10-10-10-10-10-10-10-10-	9-19 9-13 9-15 0-15 0-15
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ALIGNMENTS

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US-10-084-813-14

| Sequence 14, Application US/10084813
| Sequence 14, Application US/10084813
| Sequence 14, Application US/10084813
| GENERAL INFORMATION:
| APPLICAMY: SAXINGER:
| TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
| TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
| TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
| TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
| CURRENT FILING DATE: 2002-02-27
| PRIOR APPLICATION NUMBER: US 60/151,270
| PRIOR APPLICATION NUMBER: US 60/151,270
| PRIOR APPLICATION NUMBER: US 60/151,270
| PRIOR FILING DATE: 1999-08-27
| NUMBER OF SEQ ID NOS: 1242
| SEQ ID NO 14
| IBNGTH: 22
| TYPE: PRIOR APPLICATION: Description of Artificial Sequence: binding peptide
| COTHER INFORMATION: Description of Artificial Sequence: binding peptide
| COTHER INFORMATION: Description of Artificial Sequence: binding peptide
| COTHER INFORMATION: Description of Artificial Sequence: DIMBATCHES | DIMBATCH
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US-US-1/3-5/94-2

US-US-1/3-5/94-2

Sequence 2. Application US/09779879A

Fatent No. US20020048786A1

GENERAL INFORMATION:

APPLICANT: Rosen, Craig A.

APPLICANT: Li, Yi

APPLICANT: Li, Yi

APPLICANT: Li, Yi

APPLICANT: Ruben, Seven, M.

TITLE REFERENCE: 1488.115000A

CURRENT FILING DATE: 2001-02-09

FRICA PILING DATE: 2001-02-09

FRICA PILING DATE: 2000-02-09

FRICA FILING DATE: 2000-02-09

FRICA FILING DATE: 2000-03-09

FRICA FILING DATE: 2000-09-09

FRICA FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LINGTH: 352
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100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels C
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Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels
            TITLE OF INVENTION: Assay Method
FILE REFERENCE: PC10348APME
CURRENT APPLICATION NUMBER: US/09/759,841
CURRENT TILING DATE: 2001-01-12
PRIOR PLING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22
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Perros, Manoussos
                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-841-2
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US-09-779-879A-22
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APPLICANT: Li, Yi
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10
TITLE OF INVENTION: (CCR5 Receptor)
FILE REFERENCE: 1486.1150003
CURRENT APPLICATION NUMBER: US/09/725,285
CURRENT FILING DATE: 2000-11-29
PRIOR PAPLICATION NUMBER: 09/339,912
PRIOR APPLICATION NUMBER: 09/195,662
PRIOR APPLICATION NUMBER: 09/195,662
PRIOR PLILNG DATE: 1998-11-18
PRIOR PLILNG DATE: 1998-11-18
PRIOR FILING DATE: 1998-06-06
NUMBER: 08/466,343
PRIOR FILING DATE: 1998-06-06
NUMBER: OF SEQ ID NOS: 9
SOFTWARE: Patentin Version 3.0
SEQ ID NO 2
LENGTH: 352
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100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels
                     APPLICANT: AL-Young, Janice; Bandman, Olga, APPLICANT: AL-Young, Janice; Bandman, Olga, APPLICANT: Coleman, Roger; Wilde, Craig G.; TITLE OF INVENTION: DNA ENCODING NOVEL CHEMOKINE RECEPTORS; FILE REFERENCE: PF-0066-1 CON CURRENT FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 08/638,081
PRIOR APPLICATION NUMBER: US 08/638,081
PRIOR PILING DATE: 1996-04-26
NUMBER OF SEQ ID NOS: 6
SOFUMARE: PERL Program
SEQ ID NO 2
LENGTH: 332
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"NAME/KEY: misc_feature

"OTHER INFORMATION: Incyte ID No. US20030148294A1 478861
US-10-095-876A-2
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100.0%; Score 118; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.9e-10;
Matches 22; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
   GENERAL INFORMATION:
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APPLICANT: Li, Yi
APPLICANT: Ruben, Steven, M.

RESULT 4
US-09-759-841-2
US-09-759-841-2
; Patent No. US20010039026A1
; GENERAL INPORMATION:
APPLICANT: Rickett, Graham A
; APPLICANT: Dobbs, Susan

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WES-08-813-653-15

Sequence 15, Application US/09813653

Sequence 15, Application US/09813653

Sequence 15, Application US/09813653

Sequence 15, Application US/00064770A1

SEPERATION NO. SECONDANCY

APPLICANT: Nestor, John

APPLICANT: See, Raymond

APPLICANT: Soe, Raymond

FILE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds

FILE REPERENCE: CNO-005

CURRENT FILING DATE: 2001-03-20

PRIOR APPLICATION NUMBER: US 60/190,996

PRIOR PLING DATE: 2000-03-21

PRIOR PLING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

NUMBER OF SEQ ID NOS: 44

SEQ ID NO 15

LENGTH: 352
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Patent No. US2002064770A1
GENERAL INFORMATION:
APPLICANT: Nestor, John
APPLICANT: See, Raymond
APPLICANT: See, Raymond
APPLICANT: Tan Hehir, Christina
TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
FILE REFERENCE: CNS-005
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100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels
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Local Similarity 100.0%; Pred. No. 2e-10;
les 22; Conservative 0; Mismatches C
   FILE REFERENCE: 1488.115000C
CURRENT APPLICATION WUDBER: US/99/779,880A
FURRENT FILING DATE: 2001-02-09
PRIOR PLING DATE: 2000-02-09
PRIOR FLING DATE: 2000-02-09
PRIOR FLING DATE: 2000-02-09
PRIOR FLING DATE: 2000-03-09
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
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ORGANISM: Homo sapiens
US-09-779-880A-22
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US-09-813-653-17
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Best Local S
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| Sequence 2, Application US/09779880A |
| Patent No. US20020061834A1 |
| GENBEAL INFORMATION: |
| APPLICANT: Rosen, Craig A. |
| APPLICANT: Rosenke, Viktor |
| APPLICANT: Rosenke, Viktor |
| APPLICANT: Ruben, Steven, M. |
| TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10 |
| TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10 |
| TITLE OF ILING DATE: 2000-02-09 |
| PRIOR APPLICATION NUMBER: US 60/181,258 |
| PRIOR FILING DATE: 2000-03-09 |
| PRIOR SEQ ID NOS: 58 |
| SOFTWARE: PatentIn version 3.0 |
| SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
FILE REPERENCE: 1488-115000A
CURRENT PAPLICALION NUMBER: US,09/779,879A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,258
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 2000-02-09
PRIOR PILING DATE: 2000-03-09
PRIOR PILING DATE: 2000-03-09
PRIOR PILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PETENT NOS: 58
SOFTWARE: PETENT Version 3.0
SEQ ID NO 2.2
LENGTH: 352
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APPLICANT: Roschke, Viktor
APPLICANT: Li, Zi, Zieven, M.
APPLICANT: Ruben, Steven, M.
IIILE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNRIO
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100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels (
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100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-779-880A-2
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APPLICANT: Li, Yi, Autorian Arguerant Argueran
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APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSARY, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
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ZIP: 9260
COMPUTER READSLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                               Query Match 100.0%; Score 118; DB 9; Length 352; Best Local Similarity 100.0%; Pred. No. 2e-10; Matches 22; Conservative 0; Mismatches 0; Indels
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100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels
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ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE: , PEATURE: A OTHER INFORMATION: Deduced Amino Acid Sequence US-09-39-912A-2
; OTHER INFORMATION: Deduced Amino Acid Sequence US-09-195-662A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence: Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 APYNIVLLINTFQEFFGLINNCS 270
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, Sequence 2, Application US/09339912A
; Patent No. US:0020099176A1
; GENERAL INFORMATION:
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Patent No. US20020106742A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 9 SOFTWARE: Patentin version 3.0 SEQ ID NO 2 LENGTH: 352
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US-09-938-719-5
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APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Ruben, M.
TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGNR10 (CCR5 Receptor)
FILE REFERENCE: 1488.115002
CURRENT PILING DATE: 1998.11-18
CURRENT PILING DATE: 1998.11-18
PRICR APPLICATION NUMBER: 08/466,343
PRICR APPLICATION NUMBER: 08/466,343
PRICR PRICR APPLICATION NUMBER: 08/466,343
PRICR PRICR PRICR DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 2
LENGTH: 352
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Patent No. US2002068813A1

Sequence INCORMATION:

APPLICANT: Dragic, Tatjana

TITLE OF INVENTION: SULFATBA CRRS PEPTIDES FOR HIV-1 INFECTION

FILE REFERENCE: 2048/610/JPW/SHS

CURRENT FILING DATE: 2001-02-28

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin version 3.0

SEQ ID NO 1.
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100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0
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Pred. No. 2e-10;
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       PRIOR APPLICATION DATE: 2001-03-20
PRIOR APPLICATION NUMBER: US 60/190,946
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/190,996
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.0
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ORGANISM: Artificial Sequence: Genomic
PEATURE:
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100.0%;
Best Local Similarity 100.0%;
Matches 22; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ), ORGANISM: Homo sapiens
US-09-813-653-17
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CRGANISM: human
US-09-796-202-1
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US-09-796-202-1
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0; Mismatches
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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US-09-938-703-5
; Sequence 5, Application US/09938703
; Patent No. US20020110870A1
; GENERAL INPORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
      22; Conservative
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Matches 22; Conserve
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Sequence 5, Application US/09939226
Patent No. US20020110805A1
GENERAL INFORMATION
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSARY, GILBERT
LIBERT, FREDERICK
TITLE OF INVENEUR: AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-0-27
ATTORNEY/AGENT INFORMATION:
NAME: APLuan, Daniel E
REGISTRATION NUMBER: 43,115
REFERENCE/DOKET NUMBER: cunknown>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 322 amino acids
LENGTH: 322 amino acids
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CORRESPONDENCE ADDRESS:
ADDRESSE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
FILING DATE: 24-Aug-2001
CLASSIFICATION: «Unknown>
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 09/626,939
FILING DATE: 27-ULV-2000
ATTORNEY AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: 34,115
REFERENCE/DOCKET NUMBER: «Unknown>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acids
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                                                                                                                                                                                                                                                           249 APYNIVLLINTFQEFFGLNNCS 270
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COUNTRY: U.S.A.
ZIP: 92660
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Best Local Similarity
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US-09-939-226-5
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US-09-502-783A-2

Sequence 2, Application US/09502783A

Sequence 2, Application US/09502783A

Sequence 2, Application US/09502783A

Sequence 2, Application US/09502783A

Patent No. USEO020132269A1

APPLICANT: Li, Yi

APPLICANT: Li, Yi

TITLE OF INVENTION: Polymorlectides Encoding Human G-Protein Chemokine Receptor (CCRS)

TITLE OF INVENTION: HDGNR10

PILE REFERENCE: 1488.1150006

PILE REFERENCE: 1488.1150006

CURRENT APPLICATION NUMBER: US/09/502,783A

PRIOR APPLICATION NUMBER: 08/466,343
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APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSARY, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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COUNTRY: U.S.A.

ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IEM COMPUTER: COMPANION:
MARIE: ALTMAN DAMISE: 34,115
MARIE: ALTMAN LOBARICION:
MARIE: ALTMAN LO
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ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 118; DB 9;
ilarity 100.0%; Pred. No. 2e-10;
Conservative 0; Mismatches 0;
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US-VS-GED-209-4/,
Sequence 477, Application US/09826509
Publication No. US20030204073A1
GENERAL INFORMATION:
APPLICANT: Liaw, Chen W.
FILE REFERENCE: AREN-207
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICANT: Liaw, Chen W.
PRIOR APPLICANT: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: PATENTING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: PATENTING DATE: LIAW, CHEN W.
SEQ ID NO 477
LENGTH: 352
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Publication No. US20030064071A1

GENERAL INFORMATION

APPLICANT: Littman, Dan R.

APPLICANT: Littman, Dan R.

APPLICANT: Van Koopk, Yvette

APPLICANT: Van Koopk, Yvette

APPLICANT: Wan Koopk, Yvette

APPLICANT: Ceijtenbeck, Theo

TITLE OF INVENTION: EXTO

TITLE OF INVENTION: EXTO

TITLE OF INVENTION: (SIL)

CURRENT APPLICATION NUMBER: US/10/151,274

CURRENT FILING DATE: 2002-05-20

PRIOR PILICATION NUMBER: US/09/517,605

PRIOR PLING DATE: 2000-03-02

NUMBER OF SEQ ID NOS: 17

SEQ ID NOS: 17

SEQ ID NOS: 17

SEQ ID NOS: 17

SEQ ID NOS: 17
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100.0%; Score 118; DB 12; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0
                            Length 352;
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                                                                       Indels
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                    Query Match
100.0%; Score 118; DB 10;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                      249 APYNIVLLLNTFQEFFGLNNCS 270
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CORGANISM: Homo sapiens
US-09-826-509-477
                                                                                                                                                                                                                                             RESULT 19
US-09-826-509-477
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Publication No. US20010096221A1
GENERAL INFORMATION.
APPLICANT: LITTWAN, DAN R.
BELMEIER, WILFRIED
LANDAU, NATHANIEL R.
LIU, RONG
TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
WACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
USES THEREOF
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ZIP: 07601

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IND PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
RILNG DATE: 11-Dec-2000
CLASSIPICATION NUMBER: US 08/66,020
FILING DATE: 11-Dec-2000
CLASSIPICATION NUMBER: US 08/66,020
FILING DATE: 13-APR-1994
APPLICATION NUMBER: US 08/227,319
FILING DATE: 13-APR-1994
APPLICATION NUMBER: US 08/227,319
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-004 N2
TELEPAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
STYPE: amino acid
STYPE: protein
HYPOTHETICAL: NO
CRIGIALE TYPE: protein
HYPOTHETICAL: NO
CRIGIALE SUPPRES: SINGLE
                                                                                                                                                                                                                 Query Match 100.0%; Score 118; DB 9; Length 352; Best Local Similarity 100.0%; Pred. No. 2e-10; Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                   ) ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-734-221A-14
                                                                                                                                                                                                                                                                                                                                                                249 APYNIVLLINTFQEFFGLNNCS 270
                                                                                                                                                                                                                                                                                                                    1 APYNIVLLLNTFQEFFGLNNCS 22
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Hackensack
                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
US-09-502-783A-2
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RESULT 23
US-10-232-686-2
; Sequence 2, Application US/10232686
; Publication No. US20030023044A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Li, Yi
; TILE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFRENCE: 1488.115000N
; FILE REFRENCE: 1488.115000N
; FILE REPRENCE: 12002-09-03
; FRIOR PELICATION NUMBER: 09/39,912
; PRIOR PILING DATE: 1999-06-25
; PRIOR FILING DATE: 1999-06-25
; PRIOR FILING DATE: 1998-11-18
; RIOR FILING DATE: 1998-11-18
; RIOR FILING DATE: 1995-06-06
; SEQ ID NOS: 9
; SCFTWARE: PatentIn version 3.0
; SEQ ID NO 2
LENGTH: 352
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago CITY: Chicago ATRE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPALIBLE

COMPUTER: IBM PC COMPALIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/106,623

FILING DATE: 26-MAT-2002

CLASSIFICATION - UNKNOWN->

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 08/771,276
                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT THORNATION:
NAME: No. US20020150888Aland, Greta E REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET UMBER: 27866/33670
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-106-623-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 APYNIVLLINTFQEFFGLNNCS 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS: LENGTH: 352 amino scids
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Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CORGANISM: Homo sapiens
US-10-232-686-2
                                                                                                  COUNTRY: USA
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Sequence 20, Application US/2088A1
GENERAL INFORMATION:
APPLICANT: Gray, Patrick W.
RAPPLICANT: Checket, Vicky L.
RAPORT, Carol J.
TITLE OF INVENTION: Chemokine Receptor Materials and Methods
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                            Query Match
100.0%; Score 118; DB 13; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0
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CONTEXT USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC compatible

OPERATING SYSTEM: PC-DOS/NN-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/106,623

FILING DATE: 26-Mar-2002

CLASSIFICATION: UNKNOWN-

PRIOR APPLICATION NUMBER: 08/771,276

FILING DATE: CURROWN-

ATTORNEY/ABCHI INFORMATION:

NAME: NO. US20020150888Aland, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/33670

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECAMIN FOR SAG 1D NO: 2:

CENTRAL DATA A-744-6448

INFORMATION FOR SAG 1D NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
OTHER INFORMATION: /= "88C amino acid sequence"
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 APYNIVLLINTFQEFFGLNNCS 270
                                             249 APYNIVLLINTFQEFFGLNNCS 270
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                 1 APYNIVLLLNTFOEFFGLNNCS 22
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LENGTH: 352 antino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein FEATURE:
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US-10-106-623-20
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US-10-106-623-2
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RESULT 27
US-10-290-058A-6
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Publication No. US2033100058A1

SEQUENCE 2, Application US/10067801

SEQUENCE 2, Application No. US2033100058A1

APPLICANT: Rosen, Craig A.

FILE REFERENCE: 1488.115001

CURRENT FILING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-06-12

PRIOR PLING DATE: 2001-06-08

PRIOR PLING DATE: 2001-06-08

PRIOR PLING DATE: 2001-10-12

PRIOR PLING DATE: 2001-10-12
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                                                                                                                                                                                  US-10-086-814-1

Sequence 1, Application US/10086814

Publication No. US20030092632A1

Publication No. US20030092632A1

APPLICANT: Dragic, Tatjana

APPLICANT: Olson, Wlidam C.

TITLE OF INVENTION: SULFATED CCRS PEPTIDES FOR HIV-1 INFECTION

TITLE OF INVENTION NUMBER: US/10/086,814

CURRENT FILING DATE: 2002-02-28

NUMBER OF SEQ ID NOS: 38

SOFTWARE: Patentin version 3.1

LENGTH: 352
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Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0
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249 APYNIVLLINTFQEFFGLNNCS 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-10-067-800-2
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US-10-067-800-2
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249 APYNIVLLINTFOEFFGLINGS 270

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Selection US/10290058A

Sequence 6, Application US/10290058A

Sequence 6, Application US/10290058A

Sequence 6, Application US/20030104455A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
UPOLOGICAL Disorders Using 313, 333, 5464, 18817 or 33524

FILE REPERENCE: MPIOL-289PIRM
CURRENT APPLICATION NUMBER: US/10/290,058A

CURRENT FILING DATE: 2002-11-07

PRIOR APPLICATION NUMBER: 60/344,552

PRIOR PADIOR FILING DATE: 2001-11-07

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6

LENGTH: 352
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Sequence 22, Application US/10067800
| Publication No. US20030100058A1
| General Information No. US20030100058A1
| General Information No. US20030100058A1
| APPLICANT: Rosen, Craig A. APPLICANT: Rosen, Craig A. APPLICANT: Ruben, Stewen, M. TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
| FILE REFERENCE: 1488.115001 | COTRENT APPLICATION NUMBER: US/10/067,800 |
| CUTRENT APPLICATION NUMBER: DCT/US01/04153 |
| FRICH FILING DATE: 2001-02-09 |
| FRICH FILING DATE: 2001-02-09 |
| FRICH PRICHATION NUMBER: 06/297,257 |
| FRICH PRICHATION NUMBER: 60/297,257 |
| FRICH PRICHATION NUMBER: 60/310,458 |
| FRICH PRICHATION NUMBER: 60/310,458 |
| FRICH PRICHATION NUMBER: 60/341,725 |
| FRICH PRICATION NUMBER: 60/341,725 |
| FRICH PRICATION NUMBER: 60/341,725 |
| FRICH PRICATION NUMBER: 2001-10-12 |
| FRICH PRICATION NUMBER: 2001-10-12 |
| FRICH PRICATION NUMBER: 2001-10-12 |
| FRICH PRICATION NUMBER: 2001-13-11 |
| FRICH PRICATION N
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Best Local Similarity 100.0
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-22
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US-10-290-058A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 28
US-10-225-567A-352
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us-10-084-813-14.rapb

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US-10-164-649-52

Sequence 52, Application US/10164649

Sequence 52, Application WS/20030162943A1

Publication No. US20030162943A1

GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. US20030162943A1el Molecules of the G Protein-Coupled NUMBER OF SEQUENCES: 56

CORRESPONDENCES: 56

CORRESPONDENCES: 6

STREET: 28 State Street

CITY: Boston
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                                                                                                                                                                DB 14; Length 352;
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CONTEX: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Ploppy disk

COMPUTER: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/10/164,649

FILING DATE: 07-Jun-2002

CLASSIFICATION NUMBER: US/10/164,649

FILING DATE: 07-Jun-2002

CLASSIFICATION NUMBER: US/09/045,583

APPLICATION NUMBER: US/09/045,583

ATORNEY/AGENT INFORMATION:

NAME: Mandragoures, Amy E.

REGISTRATION NUMBER: 3,207

REGISTRATION NUMBER: 617)227-7400

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION FOR SEQ ID NO: 52:

SEQUENCE CHARACTERICATICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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100.0%; Score 118; DB 14;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                             Query Match 100.0%; Score 118; DB 14
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches C
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NOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-164-649-52
                                                                                                                                                                                                                                                                                                        249 APYNIVLLINTFQEFFGLNNCS 270
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; Publication No. US20030165988A1
; GENERAL INFORMATION:
             ; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-301-1
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US-10-071-866-1
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; Sequence 352, Application US/10225567A;
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Rough, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE SPERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT APPLICATION NUMBER: 60/257,144
; CURRENT PILING DATE: 2000-12-19
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 352
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US-10-072-301-1

Sequence 1, Application US/10072301

Publication No. US20030152913A1

GENERAL INFORMATION:

APPLICANT: Hua, Shao-bing

APPLICANT: Pauling, Michelle H.

APPLICANT: Pauling, Michelle H.

APPLICANT: Pauling, Michelle H.

APPLICANT: Pauling, WIRBMION: UNDAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNOBER

TITLE OF INVENTION: VIRUS

FILE REPERRICE: 25636-718

CURRENT FILING DATE: 2002-02-08

NUMBER OF SEQ ID NOS: 54

SOFTWARE: Patentin version 3.1
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US-10-323-314-1
US-10-323-314-1
Sequence 1, Application US/10323314
Fublication No. US20030139571A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCRS PEFTIDES FOR HIV-1 INFECTION
FILE REPERENCE: 2048/GIOLO-1/JFW/WAF/DJK
CURRENT APPLICATION NUMBER: US/10/323,314
CURRENT PILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.0
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Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0
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US-10-225-567A-352
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; ORGANISM: human
US-10-323-314-1
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LENGTH: 352
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Gaps

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Length 352;

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APPLICANT: PORSSMANN, Wolf-Georg; FORSSMANN, Ulf, ADERWANN, Knut;
APPLICANT: PORSSMANN, Wolf-Georg; FORSSMANN, Ulf, ADERWANN, Knut;
APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikola;
ITILE OF INVENTION: Diagnostic Agent and Medicanent for Examining the
ITILE OF INVENTION: Deal Surface Proteome of Tumor and Inflammation Cells and
ITILE OF INVENTION: For Treating Tumor Diseases and Inflammatory Diseases,
ITILE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction
FILE REFERENCE: 02217us
FILE REFERENCE: 2002-09-23
RIOR PAPLICATION NUMBER: US/10/239,423
CURREAT FILING DATE: 2002-09-23
RIOR APPLICATION NUMBER: DEI0016013.1
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PatentIN Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/10439845
Sequence 2, Application US/10439845
Publication No. US20030195348A1
GENERAL INFORMATION:
APPLICANT: Combadier et al.,
TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
TITLE OF INVENTION: AND THERAPEUTIC AGENTS FOR HIV INFECTION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 118; DB 14; Best Local Similarity 100.0%; Pred. No. 2e-10; Matches 22; Conservative 0; Mismatches 0;
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100.0%; Score 118; DB 14;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0;
                     CURRENT FILING DATE: 2002-05-01
PRIOR APPLICATION NUMBER: US/09/779,879A
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/187,999
PRIOR FILING DATE: 2000-03-09
PRIOR PLING DATE: 2000-03-09
PRIOR PRIOR PLING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin version 3.0
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Publication No. US20030186889A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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APPLICANT: Hua, Shao-bing
APPLICANT: Pauling, Michelle H.
APPLICANT: Dauling, Michelle H.
APPLICANT: Stu, in
TITLE OF INVENTION: HIGH THROUGHDUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST 1
TITLE OF INVENTION: FRAGMENTS DERIVED FROM MEMBRANE PROTEINS
FILE REPRENENCE: 25636-717
CURRENT APPLICATION NUMBER: US/10/071,866
CURRENT FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.1
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APPLICANT: Rosen, Craig A.
APPLICANT: Rosenke, Viktor
APPLICANT: Li, Yiktor
APPLICANT: Li, Yiktor
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNRIO
FILE REFERENCE: 1488.11500A
CURRENT APPLICATION NUMBER: US/10/135,839
CURRENT APPLICATION NUMBER: US/09/779,879A
PRIOR FILING DATE: 2001-02-09
PRIOR PELING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/187,999
PRIOR FILING DATE: 2000-03-09
PRIOR PRIOR FILING DATE: 2000-03-09
PRIOR SEQITON NUMBER: US 60/234,336
PRIOR PRIOR FILING DATE: 2000-03-09
PRIOR SEQITON NUMBER: US 60/234,336
PRIOR 
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Publication No. US20030166024A1
GENERAL INFORMATION:
APPLICANT: Roschke, Viktor
APPLICANT: Li, Yi
APPLICANT: Li, Xi
CURRENT APPLICATION NUMBER: US/10/135,839
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100.0%; Score 118; DB 14;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 APYNIVLLINTFQEFFGLNNCS 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 352
TYPE: PRT
CACANISM: Homo sapiens
US-10-071-866-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 22; Conserv
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Gaps

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Indels

Length 352;

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249 APYNIVLLINTFQEFFGINNCS 270
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                                                                                                                                                                                                                                                                                                                                                                                1 APYNIVLLINTFORFFGLINGS 22
          ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION UNDRER: 98.347
REFERENCE/DOCKET NUMBER: 08830
TELECOMMUNICATION INFORMATION:
TELERHONE: 619/678-5070
TELERAX: 619/678-509
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 APYNIVLLINTFOEFFGLNNCS
                                                                                                                                                                                       : 352 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT; ORGANISM: Homo sapiens
US-10-360-828-1
CLASSIFICATION:
                                                                                                                                                                                                                                                                  US-10-439-845-4
                                                                                                                                                                                         LENGTH:
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100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin NUMBER: US/10/439,845
FILING DATE:
FILING DATE: RAPLICATION DATA:
PRICK APPLICATION DATA:
APPLICATION NUMBER: 08/864,458
FILING DATE: MAY 28, 1997
APPLICATION NUMBER: Provisional 60/018,508
FILING DATE: MAY 28, 1996
                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/439,845
FILING DATE:
PLING DATE:
PROST APPLICATION DATA:
APPLICATION NUMBER: 08/864,458
FILING DATE: MAY 28, 1997
APPLICATION NUMBER: Provisional 60/018,508
FILING DATE: MAY 28, 1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 08830/030001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               249 APYNIVLLINTFQEFFGLINICS 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       352 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: peptide US-10-439-845-2
                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
La Jolla
            CA
USA
                                  COUNTRY: US
ZIP: 92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 37
US-10-439-845-4
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Sequence 5, Application US/10661798
; Sequence 5, Application US/10661798
; Publication No. US20040110127A1
; GENERAL INFORMATION:
   APPLICANT: Samson, Michael
; APPLICANT: Parmentier, Marc
; APPLICANT: Variant, Libert
; APPLICANT: Variant, Libert
; TITLE OF INVENTION: Screening Methods for Identifying Compounds which Decrease HIV Ent
; TITLE OF INVENTION: a Cell
; FILE REFERENCE: 9409/2023F
; CURRENT APPLICATION NUMBER: US/10/661,798
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                                                                                                                                                                                                    Indels
                                                                                                                                                                        100.0%; Score 118; DB 14;
100.0%; Pred. No. 2e-10;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 118; DB 15; Best Local Similarity 100.0%; Pred. No. 2e-10; Matches 22; Conservative 0; Mismatches 0;
08830/030001
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GENERAL INFORMATION:

APPLICANT: Li, Yi,

APPLICANT: Li, W.

APPLICANT: Ruben, Steven, M.

TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10

FILE REPERENCE: 1488.11500P

CURRENT APPLICATION NUMBER: US/10/791,905

CURRENT FILING DATE: 2004-03-04

PRICA APPLICATION NUMBER: 109/502,783

PRICA APPLICATION NUMBER: 09/502,783

PRICA APPLICATION NUMBER: 09/339,912

PRICA APPLICATION NUMBER: 09/339,912

PRICA APPLICATION NUMBER: 09/195,662

PRICA RILING DATE: 1999-06-25

PRICA RILING DATE: 1999-11-18

PRICA RILING DATE: 1995-10-6-6

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.0

LENGTH: 352

TYPE: PRT

COGANISM: Homo sapiens

US-10-791-905-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 118; DB 16; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0
         PRIOR PILLING DATE: 109/338,703
PRIOR FILING DATE: 2001-08-24
PRIOR PILLING DATE: 2001-08-24
PRIOR PILLING DATE: 2001-08-24
PRIOR PILLING DATE: 2000-07-27
PRIOR PILLING DATE: 100-07-27
PRIOR FILING DATE: 1097-04-09
PRIOR FILING DATE: 1997-04-09
PRIOR FILING DATE: 1997-03-03
PRIOR PILLING DATE: 1997-03-03
PRIOR PILLING DATE: 1996-08-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PACENTIN VEXEND 3.1
SEQ ID NO 5:
LENGTH: 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 APYNIVLLINTFQEFFGLNNCS 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 APYNIVLLINTFOEFFGLNNCS 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 APYNIVLLINTFOEFFGLNNCS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10791905; Publication No. US20040151719A1; GENERAL INFORMATION:
2003-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.1
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CORGANISM: Homo sapiens
US-10-661-798-5
  CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 40
US-10-791-905-2
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Search completed: September 28, 2004, 09:44:42 Job time : 73.875 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 28, 2004, 08:57:36; Search time 11.825 Seconds (without alignments) 178.961 Million cell updates/sec Run on:

US-10-084-813-14 118 1 APYNIVLLINTFQEFFGLNNCS 22 Title: Perfect score: 1 Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues

Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
3: pir2:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ı	chemokine (C-C) re	(d-c)	Sept	æ	probable DNA-direc	a (C-C) r	chemokine (C-C) re	Н				muscarinic acetylc			muscarinic acetylc	hypothetical prote	hypothetical prote		MIP-1 alpha recept	muscarinic acetylc	acetyl	acetyl	o U	c acetyl	uscarinic a	d des	U	muscarinic acetylc
SUMMARIES	ID	A43113	JC2443	S	JC5942	17	-11	in	G02436	m	The same	S.	\sim	S10856	ന	~	A35546	m	934	50	934	ന	951	5	111	847572	8	990	The second	012
	DB	7	N	ď	N	7	N	N	~	N	N	N	Ŋ	N	N	N	7	7	7	~	7	7	7	7	N	7	N	N	Ŋ	N
	Length	352	360	374	344	355	1075	360	355	360	383	466	466	466	466	589	490	294	300	342	359	484	589	590	590	590	639	352	478	479
ф	Query	100.	7.	•	φ.	47.5	ė.	4.	44.1	4.		4.	4.		•	•		40.7		ö	40.7	ö	ö	•	ö		ö	•	ď	ο.
	Score	금	103	0	70		54.5	53	52	52	52	52	52	52	52	51	20	4 4	4,00	4.8	4 4	44	4,00	48	48	48	48	47	47	47
	Result No.	-	N	m	4'	Ŋ	ø	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

muscarinic acetylc probable sugar tra	hypothetical prote	glutamine ABC tran	macrophage inflamm	G protein-coupled	G protein-coupled	hypothetical prote	DNA-directed RNA p	hypothetical prote	probable G protein	G protein-coupled	pentamidine resist	guanylate cyclase-	guanylate cyclase	guanylate cyclase-
S33776 T01844	T31013	E69633	I49339	S42628	332785	T28952	C29959	T25510	158186	JC5067	567163	568838	C55331	B55331
01 0	101	N	~	~	(7	ď	N	N	N	N	N	N	ď	N
479	87	216	355	374	374	613	1070	312	354	355	423	199	201	202
39.8	39.4	39.0	39.0	39.0	39.0	39.0	38.6	38.1	38.1	38.1	37.7	37.3	37.3	37.3
744	46.5	46	46	46	46	46	45.5	45	45	45	44.5	44	44	44
30	32	33	34	35	36	37	38	33	40	41	42	43	44	4.5

ALIGNMENTS

	RESULT 1
	A43113 Memokine (C-C) receptor 5 - human Nikiltarusta namna, C-C cva.e. rese
	Vitterinate indicates (-C.C.C.) CCR. C.Species: Homo sablens (man)
	C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000
	Cyncession: Atomic, 5,1000, Access, Greez, Gordon, Access, R. RiSamson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
	Biochemistry 35, 3362-3367, 1996 A:Title: Molecular cloning and functional expression of a new human CC-chemokine receptor
	A/Accession: Atomics A.modeculary
	A;FORBIGURES: 1-552
	R;Samson, M.; Libert, F., Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragosti
	M.; Imal, T.; Rana, S.; Yl, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pal Nature 382, 722-725, 1996
	A, Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of
-	A;keterence number: S71808; MUID:96345670; PMID:8751444 A;Accession: S71808
-	A; Status: nucleic acid sequence not shown; not compared with conceptual translation
	A;Molecule type: DNA
	A;Residues: 182-206;207-230 <5AM2> A:Accession: A56834
	A;Status: nucleic acid sequence not shown; not compared with conceptual translation
	A;Molecule type: DNA
	A:Residues: 1-1304;/IXCSHLAGAPAAA-RGHLLLGARKNSAVSK, <sam3. A:Cross-references: GR:X99393: NID:GISQAGA: PIDN:TAAA7767.1: PID:GISQAGA</sam3.
	A, Note: this frameshift mutation results in a non-functional receptor but confers a degre
	nd may have had a selective advantage by conterring resistance to Yersinia plague infect; PCombadiere C ibnia S X inffanv H I. Amerby D M
	7. Leukoc. Biol. 60, 147-152, 1996
	A, Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine rece
	A,Reference number: A58832; MUID:96295970; PMID:8639119 A.Arcession: A58832
	A, Molecule type: mRNA
	A, Residues: 1-352 < COM1>
	A;Cxoss-references: GB:US-Y840; NID:S162d2408; PIDN:AABL1701.1; PID:B1010.0150.0150. *Experimental gource: clone R. endotoxin-stimulated nerioberal blood monocytes
	R; Combadiere, C.
	submitted to the EMBL Data Library, May 1996
	A.Reference number: H01541
	A.AACcesson: Gulsba A.Status: translated from GR/EMBI./DDR.I
	A; Molecule type: mRNA
	A, Residues: 1-89, 'L', 91-352 <com2></com2>
	ייניאט י ניין אאראָטיָ
	rivagori, "L."; documing, "d.; dolimatokair," v.i.; dray, r.m.; diaro, i.r "Biol, Chem. 271, 17161-17166, 1996
	A,Title: Molecular cloning and functional characterization of a novel human CC chemokine
-	A;Keierence number: A58833; MUID:96291862; PMID:8663314

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Gaps

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chemokine (C-C) receptor 2, splice form A - human
NiAlternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemos Species: Homo Sapiens (man)
C;Species: Homo Sapiens (man)
C;Accession: 138450
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A;Title: Molecular cloning and functional expression of two monocyte chemoattractant prot A;Reference number: A53477; MUID:94195821; PMID:8146186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Map position: 3921-3921
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate randopsin
C; Superfamily: reansmembrane #status predicted <TM1>
F; 79-99/Domain: transmembrane #status predicted <TM2>
F; 115-136/Domain: transmembrane #status predicted <TM3>
F; 126-276/Domain: transmembrane #status predicted <TM5>
F; 208-206/Domain: transmembrane #status predicted <TM5>
F; 208-206/Domain: transmembrane #status predicted <TM6>
F; 292-309/Domain: transmembrane #status predicted <TM6>
F; 292-309/Domain: caransmembrane #status predicted <TM6>
F; 292-309/Domain: veransmembrane #status predicted <TM7>
F; 292-309/Domain: veransmembrane #status predicted <TM7>
F; 14/Binding site: carbonydrate (Asn) (covalent) #status predicted
F; 32-277, 113-190/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homb sapiens (man)
C;Species: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R.Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y. Biochem. Biophys. Res. Commun. 243, 264-268, 1998
A.Title: Cloning and characterization of a novel human chemokine receptor. A; Reference number: JC5942; MUID:98139902; PMID:9473515
A; Recession: JC5942
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-34 FRAN-
A;Cross-references: GB:U97123; NID:g2897070; PIDN:AAC39595.1; PID:g2897071
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: EMBL:U03882; NID:g472555; PIDN:AAA19119.1; PID:g472556
F_114/\mathrm{Binding} site: carbohydrate (Asn) (covalent) #status predicted F_1113-190/\mathrm{Disulfide} bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 374;
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59.3%; Score 70; DB 2; Length 344
Best Local Similarity 57.1%; Pred. No. 0.0018;
Matches 12; Conservative 4; Mismatches 5; Indels
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Pred. No. 9.6e-09;
!; Mismatches 0;
                                                                                                                                       Score 103; DB 2;
Pred. No. 9.3e-09;
2; Mismatches 0
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90.0%;
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90.0%;
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Best Local Similarity 90.0
Matches 18; Conservative
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A;Molecule type: mRNA
A;Residues: 1-374 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene: GDB:CMKBR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A pescription: G protein-coupled receptor for chemokines MIP-lalpha, MIP-lbeta and RANTE A, Note: probably acts to control granulocyte proliferation and differentiation A, Note: probably acts to control granulocyte proliferation and differentiation C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Reywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane #status predicted <TM2>
F; 67-87 (Domain: transmembrane #status predicted <TM3>
F; 103-124 (Domain: transmembrane #status predicted <TM4>
F; 193-18 (Domain: transmembrane #status predicted <TM4>
F; 182-165 (Domain: transmembrane #status predicted <TM6>
F; 253-6-257 (Domain: transmembrane #status predicted <TM6>
F; 253-6-257 (Domain: transmembrane #status predicted <TM6>
F; 253-257 (Domain: transmembrane #status predicted <TM7>
F; 253-6-257 (Domain: transmembrane #status predicted <TM7>
F; 253-257 (Domain: transmembrane #status predicted <TM7>
F; 254-257 (Domain: transmembrane #status predicted <TM7>
F; 255-257 (Domain: transmembrane #status predicted <TM7
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C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
R;Yangagami, S:; Tokuda, Y:; Ishii, K:; Tanaka, H:; Endo, N.
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
A;Title: oDNA cloning and functional expression of a human monocyte chemoattractant prot A;Reference number: JC2443; MUID:94324942; PMID:8048929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: DBBJ:D29984; NID:g531246; PIDN:BAA06253.1; PID:g531247
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. US.A. 91, 2752-2756, 1994
A;Title: Molecular cloning and functional expression of two monocyte chemoattractant prof
A;Reference number: A53477; MUID:94195821; PMID:8146186
                                                                                                              A;Residues: 1-352 <RAP>
A;Cross-references: GB:U54994; NID:g1457945; PIDN:AAC50598.1; PID:g1457946
A;Cross-references: GB:U54994; NID:g1457945; PIDN:AAC50598.1; PID:g1457946
C;Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see C;Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Map position: 3p21-3p21

S.Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate splicing; G protein-coupled receptor; glycoprotein; transmembrane #status predicted <TM1>
F;41-70/Domain: transmembrane #status predicted <TM2>
F;11-10/Domain: transmembrane #status predicted <TM3>
F;115-136/Domain: transmembrane #status predicted <TM3>
F;115-136/Domain: transmembrane #status predicted <TM3>
F;154-178/Domain: transmembrane #status predicted <TM4>
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A;Residues: 1-360 «RES»
A;Cross-references: EMBL:U03905; NID:g472557; PIDN:AAA19120.1; PID:g472558
C;Genetics:
A;Gene: GDB:CMKBR2
A;Cross-references: GDB:337364; OMIM:601267
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F;288/Bhinding site: carbohydrate (Asn) (covalent) #status predicted
F;386,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
F;340,343/Binding site: phosphate (Thr) (covalent) #status predicted
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Pred. No. 3.5e-11;
; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                Ajdane: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CKR5; ChemR13
A;Cross-references: GDB:1230510; OMIM:601373
A;Map position: 3p21-3p21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 APYNIVLLINTFQEFFGLNNCS 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 APYNIVLLLNTFOEFFGLNNCS 22
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Conservative 0
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Best Local Similarity
Matches 22; Conserv
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A;Residues: 1-360 <YAM>
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Ajorosa-references: GDB:677463
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Ajorosa-references: GDB:677463
Ajorosa-references: GDB:67221
Cjsuperfamily: vertebrate receptor; glycoprotein; phosphoprotein; transmembrane #status predicted <TM1>
F)76-97/pomain: transmembrane #status predicted <TM2>
F)112-175/Domain: transmembrane #status predicted <TM3>
F)112-175/Domain: transmembrane #status predicted <TM3>
F)12-176/Domain: transmembrane #status predicted <TM5>
F)208-226/Domain: transmembrane #status predicted <TM5>
F)208-266/Domain: transmembrane #status predicted <TM5>
F)208-206/Inolarlide bonds: #status predicted <TM5>
F)29-706,Inolarlide bonds: #status predicted <TM7>
F)29-706,Inolarlide bonds: #status predicted <TM7>
F)29-276,Inolarlide site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted F)145/Binding site: phosphate (Asn) (covalent) #status predicted F)18110ding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted F)18110ding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted F)18110ding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted F)18110ding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted F)18110ding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted F)18110ding site: phosphate (Thr) (covalent) (Thr)
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A; Biol. Chem. 270, 19495-19500, 1995
A; Title: Molecular cloning and functional expression of a novel CC chemokine receptor CDP A; Reference number: A57160; MUID:95370289; PMID:7642634
A; Accession: A57160
A; Status: preliminary; not compared with conceptual translation
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C;Species: Homo Sapiens (man)
C;Dacte: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 04-Mar-2000
C;Accession: G02436; A57237
R;Ponath, P.D.
submitted to the EMBL Data Library, February 1996
A;Reference number: H0127
A;Accession: G02436
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alternate names: C-C CKR-4
Species: Homo sapiens (man)
Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
.Cross-references: EMBL:D17510; NID:9529643; PIDN:BAA04326.1; PID:91262609;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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;Residues: 1-360 <POW>
;Cross-references: GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g971452
;Note: source clone K5-5
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Best Local Similarity 52.4%; Pred. No. 1;
Matches 11; Conservative 2; Mismatches 8; Indels
                                                                                                A,Gene: rpoB
A,Genome: chloroplast
C,Superfamily: DNA-directed RNA polymerase beta chain
C,Keywords: chloroplast, nucleotidyltransferase; transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   355 PONLVTSTLLKNTPODFFG 373
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                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 63.2%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: A57160
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chemokine (C-C) receptor 1 - human

N.Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor

C.Species: Homo sapiens (man)

C.Species: Homo sapiens (man)

C.Species: Homo sapiens (man)

C.Accession: A45177; I55671

R.Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.

R.Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.

A.Alt-425, 1993

A.Title: Molecular cloning, functional expression, and signaling characteristics of a C-Apacession: A45177

A.Accession: A45177

A.Accession: A5517

A.Accession: A5517

A.Accession: Abown

A.Molecule type: mRNA

A.Molecule type: mRNA

A.Resion and A.Molecular cloning, brank, abaractar 1: PID: G299417
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A;Title: Structure and functional expression of the human macrophage inflammatory 1 alph
A;Reference number: I55671; MUID:93240122; PMID:7683036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - Japanese black pine chlor C; Species: chloroplast Pinus thunbergiana (Japanese black pine)
C; Species: chloroplast Pinus thunbergiana (Japanese black pine)
C; Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 18-Aug-2000
C; Date: T07448
R; Wakasugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiura, M.
B; Wakasugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiura, M.
B; Wakasugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiura, M.
B; Wakasugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiura, M.
B; Reference number: 210030; MUD:95024047; PMID:7937893
A; Reference number: 210030; MUD:95024047; PMID:7937893
A; Reteres preeliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-1075 < WAK>
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A, Cross-references: GDB:138446, CMIM:601159
A, Cross-references: GDB:138446, CMIM:601159
A, Map position: 3p21-3p21
C, Superfamily: vertebrate rhodopsin
C, Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; C, Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; E, 71-91, Domain: transmembrane #status predicted <TM2>
F, 108-129/Domain: transmembrane #status predicted <TM3>
F, 140-223/Domain: transmembrane #status predicted <TM4>
F, 140-264/Domain: transmembrane #status predicted <TM5>
F, 265-223/Domain: transmembrane #status predicted <TM5>
F, 269-305/Domain: transmembrane #status predicted <TM5>
F, 269-305/Domain: transmembrane #status predicted <TM5>
F, 261-304/Domain: transmembrane #status predicted <TM5>
F, Shinding site: carbohydrate (Asn) (covalent) #status predicted
F, 34-273, 106-183/Disulfide bonds: #status predicted
F, 345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
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A;Moleoule type: mRNA
A;Mossidues: 1-355 <mrs/
A;Residues: 1-355 <mrs/>
A;Residues: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Experimental source: HL60 cells
A,Note: sequence extracted from NCBI backbone (NCBIP:124876)
R;Gao, J.
                                                                                                              252 APYNIAFFLSTFKEHFSLSDC 272
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Gaps

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Length 383; Indels

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A;Status: preliminary
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; Glycoprotein; neurotransmitter receptor; transment
F;23-48,Domain: transmembrane #status predicted <TM1>
F;61-85/Domain: transmembrane #status predicted <TM3>
F;98-119/Domain: transmembrane #status predicted <TM3>
F;139-162/Domain: transmembrane #status predicted <TM5>
F;184-207/Domain: transmembrane #status predicted <TM6>
F;184-207/Domain: transmembrane #status predicted <TM6>
F;389-409/Domain: transmembrane #status predicted <TM6>
F;421-442/Domain: transmembrane #status predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  muscarinic acetylcholine receptor M2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 24-Nov-1999
C;Accession: JH0197; D37121
R;Lai, J; Bloom, J.W.; Yamamura, H.I.; Roeske, W.R.
Life Sci. 47, 1001-1013, 1990
A;Title: Application of the rat m2 muscarinic receptor gene by the polymerase chain real A;Reference number: JH0197; MUID:91041524; PMID:2172674
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A;Residues: 1-466 <LAI>
A;Rutenbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.
J. Biol. Chem. 265, 13702-13708, 1990
A;Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues invol
A;Reference number: A37121; MUID:90337982; PMID:2380182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C,Accession: S10126
R;Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.
EMBO J. 6, 3923-3929, 1987
G protein-coupled receptor El - equine herpesvirus 2
C.Species: equine herpesvirus 2
C.Species: equine herpesvirus 2
C.Species: equine herpesvirus 2
C.Accession: S55594
B.Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J.Mol. Biol. 249; 520-528, 1995
A.Pitle: The DNA sequence of equine herpesvirus 2.
A.Pitle: The DNA sequence of equine herpesvirus 2.
A.Faccession: S55594; MUID:95302501; PMID:7783207
A.Stetus: preliminary; nucleic acid sequence not shown
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C;Species: Homo sapiens (man)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 24-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:UZ0824; NID:g695172; PIDN:AAC13788.1; PID:g695173 C;Superfamily: vertebrate rhodopsin C;Keywords: G protein-coupled receptor
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 APYNIVLLLNTF 12
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C; Superfamily: vertebrate rhodopsin
F; 36-60/Domain: transmembrane #status predicted <TM1>
F; 71-91/Domain: transmembrane #status predicted <TM2>
F; 108-129/Domain: transmembrane #status predicted <TM3>
F; 205-223/Domain: transmembrane #status predicted <TM5>
F; 240-261/Domain: transmembrane #status predicted <TM5>
F; 288-305/Domain: transmembrane #status predicted <TM5>
F; 288-305/Domain: transmembrane #status predicted <TM7>
F; 288-305/Domain: transmembrane (Ser) (covalent) (by casein kinase II) #status predicted
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C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Reywords: glycoprotein; phosphoprotein; receptor; thymus
F;2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pred
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
                                                          A.Cross-references: EMBL:U49727; NID:g1477560; PIDN:AAB09726.1; PID:g1477561
R.Crobadiere, C.; Ahuja, S.K.; Murphy, P.M.
J. Biol. Chem. 270, 16491-16494, 1995
A.Fitle: Cloning and functional expression of a human eosinophil CC chemokine receptor. A;Reference number: A57237; MUID:95348056; PMID:7622448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-106,'N',108-275,'S',277-280,'R',282-355 <COM>
A;Cross-references: GB:U28694; NID:g1199579; PIDN:AAC50469.1; PID:g1199580
A;Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC50469.
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Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: Musculus (house mouse)
Cispecies: Musculus (house mouse)
Cispecies: Musculus (house mouse)
Richosgewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A;Title: Molecular cloning of murine Co CRR.4 and high affinity binding of chemokines that the mouse common of musculus of musculus (196324; PMID:8573157
A;Residues: J.360 - HOO.
A;Residues: L-360 - HOO.
A;Residues: L-
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Pred. No. 1.4;
6; Mismatches
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PYNVAILLSSYQSILFGNDC 273
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40.08;
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Best Local Similarity 47.6'
Matches 10; Conservative
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Best Local Similarity
                   A; Molecule type: DNA
A; Residues: 1-355 < PON>
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Gaps

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RESULT 10 S55594

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Cross-references: GB:M16331; NID:g164311; PIDN:AAA30986.1; PID:g164313
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Best Local Similarity 61.5%;
Matches 8; Conservative
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505 PYNIMVLVNTFRD 517
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401 APYNVMVLINTF 412
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Matches 8; Conservative
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A;Title: Distinct primary structures, ligand-binding properties and tissue-specific expra, R,Reference number: $04326; MUID:88166632; PMID:3443095
A;Accession: $10126
A;Accession: $10126
A;Accession: SIO126
A;Molecule type: DNA
A;Residues: 1-466 <PRP>
A;Cross-references: EMBL:X15264; NID:g32319; PIDN:CAA33315.1; PID:g32320
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho
F;23-44/Domain: transmembrane #status predicted <TMA>
F;0-89/Domain: transmembrane #status predicted <TMA>
F;184-207/Domain: transmembrane #status predicted <TMA>
F;184-207/Domain: transmembrane #status predicted <TMA>
F;389-409/Domain: transmembrane #status predicted <TMA>
F;289-409/Domain: transmembrane #status predicted <TMA>
F;289-409/Domain: transmembrane #status predicted <TMA>
F;2,6,9/Binding site: carbohydrate (Asn) (covalent) #status predicted
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MESCATIAIC acetylcholine receptor, cardiac - pig

MINALternate names: muscarinic acetylcholine receptor M2

Gispecies: Sus scrofa domestica (domestic pig)

Gispecies: Sus scrofa domestica (domestic pig)

Gispecies: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 31-Dec-2000

Gispecies: A27386; A25656

Riperalta, E.G.; Winslow, J.W.; Peterson, G.L.; Smith, D.H.; Ashkenazi, A.; Ramachandran Science 236, 600-605, 1987

A; Title: Primary structure and biochemical properties of an M-2 muscarinic receptor.

A; Reference number: A27386; MUD:87206169; PMID:3107123

A; Accession: A27386

A; Molecule type: DNA; mRNA

A; Residues: 1-466 < PER>
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Wiscarinic acetylcholine receptor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Nov-1999

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Nov-1999

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Nov-1999

R;Gocayne, 0.7 Robinson, D.A.; FitzGerald, M.G.; Chung, F.Z.; Kerlavage, A.R.; Lentes, R

Proc. Natl. Acad. Sci. U.S.A. 84, 8295-8300, 1987

Proc. Natl. Acad. Sci. U.S.A. 84, 8295-8300, 1987

A;Title: Primary structure of rat cardiac beta-adrenergic and muscarinic cholinergic rec

A;Reference number: S10855; MUID:88068581; PMID:2825184
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Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.1%; Score 52; DB 2; Length 466; 66.7%; Pred. No. 1.9; cive 4; Mismatches 0; Indels
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66.7%;
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401 APYNVMVLINTF 412
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nes 8; Conservative
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les 8; Conserv
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A, Experimental source: atrial miscle
A, Experimental source: atrial miscle
A, Note: the protein sequence derived from the mRNA clones differs from that of the genomi
FCBS lett. 209, 367-372, 1986
A, Title: Primary structure of porcine cardiac muscarinic acetylcholine receptor deduced of A, Reference number: A25656, MUID:87080790; PMID:3792556
A, Reference number: A25656; MUID:87080790; PMID:379256
A, Residues: 1-329, KK, 331-466 «KUB»
A, Residues: 1-329, KK, 331-466 «KUB»
A, Residues: 1-329, KK, 331-466 «KUB»
A, Residues: Teferences: GB:X04708; MID:g1859; PIDN:CAA28413.1; PID:g1860
A, Experimental source: cardiac muscle
C, Superfamily: vertebrate rhodopsin
C, Keywords: cardiac muscle; G protein-coupled receptor; glycoprotein; heart; neurotransmic F; 23-48/Domain: transmembrane #status predicted <TM2>
F; 61-85/Domain: transmembrane #status predicted <TM3>
F; 139-162/Domain: transmembrane #status predicted <TM5>
F; 139-162/Domain: transmembrane #status predicted <TM5>
F; 139-409/Domain: transmembrane #status predicted <TM5>
F; 131-41-412/Domain: transmembrane #status predicted <TM5>
F; 13
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Acet. 1988 #sequence_revision 31-Dec-1988 #text_change 18-Feb-2000
C;Accession: A29476
R;Braun, T.; Schoffield, P.R.; Shivers, B.D.; Pritchett, D.B.; Seeburg, P.H.
Biochem. Biophys. Res. Commun. 149, 120-132, 1987
A;Tile: A novel subtype of muscarinic receptor identified by homology screening.
A;Reference number: A29476
A;Reference number: A29476
A;Reference number: A29476
A;Residues: 1-589 < ARA
A;Residues: 1-589 < ARA
A;Residues: 1-589 < CARA
A;Residues: 1-580 < CARA
A;Residues: 1-58
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A35546
muscarinic acetylcholine receptor M4 - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 22-Jan_1993 #sequence_revision 22-Jan-1993 #text_change 21-Jul-2000
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Pred. No. 3.5;
5; Mismatches 0; Indels
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R;Tietje, K.M.; Goldman, P.S.; Nathanson, N.M.
J. Biol. Chem. 265, 2828-2834, 1990
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Gispecies: Archaeoglobus fulgidus
Cidate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
Cidate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
Cidate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
Cidate: H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F.; Malder 390, 364-370, 1997
Nature 390, 364-370, 1997
Alaubors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Reference number: A69250; MUID:98049343; PMID:9389475
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Kao, J. L.; Murphy, P.M.

J. Biol. Chem. 270, 17494-17501, 1995

A)Title: Cloning and differential tissue-specific expression of three mouse beta chemokir

A)Reference number: 149339; WUID:95340546; PMID:7542241
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A;Residues: 1-300 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK90282.1; PID:g15160307; GSPDB:GN00170
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIP-1 alpha receptor like-2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1998
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DPS
A,Residues: 1-359 ARES
A,Cross-references: EMBL:U28406; NID:g881551; PID:g881552
C,Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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50.0%; Pred. No. 6.1;
rative 5; Mismatches
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40.7%; Score 48; DB 3
Best Local Similarity 52.4%; Pred. No. 5.4;
Matches 11; Conservative 3; Mismatches
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3; Mismatches
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Best Local Similarity 45.0%; Pred. No. 6
Matches 9; Conservative 3; Mismatch
                                                                                                                                          A;Gene: AGR L 3415
A;Map position: linear chromosome
C;Superfamily: inner membrane protein ugpA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 PFNSSFVLLLKVYREAFQLNN 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 PYN -- IVLLLNTFQEFFGLNN 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 PYNIVLLINTFOEFFGLNNC 21
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Best Local Similarity 50...
has 8; Conservative
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                                                                                                                                     A.Residues: 1-490 <TIE>
C.Superfamily: vertebrate rhodopsin
C.Superfamily: vertebrate rhodopsin
C.Superfamily: vertebrate rhodopsin
C.Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane #status predicted <TML>
F.42-67-Domain: transmembrane #status predicted <TML>
F.117-138/Domain: transmembrane #status predicted <TML>
F.117-138/Domain: transmembrane #status predicted <TML>
F.118-141-150main: transmembrane #status predicted <TML>
F.203-226/Domain: transmembrane #status predicted <TML>
F.413-433/Domain: transmembrane #status predicted <TML>
F.413-433/Domain: transmembrane #status predicted <TML>
F.445-466/Domain: tr
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Hy98144
hy98144
hy98145
hy98145
hy98145
C;Species: Agrobacterium tumefaciens (strain C58, Cere C;Species: Agrobacterium tumefaciens
C;Accession: H98344
A; Einu, F; Hinkle, G; Gattung, S; Miller, N; Blanchard, M; Qurollo, B; Goldman, A; Liu, F; Wollam, C; Allinger, M; Doughty, D; Scott, C; Lappas, C; Markelz, B;
C;Accession: Agrabacterium tumefacience number: Agrabacterium tumefaciente number: Agrabacterium tumefa
A;Title: Cloning and functional analysis of a gene encoding a novel muscarinic acetylchd
A;Reference number: A35546; MUID:90153912; PMID:2154460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein Atu3101 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C; Species: Agrobacterium tumefaciens C; Spacession: AG2937 R; Moc. 11-Jan-2002 #text_change 18-Nov-2002 R; Moc. D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Romero, P.; Zhang, S. Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell A; Marp, 2317-2323, 2001 A; AjAuthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577, MUID:21608550, PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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A;Cross-references: GB:AE008689; PIDN:AAL43917.1; PID:g17741468; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 50; DB 2
Pred. No. 4.2;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.7%; Score 48; DB 352.4%; Pred. No. 5.2; ive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Map position: linear chromosome
C; Superfamily: inner membrane protein ugpA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 PFNSSFVLLLKVYREAFQLNN 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 PYN--IVLLLNTFQEFFGLNN 20
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61.5%;
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Best Local Similarity 52.4%;
Matches 11; Conservative
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Status: preliminary Molecule type: DNA

A; Gene: Atu3101

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A; Accession: AG2937

| | | | ::: | : | | | | 426 PYNVMVLINTFCE 438 2 PYNIVLLLNTFOE 14 Conservative

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Local Similarity nes 8; Conserv

Query Match Best Local \$ Matches ô

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RESULT 21

A,Accession: H98344 A,Status: preliminary A,Molecule type: DNA

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Cispecies: Homo sapiens (man)
Cispecies: Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.
Richtle: Distrinct primary structures, ligand-binding properties and tissue-specific expre
A;Reference number: S04326; MUID:88166632; PMID:3443095
A;Reference number: S04326; MUID:88166632; PMID:3443095
A;Residues: 1-590 <PRR
A;Residues: 1-590 <PRR
A;Residues: 1-590 <PRR
A;Residues: Lospo <PRR
A;Residues: Lospo <PRR
Cisperfamily: Vertebrate rhodopsin
Cisperfamily: Vertebrate rhodopsin
Cisperfamily: Vertebrate specificed <TM1>
F;68-95/Domain: transmembrane #status predicted <TM2>
F;143-164/Domain: transmembrane #status predicted <TM3>
F;185-207/Domain: transmembrane #status predicted <TM5>
F;231-252/Domain: transmembrane #status predicted <TM5>
F;231-252/Domain: transmembrane #status predicted <TM5>
F;231-252/Domain: transmembrane #status predicted <TM5>
F;255-546/Domain: transmembrane #status predicted <TM6>
F;5,6,15,41/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;184-206/Domain: transmembrane #status predicted <TM4>
F;20-251/Domain: transmembrane #status predicted <TM5>
F;492-512/Domain: transmembrane #status predicted <TM6>
F;527-545/Domain: transmembrane #status predicted <TM7>
F;527-545/Domain: transmembrane #status predicted <TM7>
F;6,15,41,48,52/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                              40.7%; Score 48; DB 2; Length 589; 72.7%; Pred. No. 11;
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                                                                                                                                                                                                                                                                                       0; Indels
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3; Mismatches
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                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                            Query Match
Best Local Similarity
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Gispecies: Rattus norvegicus (Norway rat)

Cjate: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 18-Feb-2000

Cjacession: B94518; B94523; B37121; B29514

Ribonner, T. I.

Rib
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A. Molecule type: mRNA
A. Molecule type: mRNA
A. Molecule type: mRNA
A. Molecule type: mRNA
A. Cross-references: EMBL:X65865; NID:g64900; PID:g64901
C. Superfamily: vertebrate rhodopsin
C. Superfamily: vertebrate receptor; glycoprotein; neurotransmitter receptor; transmembrane #status predicted <TM1>
F:73-58/Domain: transmembrane #status predicted <TM2>
F:108-129/Domain: transmembrane #status predicted <TM3>
F:149-177/Domain: transmembrane #status predicted <TM3>
F:149-177/Domain: transmembrane #status predicted <TM5>
F:149-277/Domain: transmembrane #status predicted <TM5>
F:407-427/Domain: transmembrane #status predicted <TM5>
F:407-427/Domain: transmembrane #status predicted <TM5>
F:407-427/Domain: transmembrane #status predicted <TM5>
F:439-460/Domain: transmembrane #status predicted <TM5>
               muscarinic acetylcholine receptor MR - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Species: S-dolor laevis (African clawed frog)
C;Accession: S46657; S24948
R;Herrera, L.; Carvallo, P.; Antonelli, M.; Olate, J.
FBES Left. 352, 175-179, 1994
A;Title: Cloning of a Xenopus laevis muscarinic receptor encoded by an intronless gene.
A;Reference number: S48657; MUID:95010703; PMID:7925970
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A;Residues: 1-484 <HER>
A;Cross-references: GB:X65865; NID:g64900; PIDN:CAA46694.1; PID:g64901
R;Olate, J.
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Pred. No. 8.7;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, April 1992
A;Reference number: S24948
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Best Local Similarity 63.0%
- The Ti Conservative
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Nature 390, 249-256, 1997

Ajuthors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerr iech, J.; Harwood, C.R.; Hemaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, S.; Hardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y.; M.; Ogawara, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portecelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Sanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Togamori, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A;Accession: B69901
A;Reference number: A69580; MUID:98044033; PMID:9344377
A;Residues: 1-352 «KUN>
A;Residues: 1-352 «KUN>
A;Residues: Bobillary; nucleic acid sequence not shown; translation not shown
A;Residues: Bobillary source: strain 168
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-233;373-478 <BO2>
A; Residues: 1-233;573-478 <BO2>
A; Residues: 1-233;573-478 <BO2>
A; Residues: 1-233;573-478 <BO2>
A; Residues: 1-25; 13702-13708, 1990
A; Biol. Chem. 255, 13702-13708, 1990
A; Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues invol
A; Reference number: A37121; MUID:90337982; PMID:2380182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphor;31-56/Domain: transmembrane #status predicted <TMl>
:69-93/Domain: transmembrane #status predicted <TMl>
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submitted to GenBank, July 1987
A;Reference number: A94518
A;Accession: C94518
A;Molecule type: mRNA
A;Residues: I-178 < RDI
Science 237, 527-522, 1987
A;Title: Identification of a family of muscarinic acetylcholine receptor genes.
A;Reference number: A94293; MUID:87263421; PMID:3037705
A;Accession: C94293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    muscarinic acetylcholine receptor M4 - rat
C;Species: Rattus norvegiuus (Norway rat)
C;Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text_change 24-Nov-1999
C;Accession: C94518; C94293; \( \overline{\ov
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Pred. No. 9.1;
3; Mismatches
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C,Superfamily: omega-3 fatty acid desaturase
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Molecule type: protein
Residues: 68-130 «KUR»
Superfamily: vertebrate rhodopsin
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Matches 9; Conserv
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muscarinic acetylcholine receptor, M3 isoform - chicken
muscarinic acetylcholine receptor, M3 isoform - chicken
c;Decise acetylcholine (chicken)
c;Decise acetylcholine (chicken)
c;Decisesion: A55019
K;Gadbut, A.P.; Galper, J.B.
J. Biol. Chem. 269, 25823-25829, 1994
A;Title: A novel M-3 muscarinic acetylcholine receptor is expressed in chick atrium and A;Reference number: A55019; MUID:95014393; PMID:7929287
A;Status: preliminary
A;Status: preliminary
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C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: OS-lec-1997 #sequence_revision OS-Dec-1997 #text_change 20-Jun-2000
C;Accession: B69901
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         muscarinic acetylcholine receptor m3 - bovine
C/Species: Bos primigenius taurus (cattle)
C/Species: Bos primigenius taurus (cattle)
C/Accession: 847572
Rilee, P.H.K.; Hodges, P.K.; Glickman, F.; Chang, K.J.
Biochim. Biophys. Acta 1223; I51-154, 1994
A/Fitle: Cloning and expression of a cDNA encoding bovine muscarinic acetylcholine m3 nA/Reference number: 847572; MuID:94339178; PMID:8061048
A/Status: preliminary
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Residues: 1-590 «LEE»
Cross-references: EMBL:U08286; NID:9520465; PIDN:AAA51866.1; PID:9520466
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A,Cross-references: GB:L10617; NID:g530097; PIDN:AAA65961.1; PID:g530098
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor
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                                                   Score 48; DB 2; Length 590;
Pred. No. 11;
3; Mismatches 0; Indels
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llarity 72.7%; Pred. No. 11;
Conservative 3; Mismatches
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A,Residues: 1-590 <LEE>
A,Cross-references: BMBL:U08286; NID:g
C,Superfamily: Vertebrate rhodopsin
C,Keywords: neurotransmitter receptor
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                                    Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                 506 PYNIMVLVNTF 516
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PYNIMVLVNTF 566
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PYNIMVLVNTF
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Best Local Similarity
--hes 8; Conserve
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Matches 8; Conserv
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C. Accession: T31013
R.She, O.; Phan, H.; Garrett, R.A.; Albers, S.V.; Stedman, K.M.; Zillig, W.
R.She, O.; Phan, H.; Garrett, R.A.; Albers, S.V.; Stedman, K.M.; Zillig, W.
B.Xtremophiles 2, 417-425, 1998
Extremophiles 2, 417-425, 1998
Extremophile
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C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C;Accession: T31013
                                                                                                                                                                                    probable sugar transport protein F9D12.9 - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 24-Sep-1999
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39.4%; Score 46.5; DB 2; Length 87;
Best Local Similarity 47.4%; Pred. No. 2.6;
Matches 9; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 507;
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Pred. No. 13;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Interns: 44/1; 150/3; 359/3
A;Notes: F9912.9
C;Superfamily: glucose transport protein
C;Keywords: sugar transport; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 PFVIGMLLQFFQQFTGIN 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.8%;
50.0%;
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Best Local Similarity 50.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
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SIGL27
muscarinic acetylcholine receptor M3 - human
C;Species: Homo saptens (man)
C;Species: Homo saptens (man)
C;Species: Homo saptens (man)
C;Species: Homo saptens (man)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 24-Nov-1999
C;Accession: S10127
R;Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.
EMBO J. 6, 3923-3929, 1997
A;Title: Distinct primary structures, ligand-binding properties and tissue-specific expt
A;Accession: S10127
A;Molecule type: DNA
A;Residues: 14479 &PERS
A;Cross-references: EMBL:X15265; NID:G32321; PIDN:CAA33336.1; PID:G32322
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphc
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphc
F;32-57,Domain: transmembrane #status predicted <TM2>
F;70-94,Domain: transmembrane #status predicted <TM3>
F;70-94,Domain: transmembrane #status predicted <TM4>
F;140-122/Domain: transmembrane #status predicted <TM5>
F;140-422/Domain: transmembrane #status predicted <TM5>
F;140-422/Domain: transmembrane #status predicted <TM6>
F;122-216/Domain: transmembrane #status predicted <TM6>
F;140-422/Domain: transmembrane #status 
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S13776
muscarinic acetylcholine receptor m4 - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 24-Nov-1999
C;Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 24-Nov-1999
C;Accession: 833776; 833135
R;van Koppen, C.J.; Lenz, W. N. N. M.
Biochim. Biophys. Acta 1173, 342-344, 1993
A;Title: Isolation, sequence and functional expression of the mouse m4 muscarinic acetyl
A;Reference number: 833776; MUD:93305731; PMID:7916637
A;Recession: 833776; MUD:93305731; PMID:7916637
A;Residues: 1-479 < KOP>
A;Residues: 1-479 < KOP>
A;Residues: EMBL:X63473; NID:9296913; PIDN:CAA45071.1; PID:9296914
C;Superfamily: vertebrate rhodopain
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphot c; Reywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphot c; Reywords: G protein-coupled status predicted < TMIS>
F;69-33/Domain: transmembrane #status predicted < TMIS>
F;69-33/Domain: transmembrane #status predicted < TMIS>
F;402-422/Domain: transmembrane #status predicted < TMS>
F;402-422/Domain: transmembrane #status predicted < TMS>
F;434-455/Domain: transmembrane #status p
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Pred. No. 13;
4; Mismatches 0; Indels
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Pred. No. 13;
4; Mismatches 0; Indels
                                                    Indels
                                                          ;
0
Pred. No. 12;
4; Mismatches
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           63.6%;
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Matches 7; Conservative
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Best Local Similarity 63.0.
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415 PYNVMVLVNTF 425
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415 PYNVMVLVNTF 425
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           Best Local Similarity 63.6
Matches 7; Conservative
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414 PYNVMVLVNTF 424
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Genomics 18, 175-184, 1993
Affilte: Identification, chromosomal location, and genome organization of mammalian G-pro
A;Reference number: A48909; MUID:94116980; PMID:8288218
A;Accession: Ç48909
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52785
G protein-coupled receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 24-Nov-1999
C;Accession: 332783
R;Kouba, M.; Vanetti, M.; Wang, X.; Schaefer, M.; Hoellt, V.
R;EBS Lett. 321, 173-178, 1993
A;Title: Cloning of a novel putative G-protein-coupled receptor (NLR) which is expressed A;Reference number: S32785; MUID:9328948; PMID:8386678
A;Accession: S32785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-374 <ROU>
A;Cross-references: GB:X71463; GB:S59748; NID:g599926; PIDN:CAA50582.1; PID:g599927
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Sammons, i.; Murray, J.
Submitted to the EMBL Data Library, July 1996
A;Pseference number: 220547
A;Reference numbe
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A;Introns: 41/1; 92/3; 159/1; 302/3; 358/1; 382/1; 433/2; 464/1; 512/3; 567/3
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                                                                                                                                                                  A Status: preliminary; nucleic acid sequence not shown
A; Molecule type: mRNA
A; Molecule type: mSNA
A; Residues: 151-269 < WILL>
A; Cross-references: GB: 1220312; NID: 9438798; PIDN: AAA16852.1; PID: 9438799
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; transmembrane protein
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Pred. No. 14;
6; Mismatches
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Pred. No. 14;
6; Mismatches
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Pred. No. 23;
2; Mismatches
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25.6%;
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Best Local Similarity 25.6%;
Matches 11; Conservative
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66.7%;
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Best Local Similarity 66.73
Best Local 8; Conservative
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Best Local Similarity 25.6
Matches 11; Conservative
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iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Porteclie Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tosato, V.; Uchiyama, A; Authors: Yoshikawa, H.; Zumatein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Uchiyama, A; Authors: Yoshikawa, H.; Zumatein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Uchiyama, A; Reference number: A69580; MUID:98044033; PMID:9384377
A; Rocession: E69633
A; Molecule type: DNAy; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-216 <KUN>
A;Cross-references: GB:Z99117; GB:Z99118; GB:AL009126; NID:92635200; PIDN:CAB14703.1; PI
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   macrophage inflammatory protein-1 alpha receptor - mouse C;Species: Mus musculus (house mouse) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999 C;Accession: 149339 C;Accession: 149339 R;Gao, J.L.; Murphy, P.M. J. Biol. Chem. 270, 17494-17501, 1995 A;Title: Cloning and differential tissue-specific expression of three mouse beta chemoki A;Reference number: 149339; MUID:95340546; PMID:7542241 A;Accession: 149339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G protein-coupled receptor Gpcr6 - mouse
N.Alternate names: interleukin-8 receptor homolog; muBLR1 protein
() Species: Mus musculus (house mouse)
() Species: Mus musculus (house mouse)
() Accession: S42628; C48909
() Accession: S42628; MulD:9409211; PMID:8405054
A) Accession: S42628
A) Accession: S42628
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A;Cross-references: EMBL:X71788; NID:g2598563; PIDN:CAA50673.1; PID:g433947
A;Cross-references: EMBL:X71788; NID:g2598563; PIDN:CAA50673.1; PID:g433947
R;Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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A;Residues: 1-355 <RES>
A;Cross-references: EMBL:U28404; NID:g881547; PIDN:AAA69153.1; PID:g881548
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.0%; Score 46; DB 2; Length 355; 35.0%; Pred. No. 13; vative 5; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: glnM C; Superfamily: histidine permease protein M
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les 11; Conserv
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RESULT 35

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62

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Query Match

Matches

C;Genetics:

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Gaps

5

Length 354; 4; Indels

Score 45; DB 2; Pred. No. 19; 1; Mismatches

459 ILNTFNKIFGLN 470

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-354 <RES>
A;Cross-references: EMBL:U04808; NID:g2558635; PIDN:AAB87093.1; PID:g439861
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: September 28, 2004, 09:07:10 Job time : 13.075 secs
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                                                                                                                                                                                                                                                                                                                                             2 PYNIVLLLNT--FQEFF 16
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58.8%;
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les 10; Conservative
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Best Local S:
Matches 10
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                                                                               RESULT 38

ONA-directed RNA polymerase (EC 2.7.7.6) beta chain - spinach chloroplast

DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - spinach chloroplast

C;Species: chloroplast Spinacia oleracea (spinach)

C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 18-Jun-1999

C;Accession: C29959

R;Hudson, G;S.; Holton, T.A.; Whitfeld, P.R.; Bottomley, W.

A;Hudson, G;S.; Holton, T.A.; Whitfeld, P.R.; Bottomley, W.

A;Title: Spinach chloroplast rpoBC genes encode three subunits of the chloroplast RNA pc

A;Reference number: A29959; MUID:88316931; PMID:3045324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Harrison, J.K.; Barber, C.M.; Lynch, K.R.
Neurosci. Lett. 169, 85-89, 1994
A;Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and
A;Reference number: I58186; MUID:94323113; PMID:8047298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein C04E6.10 - Caemorhabditis elegans
C;Species: Caemorhabditis elegans
C;Species: Caemorhabditis elegans
C;Date: 15-C0c1-1999 #sequence_revision 15-Cot-1999 #text_change 02-Jun-2000
C;Accession: T2510
R;Bentley, D.; Gattung, S.
Submitted to the EMBL Data Library, April 1997
A;Description: The EMBL Data Library, April 1997
A;Reference number: 22043
A;Accession: T25510
A;Reference number: 22043
A;Accession: T25510
A;Reference: T25510
A;Reference: T25510
A;Reference: BMBL:U97012; PIDN:AAB52330.1; GSPDB:GN00023; CESP:C04E6.10
A;Residues: 1-312 <BMS.
A;Coss-references: EMBL:U97012; PIDN:AAB52330.1; GSPDB:GN00023; CESP:C04E6.10
A;Experimental source: strain Bristol N2; clone C04E6
C;Genetics:
A;Gene: CESP:C04E6.10
A;Map position: 68/2; 97/2; 148/3; 241/3; 263/1
C;Superfamily: Caenorhabditis hypothetical protein C49G7.2
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C;Accession: IS8186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                             A)Accession: C29959
A;Molecule type: DNA
A;Residues: 1-1070 cHUD>
A;Cross-references: GB:MS5297; NID:g295119; PIDN:AAA84637.1; PID:g295121
C;Genetics:
A;Gene: rpoB
A;Gene: chloroplast
C;Superfamily: DNA-directed RNA polymerase beta chain
C;Keywords: chloroplast; nucleotidyltransferase; transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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ب
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78 ITYILNGFCTYFGLSTCA 95
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us-10-084-813-14.rsp

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September 28, 2004, 08:55:11; Search time 6.875 Seconds (without alignments)
166.624 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                          OM protein - protein search, using sw model
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US-10-084-813-14 118 1 APYNIVLLINTFQEFFGLNNCS 22

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		ο,					Q95nc0 hylobates m	hyloba		pan t	P56441 papio hamad	O97881 pongo pygma	097880 pygathrix b	097882 pygathrix n	097878 trachypithe		mus mue	rattus	018793 macaca mula	P41597 homo sapien		mus m	homo	pinus	P51679 homo sapien	homo	rattı	mus	a7 pan	P08172 homo sapien	9erz4 mus	P06199 sus scrofa	1098
ID	CKR5 CERAE	CKR5 CERPY	CKR5 CERTO	CKR5 GORGO	CKR5 HUMAN	CKRS HYLLE	CKR5 HYLML	CKR5 HYLSY	CKR5 MACMU	CKR5_PANTR	CKR5_PAPHA	CKR5 PONPY	CKR5 PYGBI	CKR5 PYGNE	CKR5_TRAFR	CKR5 TRAPH	CKR5 MOUSE	CKR5_RAT	CKR2 MACMU	CKR2 HUMAN	CKR2_RAT	CKR2 MOUSE	CKR1 HUMAN	RPOB PINTH	CKR4_HUMAN	CKR3 HUMAN	CKR3_RAT	CKR4_MOUSE	ACM2_PANTR	ACM2 HUMAN	ACM2 MOUSE	ACM2_FIG	ACM2_RAT
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P56492 cercopithec	P56483 macaca mula	P56482 macaca mula	P17200 gallus gall	O28255 archaeoglob	P51678 mus musculu	P30544 xenopus lae	Q9erz3 mus musculu	P08483 rattus norv	P41984 bos taurus	Q9n2a3 gorilla gor	P20309 homo sapien	
CKR3 CERAE	CKR3 MACMU	CKR1 MACMU	ACM4 CHICK	HI82 ARCFU	CKR3 MOUSE	ACM4 XENLA	ACM3 MOUSE	ACM3 RAT	ACM3 BOVIN	ACM3 GORGO	ACM3_HUMAN	
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355	355	355	490	342	359	484	589	589	590	290	290	
43.6	43.6	43.2	42.4	40.7	40.7	40.7	40.7	40.7	40.7	40.7	40.7	
51.5	51.5	51	20	48	48	48	48	48	48	48	48	
34	35	36	37	38	33	40	41	42	43	44	45	

ALIGNMENTS

RESULT 1

CKRS_CERAE CKRS_CERAE DD CKRS_CERAE STANDARD; PRT; 352 AA.							MEDLINE=98001387; PubMed=9343222; Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.;					Murayama Y., Matsunaga S., Inoue-Murayama M.; "chNi semiance of lfrican green monkey CCR-5 chemokine receptor			-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MiP-I- MIP-1-beta and RANTES and subsequently transduces a signal b			! .					modified and this statement is not removed. Usage by and for commercial				EMBL; U83325; AACS1796.1; EMBL; AB015944; BAA31328.1;				G-protein coupled	Polymorphism.	200
888	Edda	SSS	88	88	Z S	RC	Z Z	E I	RT	N K	RP	E E	Z E	RL	ខ្លួ	8	ខ្លួ	8	36	S	8	նչ	88	ខ្លួ	38	H H	K K	DR	H 6	3 2	₹ 🛣	¥ ₽	4

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Query Match

Best Loc Matches

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CKR5_CERTO STANDARD; PRT; 352 AA.
062743, 062744; 062745; 062746;
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKS).
CCR5 OR CMRBR5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      differentiation.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
             PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

DOMAIN

EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                      extracellular (Potential)

7 (Potential).

CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                     SULFATION (BY SIMILARITY)
SULFATION (BY SIMILARITY)
SULFATION (BY SIMILARITY)
                                                                                                                                                                                          4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                         EF17D67CBCCC3DB0 CRC64;
                                                                                            CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 118; DB 1;
Pred. No. 4.7e-11;
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                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 APYNIVLLINTFQEFFGLNNCS 270
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GPCRRHODOPSN
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Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;
Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;
Mutations in CRS-coding sequences are not associated with SIV
carrier status in African nonhuman primates.",
AIDS Res. Hum. Retroviruses 15:931-939(1999).
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and cubsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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15-MAR-2004 (Rel. 43, Last enquence update)
15-MAR-2004 (Rel. 43, Last annotation update)
C_C_chemokine_receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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             CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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Les 22; Conserv
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MEDLINE=97268667; PubMed=9108095;

Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
"Differential utilization of CCR5 by macrophage and T cell tropic simian immunodeficiency virus strains.";
Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).

-: FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by
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EMBL; AF051902; AAC39830.1; -.
EMBL; AF051904; AAC39831.1; -.
EMBL; AF051904; AAC39831.1; -.
EMBL, AF051904; AAC39831.1; -.
InterPro; IPR00076; GPCR_Rhodpsn.
Print PR00001; 7tm 1; 1.
PROSITE; PR00237; GPRATBIN RECEP F1 1; 1.
PROSITE; PS00237; GPROTBIN_RECEP_P1 2; 1.
PROSITE; PS00237; GPROTBIN_RECEP_P1 2; 1.
PROSITE; PS00240; GPROTBIN_RECEP_P1 2; 1.
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CRR-5) (CC-CKR-5) (CC-CKR-5)
CCR5 OR CKKRRS.
GCR5 OR CKKRRS.
GORILla gorilla (Lowland gorilla).
Bukaryota; Metazoa; Choqata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
NCBI_TAXID=9595;
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Y -> D (IN ISOLATE 097).
Y -> D (IN ISOLATE 097).
M -> K (IN ISOLATE 097).
L -> V (IN ISOLATE 089).
V -> G (IN ISOLATE 089).
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100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels
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T 15-WAR-2004 (Rel. 34, Last sequence update)

C C chemokine receptor type 5 (C-C CRR-5) (CCR-5) (CCR5)

E (HIV-1 fusion co-receptor) (CHEMR13) (CD195 antigen).

C CRS C CKRSES.

N CCRS OR CKRSES.

C Homo sapiens (Human).

C Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or
                                                                   SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 118; DB 1; Length 352; 100.0%; Pred. No. 4.7e-11; ive 0; Mismatches 0; Indels (
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Raport C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.; "Molecular cloning and functional characterization of a novel human CC chemokine receptor (CCS) for RANTES, MIP-lbeta, and MIP-lalpha."; J. Biol. Chem. 271:17161-17166(1996).
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MEDLINE-88001387; PubMed-9343222;
Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.;
Kuhmann C.E., platt E.J., Kozak S.L., Kabat D.;
implicate specific amnon acids in infections by simian and human immunodeficiency viruses.";
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MEDLINE-98022612; PubMed-9359654;
Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn Ho D.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.", AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
                                                                                                                                               MEDIINE=96295970; PubMed=8699119;
Conbadierc C., Ahuja S.K., Tiffany H.L., Murphy P.M.;
"Cloning and functional expression of CC CKR5, a human monocyte
chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and
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"cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie CDNA resource center (www.cdna.org)."; Submitted (JAN-2003) to the EMBL/GenBank/DDBU databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
MEDLINE=96260017; PubMed=8649511;
Deng H., Liu R., Ellmeier W., Choe S., Unutmaz D., Burkhart M., di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B., Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
"Identification of a major co-receptor for primary isolates of
                                                                                                                                                                                                                                                          υ×.
                                                                                                                                                                                                                                                    McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson I Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz I Gnoj L., 1a Bastide M., Kaplan N., Greco T., Touchman J., Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D., Sagripanti J.L., Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND VARIANT ARG-178.
Magierowska M., Barre-Sinoussi F., Issafras H., Theodorou I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
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                                        SEQUENCE FROM N.A.
MEDLINE=96291862; PubMed=8663314;
 CC-chemokine receptor gene.";
Biochemistry 35:3362-3367(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99189752; PubMed=10089882; P., Wyatt R., Cayabyab M., Arzan M., Mizzabekov T., Kolchinaky P., Wyatt R., Cayabyab M., Gerzand N.P., Gerzand N.P., Gerzand N.P., Garand O. Sodroski J., Choe H.; "Tyrosine sulfation of the amino terminus of CCRS facilitates HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glycosylation.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                             entry into CD4+ cells is mediated by the chemokine receptor
Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,
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ARCOLLSIN, AABGSTOLL;

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EMBL, U54994, AAC50598.1, -..
EMBL, U57840, AAB1771.1, -..
EMBL, U95866, AAB57793.1, -..
EMBL, U93326, AAC51797.1, -..
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                                                                                                                                                                                                                    CC-CKR-5.";
Nature 381:667-673(1996)
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AAB65732.1;

AF011532;

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352 AA.
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352 AA;
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EMBL; AF011533; AAB65733.1; -.

BRML; AF011535; AAB65733.1; -.

BRML; AF011536; AAB65735.1; -.

BRML; AF011536; AAB65736.1; -.

BRML; AF011536; AAB65736.1; -.

BRML; AF011537; AAB65736.1; -.

BRML; AF011537; AAB65736.1; -.

BRML; AF052539; AAD18131.1; -.

BRMC; GO:0005887; Cintegral to plasma membrane; TAS.

GO; GO:0005887; Cintegral to plasma membrane; TAS.

GO; GO:0007267; P:cell-cell signaling; TAS.

GO; GO:0007267; P:chemotraxis; TAS.

GO; GO:0007267; TAS.

GO; GO:00
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MRDLINE=99416438; PubMed=10486970;

MRDLINE=99416438; PubMed=10486970;

Mang Y.-W., Ryder O.A., Zhang Y.-P.;

"Sequence evolution of the CCR5 chemokine receptor gene in primates.";

Mol. Balol. Bvol. 16:1145-1154 (1999).

-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

MIP-1-beta and RANTES and subsequently transduces a signal by

increasing the intracellular calcium ions level. May play a role

in the control of granulocytic lineage proliferation or
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-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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30-WAY-2000 (Rel. 39, Last sequence update)
30-WAY-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5)
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Wakaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates; Catarrhini, Hylobatidae, Hylobates. VGBI_TaxID=61853;
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(YPOPLASMIC (POTENTIAL).

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EXTRACELLULAR (POTENTIAL).

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CKR5_HYLLE
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the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
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AMBDINE=99416436; PubMed=10486970;

Zhang Y.-W., Ryder O.A., Zhang Y.-P.;

Sequence evolution of the CCR5 chemokine receptor gene in primates.";

Mol. Biol. Evol. 16:1145-1154(1999).

-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

MIP-1-beta and RANTES and subsequently transduces a signal by

increasing the intracellular calcium ions level. May play a role

in the control of granulocytic lineage proliferation or

differentiation.
                                                                                                                                                                                                             EMBL; AP075451; AAD1965.1; -
EMBL; AP075451; AAD1965.1; -
InterPro; ITR000276; GPCR_Rhodpsn.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00267; GPROTEIN RECEP_F1 1; 1.
PROSITE; PS02626; GPROTEIN_RECEP_F1 2; 1.
PROSITE; PS0262; GPROTEIN_RECEP_F1 3.
EXTRACELLULAR (POTENTIAL).
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15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5)
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-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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Hylobates moloch (Silvery gibbon).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

Mammalia, Butheria, Primates, Catarrhini, Hylobatidae, Hylobates.
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Sequence evolution of the CCR5 chemckine receptor gene in primates.";
Mol. Biol. Evol. 16:1145-1154(1999)
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MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
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093505;
15-0838-2004 (Rel. 43, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
CCR5 OR CWKBR5.
                                                               EMBL; AFI77899; AAK43382.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
PRAM; PR0001; 77.m_1; 1.
PRINTS; PR00137; GPCRHODPSN.
PROSITE; PS00237; GPCRHODPSN.
PROSITE; PS50262; G-PROTEIN_RECEP_FI_1; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN

EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      differentiation.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
NCBI_TaxID=9590;
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.

SULFATION (BY SIMILARITY).

SULFATION (BY SIMILARITY).

SULFATION (BY SIMILARITY).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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352 AA;
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les 22; Conserv
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CKR5_HYLSY
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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ID CKRS MACMU STANDARD, PRT, 352 AA.

CRS 10-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-PER-2003 (Rel. 41, Last annotation update)

DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCRS).

GN CCRS OR CMCBRS.
                                                                                                                                                    EMBL; AF177884; AAK43367.1; -.
InterPro; IPR00276; GPCR_Rhodpsn.
PRIMTS; PR00217; Trum 1; 1.
PRIMTS; PR00237; GPCRFHOOPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1 1; 1.
PROSITE; PS50262; GPROTEIN_RECEP_F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN.

EXTRACELLULAR (POTENTIAL).
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Macaca nemestrina (Pig-tailed macaque)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
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Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
Newman W., Gerard N., Gerard C., Sodroski J.;
"Utilization of C-C chemokine receptor 5 by the envelope
"Utilization of C-C chemokine receptor 5 by the envelope
glycoprofeins of a pathogenic simian immunodeficiency virus,
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                                                                                                                                                                                                                                                                                                                                                                                               1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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SULFATION (BY SIMILARITY)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
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MEDLINE=97213934; PubMed=9060623;
Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
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NCBI_TaxID=9544, 9541, 9545;
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Genetically divergent strains of simian immunodeficiency virus use CRS as a coreceptor for entry."; J. Virol. 71:2705-2714(1997).

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- FINCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-betta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or in the control of granulocytic lineage proliferation of differentiation. Subcritical membrane protein. Subcritical integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors. SEQUENCE FROM N.A.
SPECIES—M.mulatta;
SPECIES—M.mulatta;
Marguline=2135416; PubMed=11461684;
Margulies B.J., Hauer D.A., Clements J.E.;
"Identification and comparison of eleven rhesus macaque chemokine (GLCNAC. . .) (POTENTIAL) 7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY). 1 (POTENTIAL). CYTOPLASMIC (POTENTIAL). 2 (POTENTIAL). EXTRACELLULAR (POTENTIAL) 4 (POTENTIAL). EXTRACELLUIAR (POTENTIAL) 5 (POTENTIAL). CYTOPLASMIC (POTENTIAL). 6 (FOIENTIAL). EXTRACELLULAR (POTENTIAL) 3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL). -> I (IN REF. 3) -> M (IN REF. 3) AIDS Res. Hum. Retroviruses 17:981-986(2001) 6 (POTENTIAL) SULFATION (SULFATION (SULFATION (N-LINKED (G 301 352 178 241 292 352 AA; SEQUENCE FROM N.A. TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEM DISULFID MOD RES MOD RES CARBOHYD CONFLICT CONFLICT SEQUENCE DOMAIN TRANSMEM FRANSMEM FRANSMEM RES DOMAIN DOMAIN DOMAIN

Gaps . 0 Length 352; Indels Query Match 100.0%; Score 118; DB 1; Best Local Similarity 100.0%; Pred. No. 4.7e-11; Matches 22; Conservative 0; Mismatches 0;

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249 APYNIVLLINIFQEFFGLNNCS 270 1 APYNIVLLINTFQEFFGLNNCS 22 셤 à

RESULT 10

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Submitted (Aug-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
-!- FUNCTION: Receptor for a document of transduces a signal by
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B., SEQUENCE FROM N.A.
MEDLINE=97426118; PubMed=928282;
Aacharova V., Zachar V., Goustin A.S.;
"Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
HIV type 1 host."; PS6440; 002778; 15-UL-1998 (Rel. 36, Last sequence update) 15-UL-1998 (Rel. 36, Last sequence update) 16-CCT-2001 (Rel. 40, Last annotation update) C-C chemokine receptor type 5 (C-C CKR-5) (CCC-CKR) -i- SUBCELLULAR LOCATION: Integral membrane protein. SEQUENCE FROM N.A.

MEDDLINE=9726869; PubMed=9108095;

Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,

Sharron A., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,

Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;

Pifferential utilization of CCR5 by macrophage and T cell tropic

simian immunodeficiency virus strains.";

Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997). CCRS OR CMKBRS.

Pan troglodytes (Chimpanzee).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. "HIV type 1 subtypes, coreceptor usage, and CCRS polymorphism."; AIDS Res. Hum. Retroviruses 13:1357-1366(1997). MEDLINE=98090115; PubMed=9430250; Birlet J.-G., Butor C.; Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.; Chimpanze CKR4 and CKB5 act as coreceptors for HIV type 1."; AIDS Res. Hum. Retroviruses 13:1583-1587 SEQUENCE FROM N.A. Zhang Y.; Zhang Y.; Tyder O.A., Zhang Y.; Ryder O.A., Zhang Y.; Sequence comparison of the CCRS gene in primates and primate Zimmerman P.A., Buckler-White A., Alkhatib G.; Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases AIDS Res. Hum. Retroviruses 13:1159-1161(1997). 352 AA. PRT; SEQUENCE FROM N.A. MEDLINE=98022612; PubMed=9359654; STANDARD; differentiation. SEQUENCE FROM N.A. SEQUENCE FROM N.A. PANTR D.D.;

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58B96C85909FACB2 CRC64;

40507 MW:

Tue Sep 28 15:49:58 2004

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                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SPECIES=P.anubis;
SPECIES=P.anubis;
Benton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RAWTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
                                                                                          EMBL; AR10529U; AMAGES 30.1; --
EMBL; AR023452; AGC63830.1; --
InterPro; IPR000276; GPCR.Rhodpsn.
Pfam; PR00001; 7tm 1; 10.7 m.1; 10.7 m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBCELLULAR LOCATION: Integral membrane protein.
  "Differential utilization of CCR5 by macrophage and T cell tropic simian immunodeficiency virus strains."; Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
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352 AA;
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     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

DOMAIN 30

EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
16-UUL-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CRR-5) (CC-CRR-5) (CCRS OR CMKBRS.
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CYTOPLASHIC (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASHIC (POTENTIAL).
BY SIMILARITY.
SULFATION (BY SIMILARITY).
N'LINKED (GICNAC. . .) (POTENTIAL).
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Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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MEDLINE=97268687; PubNed=9108095;
Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
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Pred. No. 4.7e-11;
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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4A33E698B80FE34C CRC64;
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Papio hamadryas (Hamadryas baboon), and Papio anubis (Olive baboon).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 APYNIVLLLNTFQEFFGLNNCS 270
                                                                                                                                                                                                                                    EMBL; U89797; AAC03717.1; -.
EMBL; AF177894; AAK43377.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 APYNIVLLINTFQEFFGLNNCS 22
                                                                                                                                         EMBL, U94329; AAB58446.1; -.
EMBL, AF0111342; AAB65742.1; -.
EMBL, U97666; AAC51670.1;
EMBL, AF011540; AAB65740.1; -.
                                                                                                                     EMBL; AF005663; AAB62557.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40539 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cercopithecinae, Papio.
NCBI_TaxID=9557, 9555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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P56441;
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Score 118; DB 1; Length 352; Pred. No. 4.7e-11; Indels

0

Gaps

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(POTENTIAL)

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                                                                                                                                                                                                                      MEDLINE=99416438; PubMed=10486970;
MEDLINE=99416438; PubMed=10486970;
Zhang Y.-W., Zhang Y.-P.;
Zhang Y.-V., Zhang Y.-P.;
Sequence evolution of the CCR5 chemokine receptor gene in primates.";
Mol. Biol. Evol. 16:1145-1154(1399).
-!-FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
-!-FUNCTION: Receptor for a Bubsequently transduces a signal by
MIP-1-beta and RANTES and undergenently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AF075446; AAD19858.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Prints, PR000217; GPCRRADOPSN.
PRINTS; PR00237; GPCRRADOPSN.
PROSITE; PS00237; GPROTEIN_RECEP_FI_1; 1.
PROSITE; PS50262; GPROTEIN_RECEP_FI_2; 1.
30 EXTRACELLULAR (POTENTAL).
                                                         30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
30-RAY-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5)
                                                                                                                                                                                                                                                                                                                                                                       differentiation.
-!- SUBCELLUTAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                        Pongo pygmaeus (Orangutan).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pongo.
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CYTOPLASMIC (POTENTIAL).

EXTRACELLURA.

(POTENTIAL).

T (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

SULFATION (BY SIMILARITY).

SULFATION (BY SIMILARITY).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                           352 AA
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Best Local Similarity 100.
Matches 22, Conservative
                           STANDARD;
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14
15
352 AA;
                                                                                                                                                                                            NCBI_TaxID=9600;
                         CKRS PONPY 097881;
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DOMAIN
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            CKR5_PONPY
RESULT
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ö Gaps ö Score 118; DB 1; Length 352; Pred. No. 4.7e-11; Mismatches 0; Indels C 1 APYNIVLLINTFQEFFGLNNCS 22 ..

249 APYNIVLLINTFQEFFGLNNCS 270

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RESULT

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                                                                                                                                                                                                                                                                                                                                              MEDINE=99416438; PubMed=10486970;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Sequence evolution of the CCRS chemokine receptor gene in primates.";
"Sequence evolution of the CCRS chemokine. Binds to MIP-1-alpha,
"Include Evol. 16:1145-1154(1999).
"Increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation."
                097880;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CRR-5) (CC-CKR-5) (CCR5).
CCR5 OR CMRRS.
Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 118; DB 1; Length 352; 100.0%; Pred. No. 4.7e-11; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
SULFATION (BY SIMILARITY).
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        352 AA.
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Best Local Similarity 100.
Matches 22; Conservative
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352 AA;
                                                                                                                                NCBI_TaxID=61621;
CKRS PYGBI
ID CKRS PYGBI
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TRANSMEM
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1 APYNIVLLLNTFQEFFGLNNCS 22

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352 AA.

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                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=99416418; PubMed=10486970;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
"Sequence evolution of the CCR5 chemokine receptor gene in primates.";
Mol. Biol. Evol. 16:1145-1154(1999).
                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or
                                                                                                                                                                                             Pygathrix nemeus (Dove langur).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae, Colobinae,
                                                                                                                      30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
38-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR5)
                                                                                                                                                                                                                                                                                                                                                                                                                            differentiation.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS, PRO0237; GFCRHODOPSN.
PROSITE: PS00237; GFROTEIN RECEP F1 1; 1.
PROSITE; PS00262; G_PROTEIN_RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOWAIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 100.0%; Score 118; DB 1; 2 Similarity 100.0%; Pred. No. 4.7e-11; 22; Conservative 0; Mismatches 0;
249 APYNIVLLINTFQEFFGLNNCS 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF075448; AAD19860.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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                                                                                           STANDARD;
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260
277
301
352
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                                                                                                                                                                                                                                                            NCBI_TaxID=54133;
                                                                                         CKR5 PYGNE
097882;
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DISULFID
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                                                                              CKR5_PYGNE
                                                             RESULT 14
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                                                                                                                                                                                                                                                                                                                                                               Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
"Sequence evolution of the CCR5 chemokine receptor gene in primates.";
Mol. Biol. Evol. 16:1145-1154(1999).
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
                                                                                                                                                                                                                                Trachypithecus francoisi (Francois' langur) (Indochinese langur).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                                                                                                            30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemoking receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 differentiation.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00237; GFCRHODOPSN.
PROSITE; PS00237; G_PROTEIN RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN 30 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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SULFATION (BY SIMILARITY)
SULFATION (BY SIMILARITY)
SULFATION (BY SIMILARITY)
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 118; DB 1;
Fred. No. 4.7e-11;
Mismatches 0;
                                                                                                                  352 AA
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                 249 APYNIVLLLNTFQEFFGLNNCS 270
1 APYNIVLLLNTFQEFFGLNNCS 22
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=99416438; PubMed=10486970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF075442; AAD19854.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40496 MW;
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ilarity 100.0%;
Conservative 0
                                                                                                                  STANDARD;
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Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                  NCBI_TaxID=54180;
                                                                                                                                                                                                                CCR5 OR CMKBR5.
                                                                                                                  TRAFR
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                                                                                                                  CKR5_TRA
097878;
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Best Local Similarity Matches 22; Conserv

BY SIMILARITY.
SULFATION (BY SIMILARITY).
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W, FE4F9D9BD3B3E861 CRC64;

CYTOPLASMIC (POTENTIAL).

(POTENTIAL)

EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).

2 (POTENTIAL). EXTRACELLULAR (POTENTIAL) 3 (POTENTIAL). CYTOPLASMIC (POTENTIAL). 4 (POTENTIAL).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99416438; PubMed=10486970; Zhang Y.-W., Ryder O.A., Zhang Y.-P.; Zhang Y.-W., Ryder O.A., Zhang Y.-P.; Sequence evolution of the CCR5 chemokine receptor gene in primates."; Mol. Biol. 2vol. 16:1145-1154(1999).
-! FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-bete and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or
                                                                                                                                                                                                                                                                                                                                                       Trachypithecus phayrei (Phayre's leaf monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
38-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCRS OR CMKBRS.
Trachypithecus phayrei (Phayre's leaf monkey).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

DOMAIN

EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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EXTRACELLULAR (POTENTIAL).
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ILGETRO; 1PR000276; GFCR_Rhodpsn.
Pfan; PP00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
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352 AA;
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Length 352;

Score 118; DB 1; Pred. No. 4.7e-11;

100.0%;

Best Local Similarity

Query Match

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Guo B., Kuno K., Harada A., Matsushima K.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level.
-!- SUBCELULUAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
-the nonhematopoietic cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chemoattractant protein 1) and murine macrophage inflammatory protein lalpha receptors: evidence for two closely linked C-C chemokine receptors on chromosome 9.";
J. Biol. Chem. 271:7551-7558(1996).
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MEDLINE=97404635; PubMed=9261347;
Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,
Mang Z.X., Guo H.H., Du JG., Accavitti M.A., Doms R.W., Peiper S.C.;
"Two distinct CCRS domains can mediate coreceptor usage by human
                                                                                                                                                                    CKRE_MOUSE STANDARD; PRT; 354 AA.
P51682; O35313; O35891; P97308; P97405; Q61867;
P1-CCT-1996 (Rel. 34, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-CT-2003 (Rel. 42, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (MIP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tharo I.F.; Molecular cloning and functional expression of murine JE (monocyte)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6
MEDLINE=S8001387; PubMed=934322;
Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.;
Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.;
Folymorphisms in the CCR5 genes of African green monkeys and mice implicate specific amino acids in infections by simian and human immunodeficiency viruses.";
J. Virol. 71:8642-8656(1997).
                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Makaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-CSTBL/6 X. CBA; TISSUE=Thymus;

MEDIINE=96278910; PubMed=8662890;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L.,
Charo I.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=129/Ola;
Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                  249 APYNIVLLLNTFOEFFGLNNCS 270
22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=129/SvJ; TISSUE=Spleen;
MEDLINE=96205938; PubMed=8631787;
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J. Virol. 71:6305-6314(1997).
  1 APYNIVLLINTFQEFFGLNNCS
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                                                                                                                                                                                                                                                                                                                            alpha receptor).
CCRS OR CMKBRS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i-FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level.
-i-SUBGELULAR LOCATION: Integral membrane protein.
-i-SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Sprague-Dawley;
MEDLINE=S8138173; WabMed=9655467;
MEDLINE=98138173; WabMed=9655467;
Defiancy Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
Defiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
"Chemokine receptor expression in cultured glia and rat experimental
allergic encephalomyelitis";
J. Neuroimmunol. 86:1-12(1998).
                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                    01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (MIP-1
                                                                                                                                                                                                                                                                                                              STRAIN=Wistar; TISSUE=Brain;
BribINE=98334064; bubmed=9670989;
Spleiss O., Gourmala N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,
Berger M., Gebicke-Haerter P.J.;
                                                                                                                                                                                                                                                                                                                                                                                       Berger M., Gebicke-Haerter P.J.;
"Cloning of rat HTV1-chemokine coreceptor CKR5 from microglia and
upregulation of its mRMs in ischemic and endotoxinemic rat brain.";
J. Neurosci. Res. 53:16-28(1998).
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Fred. No. 5.1e-09;
1; Mismatches 1; Indels
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77EDB368AA4C868D CRC64;
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                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
30-MAY-2000 (Rel. 39, Last ann
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                                                                                                                    alpha receptor).
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PROSITE; PRO0237; GPCRRHODOPSN.

PROSITE; PRO1237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS0262; G-PROTEIN RECEP F1 2; 1.

PROSITE; PS0262; G-PROTEIN FRECEP F1 2; 1.

PROSITE; PS0262; G-PROTEIN FRECEP F1 3; 1.

EXTRACELLULAR (POTENTIAL).
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  -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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                                                                                                                                                                                                                                      EMBL; U47036; AAC52454.1; --
EMBL; X94151; CAA63867.1; --
EMBL; U68565; AAB3723.1; --
EMBL; U68565; AAC53386.1; --
EMBL; AF022990; AAC53389.1; --
EMBL; AF022990; AAC53389.1; --
EMBL; AF022990; AC53389.1; --
EMBL; D83648; BA12024.1; --
MGD; MG1:107182; CCr5.
GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
GO; GO:0006952; P:defense response; IMP.
InterPro; IPR00276; GPCR. Rhodpsn.
PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELULAR (POTENTIAL).
3 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
BY SIMILARITY
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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208
354 AA;
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CKRS_RAT
ID _CKRS_RAT
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Matches

354 AA.

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Length 360;

4B2552BCE913FE9F CRC64;

41139 MW;

BY SIMILARITY

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113 1
360 AA;
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptors.",
AIDS Res. Hum. Retroviruses 17:981-986(2001).
-!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
Transduces a signal by increasing the intracellular calcium ions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0237; GFCRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=A; ,
IsoId±018793-2; Sequence=Not described;
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE-21544167, bubwed=11461684;
Margulies B.J., Hauer D.A., Clements J.E.;
"Identification and comparison of eleven rhesus macaque chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
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CYTODIASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
SULFATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                               (Monocyte chemoattractant protein 1 receptor) (MCP-1-R) CCR2 OR CMKBR2.
Macaca mulatta (Rhesus macaque).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLÜLAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                           360 AA.
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IsoId=D18793-1; Sequence=Displayed;
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                     252 PYNIVLLITFQEYFGLNNCS 272
                         22
                   PYNIVLLINTFQEFFGLNNCS
                                                                                                                                                                                                           STANDARD;
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CARBOHYD
MOD_RES
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CKR2_MACMU

DCKR2_MACMU

O18793

DT 16-0CT-1

DE CCC O18793

OC CR2 OI

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OC CR3 OI

OC CR4 OI

OC CR4 OI

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MEDIINE=20501139; PubMed=11046064; Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V., Chakravarty L., Kolattukudy P.E.; "Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that has tyrosine sulfation in a conserved extracellular N-terminal region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDIAGE 8995400; MEDIAGE 870664; MEDIATE 97150664; PubMed 8995400; MEDIATE 97150664; MAY MAND IL.-M., Myers S.J., Tsou C.-L., Gosling J., Arai H., Charo I.F.; "Organization and differential expression of the human monocyte chemoattractant protein I receptor gene. Evidence for the role of the carboxyl-terminal tail in receptor trafficking."; J. Biol. Chem. 272:1038-1045(1997).
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternative splicing of the carboxyl-terminal tails.";
Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
C-C chemokine receptor type 2 (C-C CRR-2) (CC-CKR-2) (CCR2)
(Monocyte_Chemoattractant protein 1 receptor) (MCP-1-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryotta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz J
Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J.,
Muzny D., Chen C.N., Bvans C., Fitzgerald M., See L.H., Tang P
Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
Watanabe M., Doggett N., Gardia D., Sagripanti J., Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94195821; PubMed=8146186; Charo I.F., Myers S.J., Herman A., Franci C., Connolly A.J., Coughlin S.R.; Molecular cloning and functional expression of two monocyte "Molecular cloning and functional expression of two monocyte spli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDINE-94324942; PubMed=8048929; Yamagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.; "CDNA cloning and functional expression of a human monocyte
Score 103; DB 1; Length 36 Pred. No. 1.1e-08; 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chemoattractant protein 1 receptor.";
Biochem. Biophys. Res. Commun. 202:1156-1162(1994)
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                                                                                                                                                                                               258 PYNIVILLNTFOEFFGLSNC 277
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   Query Match
Best Local Similarity 90.0%;
Matches 18; Conservative ;
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CKR2_RAT
ID _CKR2_RAT
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MIM; 601267; -.

MIM; 601267; -.

MIM; 601267; C: integral to plasma membrane; TAS.

GO; GO:0005867; C:soluble fraction; TAS.

GO; GO:0005969; P:achimicrobial humoral response (sensu Inver. . .; TAS.)

R GO; GO:0006969; P:achimicrobial humoral response; TAS.

GO; GO:0006969; P:achimicrobial humoral response; TAS.

GO; GO:0005969; P:achimicrobial humoral response; TAS.

GO; GO:0005969; P:achimicrobial humoral response; TAS.

GO; GO:0005969; P:achimicrobial humoral response; TAS.

GO; GO:000526; P:achimicrobial humoral response; TAS.

GO; GO:000526; P:achimicrobial humoral response; TAS.

GO; GO:000526; P:achimicrobial humoral response; TAS.

GO; GO:0007194; P:achimicrobial humoral humo
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BY SIMILARITY.
SLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGR
                    -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.

Transduces a signal by increasing the intracellular calcium ions level. Alternative coreceptor with CD4 for HIV-1 infection.
-!-SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                            PTM: N-glycosylated.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
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                                                                                                                                                                                                                                                                                                                             IsoId=P41597-2; Sequence=VSP_001893;
                                                                                                                                                                                                                                   Name=A;
IsoId=P41597-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U03882; AAA19119.1; EMBL; U03905; AAA19120.1; EMBL; U03904; BAA612120.1; EMBL; U09924; BAA651637.1; EMBL; U80924; AAC51636.1; EMBL; U95626; AAB57791.1; EMBL; U95626; AAB57791.1; EMBL; U95626; AAB57792.1; EMBL; AF54500; AAN16400.1; PIR; JCA443; JC2443; JCC72; JC2443; JCC72; JC2443; JCC72; JC2443; JCC72; JC2443; JCC72; JC2443; JCC72; JC2443; JC2443; JCC72; JCC72; JCC72; JC2443; JCC72; JCC
   J. Immunol. 165:5295-5303(2000)
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                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  055193;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- INDUCTION: In animals in which experimental allergic encephalomyelitis (EAE) has been induced.
                         QCPVFYRETVDGVTSTNTPSTGEQEVSAGL (in
                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                      Score 103; DB 1; Length 374; Pred. No. 1.1e-08; i Mismatches 0; Indels
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                               /FIId=VSP 001893.
V -> I (in dbSNP:1799864).
/FIId=VAR_014339.
G -> E.
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INTERFO; IPR000276; GPCR_Rhodpsn.
PFLMTS; PR00037; TPM_1; J.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50425; G_PROTEIN_RECEP_F1_2; 1.
G_PROTEIN; PS50425; G_PROTEIN_RECEP_F1_2; 1.
ENGSTTE; PS50425; G_PROTEIN_RECEP_F1_2; 1.
ENGSTTE; PS50425; G_PROTEIN_RECEP_F1_2; 1.
ENGSTTE; PS50425; G_PROTEIN_RECEP_F1_2; 1.
ENTRACEILULAR (POTENTIAL).
                                                                                                                                                                 7FTIG=VAR 014340.
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     GKGKSIGRAPEASLQDKEGA
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MEDLINE=98318173; PubMed=9655467;
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                                                                                                                                                                                                                                             87.3%;
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CYTOPLASMIC (POTENTIAL).

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modified and this statement is not removed.
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                                                                              EMBL; U47035; AAC52453.1; -. EMBL; U51717; AAC52557.1; -.
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Bust Local Similarity 70.00,
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Homo sapiens (Human).
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373 AA;
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SEQUENCE
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CKR1_HUMAN
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SEQUENCE FROM N.A.

MEDLINE=97026720; PubMed=8872898;

MEDLINE=97026720; PubMed=8872898;

MEDLINE=97026720; PubMed=8872898;

Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse transcriptase-polymerase chain reaction does not detect mRNA for the KC or new MCP-1 receptor.";

If I Neurosci. Res. 45:382-391(1996).

II TISSUE SPECIFICITY: Integral membrane protein.

II SUMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Charo I.F., "Monthly and functional expression of murine JE (monocyte "Molecular cloning and functional expression of murine JE (monocyte chemoattractant protein 1) and murine macrophage inflammatory protein receptors: evidence for two closely linked C-C chemokine receptors on chromosome 9.";
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSISE 3, GEITT2; PRITE 3/3 MA.
PSISE 3, GEITT2; S. Created)
10.CCT-1996 (Rel. 34, Created)
28-FEB-2003 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR-2)
CCR2 OR OWKBR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kurihara T., Bravo R.;
Cloning and functional expression of mCCR2, a murine receptor for
the C-C chemokines JE and FIC.";
J. Biol. Chem. 271:11603-11606(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L., Charo I.F.,
                                                                                                                                                                                                                                                              ..
0
                                                                                                                                                                                                                 73.7%; Score 87; DB 1; Length 373; 75.0%; Pred. No. 3.5e-06; ive 2; Mismatches 3; Indels
                EXTRACELLULAR (POTENTIAL)
                                                                            POTENTIAL.
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                           2E7BB012F5D6FD09 CRC64;
                                                         CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                          BY SIMILARITY
                                        POTENTIAL.
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                                                                                                                                                                                                                                                                                                                       271 PYNIVLFLTTFQEFLGMSNC 290
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MEDLINE=96205938; PubMed=8631787;
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                                                                                                                                                                                                                                                                                                2 PYNIVLLINTFORFFGLNNC 21
                                                                                                                                                                             42763 MW;
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                                                                                                                                       323
126
373 AA;
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Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                         CKR2 MOUSE
                                                                                               DOMAIN
TRANSMEM
                                    TRANSMEM
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SEQUENCE
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TRANSMEM
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CKR2 MOUSE
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01-0CT-1993 (Rel. 27, Last sequence update)
15-MR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor type 1 (CC (CR-1) (CC-CKR-1) (CCR-1) (CCR (Macrophage inflammatory protein-1 alpha receptor) (MIP-lalpha-R) (RANTES-R) (HM145) (LD78 receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Pred. No. 6.3e-05;
2; Mismatches 4; Indels
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MEDLINE=93161416; PubMed=7679328;
Neote K., Digregorio D., Mak J.Y., Horuk R., Schall T.J.;
Neote Clar cloning, functional expression, and signaling
characteristics of a C-C chemokine receptor.";
Cell 72:415-425(1993).
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6 (POTENTIAL).
EXTRACELULAR (POTENTIAL).
7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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-> G (IN REF. 1).
-> G (IN REF. 1).
FA012C10F4C9325A CRC64;
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
Usage
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Y -> H (IN REF
                                                                                                                                                                                                                                                                                                                Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

G-protein coupled receptor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 (POTENTIAL)
CYTOPLASMIC (
                   entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
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us-10-084-813-14.rsp

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Score 56; DB 1; Length 355; Pred. No. 0.24;
BY SIMILARITY.
E -> D (IN REF. 3).
B2C100FFED275985 CRC64;
                                                             41172 MW;
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                                                                                                                 Query Match
Best Local Similarity 40.0%;
Matches 8; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                          355 AA;
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Best Local Similarity
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01-NOV-1995
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      DISULFID
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM, 601159; -. Gintegral to plasma membrane; TAS.
GO; GO:0005887; C:integral to plasma activity; TAS.
GO; GO:0004950; F:chemokine receptor activity; TAS.
GO; GO:0007155; P:cell adhesion; TAS.
GO; GO:0007165; P:cell auxface receptor linked signal transdu. . .; TAS.
GO; GO:0007167; P:cell-cell signaling; TAS.
GO; GO:0007204; P:chemotaxis; TAS.
GO; GO:0007204; P:chemotaxis; TAS.
GO; GO:0007187; P:chemotaxis; TAS.
GO; GO:0007187; P:chemotaxis; TAS.
GO; GO:0006995; P:immune response; TAS.
GO; GO:0006994; P:immune response; TAS.
GO; GO:0006994; P:immune response; TAS.
GO; GO:0007125; P:immune response; TAS.
GO; GO:0007125; P:immune response; TAS.
                                                                                                                                                                                                                                                                                                                                                   Nomura H., Nielsen B.W., Matsushima K.;
"Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chemotactic peptide receptors.";
Int. Immunol. 5:1239-1248 (1993).
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1 delta, RANTES, and MCP-3 and, less efficiently, to MIP-1-beta or MCP-1 and subsequently transduces a signal by increasing the intracellular calcium ions level. Responsible for affecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stem cell proliferation.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUB SPECIFICITY: Widely expressed in different hematopoietic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
            [2]
SEQUENCE FROM N.A.
MEDLINE=93240122; PubMed=7683036;
Gao J.-L., Kuhns D., Tiffany H.L., McDermott D., Li X., Francke
Murphy P.M.;
                                                                                                                                                  "Structure and functional expression of the human macrophage inflammatory protein 1 alpha/RANIES receptor."; J. Exp. Med. 177:1421-1427(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0237; GPCRRHODOSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS00262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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MEDLINE=94092629; PubMed=7505609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L09230; AAA58408.1; -.
EMBL; L10918; AAA36543.1; -.
EMBL; D10925; BAA01723.1; -.
PIN; A45177; A45177; A45177.
Genew; HGNC:1602; CCR1.
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                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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RISSP. 205WU7; 1140.

RISSP. 205WU7; 1140.

RICEPPO; IPR007121; RNA_Dol_BD.

RICEPPO; IPR007641; RNA_Dol_Rpb2_1.

RICEPPO; IPR007642; RNA_Dol_Rpb2_1.

RICEPPO; IPR007642; RNA_Dol_Rpb2_2.

RICEPPO; IPR007642; RNA_Dol_Rpb2_6.

RICEPPO; IPR007641; RNA_Dol_Rpb2_6.

RICEPPO; IPR007641; RNA_Dol_Rpb2_7.

REFAM: PF04561; RNA_Dol_Rpb2_2; 1.

REFAM: PF04562; RNA_Dol_Rpb2_2; 1.

REFAM: PF04560; RNA_Dol_Rpb2_2; 1.

REFAM: PF04560; RNA_Dol_Rpb2_7; 1.

REPAM: PF04560; RNA_DOL_RPPA; 1.22470 MM; 00677BC6D8F26ACR CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suginta M.;
Suginta M.;
"Loss of all ndh genes as determined by sequencing the entire
"Loss of all ndh genes as determined Pinus thunbergii.";
chloroplast genome of the black pine Pinus thunbergii.";
Proc. Natl: Acad. Sci. U.S., 91:9794-9798(1994).
-!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
of DNA into RNA using the four ribonucleoside triphosphates as
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBINIT: In chloroplasts, the RNA polymerase is composed of four subunits: alpha, beta, beta', and beta'.
-!- SUBCELLULAR LOCATION: Chloroplast.
-!- SIMILARITY: Belongs to the RNA polymerase beta chain family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CATALYIC ACTIVITY: N nucleoside triphosphate = N diphosphate + {RNA}(N).
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Pinus.
NCBI_TaxID=3350;
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MEDLINE=95024047; PubMed=7937893;
Wakasugi_T., Tsudzuki J., Ito S., Nakashima K., Tsudzuki T.,
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6)
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Pred. No. 1.2;
    6; Mismatches
                                                                                                                                                                          254 PYNLTILISVEODFLETHEC 273
                                                                                     2 PYNIVLLINTFOEFFGLNNC 21
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(Rel. 32, Last seq
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Imai T., Chantry D., Raport C.J., Wood C.L., Nishimura M., Godiska R.,
Yoshie O., Gray P.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION, TISSUE SPECIFICITY, AND PHOSPHORYLATION.
MEDLINE-20219238; PubMed=10754297;
Inndjerdingen M., Damaj B., Maghazachi A.A.;
"Human NK cells express CC chemokine receptors 4 and 8 and respond to thymus and activation-regulated chemokine, macrophage-derived chemokine, and I-309.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campbell J.J., Haraldsen G., Pan J., Rottman J., Qin S., Ponath P., Andrew D.P., Warnke R., Ruffing N., Kassam N., Wu L., Butcher E.C.; "The chemokine receptor CCR4 in vascular recognition by cutaneous but not intestinal memory T cells.";
Nature 400:776-780 (1999).
                                                                                                                                                                                                                                                                                  Power C.A., Meyer A., Nemeth K., Bacon K.B., Hoogewerf A.J., Proudfoot A.E.I., Wells T.N.C.; "Molecular coloning and functional expression of a novel CC chemokine receptor cDNA from a human basophilic cell line."; J. Biol. Chem. 270:19495-19500(1995).
 Gaps
                                                                                   CKR4 HUMAN STANDARD; PRT; 360 AA.
PS1679; Q9ULY6; Q9ULY7;
01-OCT-1996 (Rel. 34, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
C-C chenokine receptor type 4 (C-C CKR-4) (CC-CKR-4)
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND VARIANTS VAL-130 AND SER-178.
MEDLINE=21040311; PubMed=11196669;
MEDLINE=21040311; Tuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki Hirai K., Tokunaga K.;
Hirai K., Tokunaga K.;
"New variations of human CC-chemokine receptors CCR3 and CCR4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yoshie O.;
                                                                                                                                                                                           Homo sapiens (Human).
Vertebrata; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Macrophage-derived chemokine is a functional ligand for the CC
                                                                                                                                                                                                                                                                                                                                                                                                                                               Kopatz S.A., Aronstam R.S., Sharma S.V.; "cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org)."; submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
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Imai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yosh
The T cell-directed CC chemokine TARC is a highly specific
biological ligand for CC chemokine receptor 4.";
J. Biol. Chem. 272:15036-15042(1997).
 Indels
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2; Mismatches
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Biol. Chem. 273:1764-1768(1998).
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                                                                                                                                                                                                                                                              TISSUE=Spleen;
MEDLINE=95370289; PubMed=7642634;
                                 2 PYNIV---LLLNTFQEFFG 17
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 12; Conservative
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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1. Immunol. 164:4046-4054(2000).

1. FUNCTON: High affinity receptor for the C-C type chemokines TARC/SCYA17 and MUC/SCYA22. The activity of this receptor is mediated by G(i) proteins which activate a phosphatidylinositol-calcium second messenger system. Can function as a chemoattractant homing receptor on circulating memory lymphocytes and as a coreceptor for some primary HIV-2 isolates. In the CNS, could mediate hippocampal-neuron survival.

1. SUBCELLUIAR LOCATION: Integral membrane protein.

2. PETSUB SPECIFICITY: Predominantly expressed in the thymus, in peripheral blood leukocytes, including T cells, mostly cd4+ cells, and an monocytes. Detected also in macrophages, IL-2-activated natural killer cells and skin-homing memory T cells, mostly the ones expressing the cutaneous lymphocyte antigen (CLA). Expressed in brain microvascular and coronary artery endothelial cells. PHOSPHORYLATION ON YET UNDEFINED SER/PHR REIDUES, MOST PROBABLY BY BESTPURE ADARBATORY RIBER CELLS, SURVAZ BINDING INDUCES.

2. PETM: IN NATURAL KILLER CELLS, SURVAZ BINDING INDUCES.

2. PHOSPHORYLATION ON YET UNDEFINED SER/PHR REIDUES, MOST PROBABLY BY BESTPURE ADARBATORY. IN NATURE STANDING INDUCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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R GO; GO:0005887; C:integral to plasma membrane; TAS.

R GO; GO:0006950; F:chemotaxis; TAS.

R GO; GO:0006955; P:chemotaxis; TAS.

R GO; GO:0006955; P:chemotaxis; TAS.

R GO; GO:0006955; P:immune response; TAS.

R GO; GO:0006955; P:immune response; TAS.

DR GO; GO:0006954; P:immlamatory response; TAS.

DR PROSTE; P:immlamatory response; TAS.

DR PERM: PRO001; TRM 1; 1.

DR PERM: PRO001; TRM 1; 1.

DR PROSTE; PS:02237; GPCREHODOPSN.

DR PROSTE; PS:02237; GPCREHODOPSN.

DR PROSTE; PS:02237; GPCREHODOPSN.

RW G-protein coupled receptor; Transmembrane; Glycoprotein; KW Phosphorylation; Polymorphism.

RXW Phosphorylation; Polymorphism.

RXTRARGELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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/FTId=VAR_010669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X85740; CAA59743.1; --
EMBL; AB023888; BAA86965.1; --
EMBL; AB023899; BAA86966.1; --
EMBL; AB023891; BAA86967.1; --
EMBL; AB023891; BAA86968.1; --
EMBL; AB023892; BAA86969.1; --
EMBL; AB022892; BAA86969.1; --
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MIM; 604836; -.
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EMBL; AY322539; AAPE
PIR; AS7160; AS7160.
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rare TATA-less promoter structure conserved between Drosophila
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EMBL, AA8023887; BAA86964.1; --
EMBL, AF247361, AAL85154.1; --
EMBL, AY221.092; AAA065970.2; --
EMBL, BC033514; AAH33514.1; --
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                                           Genomics 80:86-95(2002).
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Genew; HGNC:1604; CC
                                                                                           SEQUENCE FROM N.A.
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      a rare humans.
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Xiao L., Weiss S., Qari S., Rudolph D., Hodge T., Lal R.;

"Partial resistance to infection by syncytium-inducing primary HIV-1
in exposed uninfected individuals homozygous for CCR5 32bp deletion.";

Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=21040311; PubMed=11196669;
Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Combadiere C., Ahuja S.K., Murphy P.M.; "Cloning and functional expression of a human eosinophil CC chemokine receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Transcription regulation of human chemokine receptor CCR3: evidence
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96281895; PubMed=8676064; Conath P.D., Qin S., Post T.W., Mang J., Wu L., Gerard N.P., Newman W., Gerard C., Mackay C.R.; "Molecular cloning and characterization of a human ectaxin receptor
                                                                                                                                                                                                                                                                                                          CKR3 HUMAN STANDARD; Q9ULY8; 355 AA.

D15677; Q15748; Q86ND2; Q9ULY8;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-YAR-2004 (Rel. 43, Last annotation update)
C-C chemoxine receptor 43, Last annotation update)
(CKR3) (Bosinophil eotaxin receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96235044; PubMed=8642344; Daugherty B.L., Siciliano S.J., Demartino J.A., Malkowitz L., Siciliano S.J., Demartino J.A., Malkowitz L., Sirotina A., Springer M.S.; "Cloning A., Springer M.S.; ectaxin a expression, and characterization of the human eosinophil eotaxin receptor:"; J. Exp. Med. 183:2349-2354(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-22074933; PubMed=12079287;
Vijh S., Dayhoff D.E., Wang C.E., Imam Z., Ehrenberg P.K.,
Michael N.L.;
                                                                    44.9%; Score 53; DB 1; Length 360; 52.4%; Pred. No. 0.71;
                                                                                                                  8; Indels
    /FTId=VAR_010670.
S1EBE12AD1FAFABF CRC64;
                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expressed selectively on eosinophils.";
J. Exp. Med. 183:2737-2748(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Combadiere C., Ahuja S.K., Murphy P.M.; J. Biol. Chem. 270:30235-30235(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. Chem. 270:16491-16494(1995).
                                                                                                                                                                                     257 PYNIVLFLETLVELEVLQDCT 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Monocytes;
MEDLINE=95348056; PubMed=7622448;
                                                                                                                                                           2 PYNIVLLINTFQEFFGLNNCS 22
                             41402 MW;
                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                360 AA;
                                                                  Query Match
Best Local Similarity
Matches 11; Conserv
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                             SEQUENCE
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                                                                                                                                                                                                                                                                     RESULT 26
CKR3_HUMAN
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                                                                                                                                                                                                                                                                                          RESURENCE FROM N.A.

RESURENCE FROM N.A.

RESURENCE TESSUES A.D. GOLDING E.A., GROUSE L.H., Derge J.G.,

RETAUSPERG R.L., Felngold E.A., Grouse L.H., Derge J.G.,

RA STAUSBERG R.L., Felngold E.A., Grouse L.H., Schamen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

R. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hableh F.,

R. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hableh F.,

R. Schards S.A., Nogham P.J., Nogham R.P., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Sosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.

RA Wilting M., Madan A., Young A.C., Shevohenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schenn J.E., Jones S.J.M., Marra M.A.;

RA Generation and initial analysis of more than 15,000 full-length

RT Human and mouse cDNA sequences.",

PROC. 1-- FUNCTION: Receptor for a C.C type chemokine. Binds to ectaxin,

cotaxin-3, MCP-3, MCP-4, RANTES and MIP-1 delta. Subsequently

cotaxin-3, MCP-3, MCP-4, RANTES and MIP-1 delta. Subsequently

ransyches BPECIFICITY: In ecsinophils as well as trace amounts in

cotaxin-bullar LOCATION: Integral membrane protein.
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GO; GO: 0005887; C:integral to plasma membrane; TAS.
GO; GO: 0004950; F:chemokine receptor activity; TAS.
GO; GO: 00004950; F:chemokine receptor activity; TAS.
GO; GO: 00007155; P:cell adhesion; TAS.
GO; GO: 00007155; P:cellular defense response; TAS.
GO; GO: 00007204; P:cytosolic calcium ion concentration elevation; TAS.
GO; GO: 00007188; P:chemotaris; TAS.
GO; GO: 00007189; P:chemotaris; TAS.
GO; GO: 00007125; P:intamatory response; TAS.
InterPro; IRF000204; GPCR_Rhodpsn.
PFEmi, PF00001; 7rm 1; 1.
PRINTS; PRÇ0217; GPCRRHODOSN.
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Kopatz S.A., Aronstam R.S., Sharma S.V.; "cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org)."; Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                        EMBL; AF003954; AAC03337.1; -.
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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nes 10; Conserv
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P51680;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
STRAIN=Wistar; TISSUE-Spleen;
MEDLINE=98318173; PubMed=9655467;
Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
Defiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
"Chemokine receptor expression in cultured glia and rat experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                   C -> S (polymorphism found in about 7% the population; may show reduced activity.

FridavAR 010668.

S -> T (IN REF. 4 AND 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CKR3 RAT STANDARD; PRT; 359 AA.
054814; 055169;
30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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                                                                                                                                                                                                                                                                                                                                                                                                44.1%; Score 52; DB 1; Length 355; 40.0%; Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                              6; Indels
G_PROTEIN_RECEP_F1_1; 1.
G_PROTEIN_RECEP_F1_2; 1.
receptor; Transmembrane; Polymorphism.
34 EXTRACELLULAR (POTENTIAL).
                                                           1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                   4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                        3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                           BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                              6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||: :|||::||
|PYNVAILLSSYQSILFGNDC 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 PYNIVLLLNTFQEFFGLNNC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         allergic encephalomyelitis.";
J. Neuroimmunol. 86:1-12(1998).
                                                                                                                                                                                                                                                                                                                                                                   41043 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCR3 OR CMKBR3.
Rattus norvegicus (Rat).
                                                            276
355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 8; Conserv
   PS00237;
PS50262;
                 PROSITE; PS50262;
G-protein coupled
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   PROSITE;
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STRAIN=CSPEL/6 X CBA, TISSUE=Thymus;
STRAIN=CSPEL/6 X CBA, TISSUE=Thymus;
MRDIMED-6613624; PubMed=8573157;
Hoogewerf A.J., Black D., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
"Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to murine and human CC CKR-4.";
Biochem. Biophys. Res. Commun. 218:337-343(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                đ
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01-0CT-1996 (Rel. 34, Last sequence update)
15-MXR-2004 (Rel. 43, Last annotation update)
C.C. chemokine receptor type 4 (C-C CKR-4) (CC-CKR-4) (CCR-4).
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STRAIN=C57BL/6; TISSUE=Cytotoxic T-cell;
MEDLINE=97335974; PubMed=9192769;
Youn B.-S., Kim S.-H., Lyu M.S., Kozak C.A., Taub D.D., Kwon B.S.;
Youn B.-S., Kim Sg and characterization of a cDNA, CHENRI, encoding chemokine receptor with a homology to the human C-C chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 52; DB 1; Length 359;
Pred. No. 1;
3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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880F682984F501DA CRC64;
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EXTRACELLULAR (POTENTIAL)
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InterPro; IRR000276; GPCR_Rhodpsn.
Pf.an, PR00017 7tm 1; 1.
PRINTS; PR000237; GPRRHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; GPROTEIN RECEP_F1_2; 1.
G-POTCHEN COUPLED 43 PROTEIN RECEP_F1_2; 1.
G-POTCHEN COUPLED 43 PROTEIN RECEP_F1_2; 1.
TRANSMEM 44 64 POTENTIAL.
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183
194
                                                                                  TRANSMEM
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                                                                                             TRANSMEM
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NON TER TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEM MOD_RES MOD_RES MOD_RES SEQUENCE Query Match Best Local DISULFID Q9N2A7 DOMAIN DOMAIN CHRM2 Matches RESULT 셤 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL utstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). and B-cells. -!- DEVELOPMENTAL STAGE: Low expression at 7.5 dpc and 12.5 dpc in the Buser R., Conquet F., Proudfoot A.E.I., Wells T.N.C., Power C.A., "A key role for CC chemokine receptor 4 in lipopolysaccharide-induced endotoxic shock."; J. Exp. Med. 1911.1755-1764 (2000).

-!- FUNCTION: High affinity receptor for the C-C type chemokines TARC/SCYA17 and MDC/SCYA2. The activity of this receptor is mediated by G(i) proteins which activate a phosphatidylinositol-calcium second messenger system. Could play a role in lipopolysaccharide (LPS)-induced endotoxic shock. In the CNS, could mediate hippocampal-neuron survival.
-!- SIBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Expressed in the thymus, macrophages and Tyolk sac.
-!- PTH: IN NATURAL KILLER CELLS, SCYA22 BINDING INDUCES
PHOSPHORYLATION ON YET UNDEFINED SER/THR RESIDUES, MOST PROBABLY
BY BETA-ADRENERGIC RECEPTOR KINASES 1 AND 2 (BY SIMILARITY).
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors. (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL). CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL). -> A (IN REF. 2). -> S (IN REF. 2). 97BDB8C96D259AE3 CRC64; 3 (POTENTIAL). CYTOPLASMIC (POTENTIAL). 4 (POTENTIAL). EXTRACELLULAR (POTENTIAL) 6 (FOIENTIAL). EXTRACELLULAR (POTENTIAL) RACELL. (POTENTIAL). CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL). (POTENTIAL) (POTENTIAL) (POTENTIAL) BY SIMILARITY T -> I (IN R N-LINKED N-LINKED N-LINKED MEDLINE=20273981; PubMed=10811868; ٨ ^ ^ 41462 MW; EMBL; X90862; CAA62372.1; -. EMBL; U15208; AAA92582.1; -. 241 246 293 311 360 AA; CONFLICT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Isolate 220;
Kitano T., Kobayakawa H., Saitou N.;
Kitano T., Kobayakawa H., Saitou N.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RESPRONSES,
CELLULAR RESPONSES, INCLUDING INHIBITION OF POTASSIUM CHANNELS
THROUGH THE ACTION OF PROTEINS. PRIMARY TRANSDUCING EFFECT IS
ADENYLATE CYCLASE INHIBITION.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AB041392; BAA94477.1;
InterPro; IPR000276; GPCR_Rhodpsn.
PRIMTS; PR0001; 7mm_1; 1.
PRIMTS; PR000137; GPCRTEIN RECEP_F1_1; 1.
PROSITE; PS00237; GPROTEIN RECEP_F1_2; 1.1;
PROSITE; PS00263; GPROTEIN RECEP_F1_2; 1.7
Postsynaptic membrans; Ionic Channel; Glycoprotein; Transmembrane; Phosphorylation; Multigene family; G-protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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0
  Length 360;
                                                  8; Indels
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PHOSPHORYLATION (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
12B0324E13D37DDF CRC64;
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                             15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
17-MAR-2004 (Rel. 43, Last annotation update)
Muscarinic acetylcholine receptor M2 (Fragment).
  DB 1;
                                                                                                                                                                                                                                                                             440 AA
44.1%; Score 52; DB ilarity 47.6%; Pred. No. 1; Conservative 3; Mismatches
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                                                                                                  2 PYNIVLLINTFOEFFGLNNCS 22
                                                                                                                                                                                                                                                                                STANDARD;
                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9598;
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48854 MW;

440 AA;

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Genew; HGNC:1951; CHRM2.
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                                                                                                                                                                 3D-structure.
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                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-88166632; PubMed=3443095;
Peralta B.G., Ashkenazi A., Winslow J.W., Smith D.H.,
Ramachandran J., Capon D.J.;
"Distinct primary structures, ligand-binding properties and tissuespecific expression of four human muscarinic acetylcholine
                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDILME-87263421; PubMed=3037705;
BONNEY T.I., Buckley N.J., Young A.C., Brann M.R.;
"Identification of a family of muscarinic acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Brain;
Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
"cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie CDNA resource center (www.cdna.org).";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                               .
0
          Score 52; DB 1; Length 440;
Pred. No. 1.2;
4; Mismatches 0; Indels
                                                                                                                     ACM2 HUMAN STANDARD; PRT; 466 AA. P08172; Q9P1X9; 01-AUG-1988 (Rel. 08, Created) 01-AUG-1988 (Rel. 08, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Muscarinic acetylcholine receptor M2. CHRM2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M16404; AAA51570.1; -.
EMBL; X15264; CAA33335.1; -.
EMBL; AF496916; AAM18939.1; -.
EMBL; AB041391; BAA94476.1; -.
PIR; S10126; S10126.
                                                                                                                                                                                                                                                                                                                                                                                       receptors.";
EMBO J. 6:3923-3929(1987).
                                                                                                                                                                                                                                                                                                    Science 237:527-532(1987).
                                                                375 APYNVMVLINTF 386
   1 APYNIVLLINTF 12
                                                                                                                                                                                                  Homo sapiens (Human)
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                                                                                                              ACM2 HUMAN
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MIN, 118493; ...
R MIX, 118493; ...
R GO; GO:0005887; C:integral to plasma membrane; TAS.
R GO; GO:0004881; F:muscarinic acetylcholine receptor activity; TAS.
R GO; GO:0007207; P:muscarinic acetyl choline receptor, phospho. .; TAS.
R GO; GO:0007307; P:muscarinic acetyl choline receptor, phospho. .; TAS.
R GO; GO:0007309; P:neurogenesis; TAS.
R GO; GO:0008016; P:requlation of heart rate; TAS.
R GO; GO:0008016; P:requlation of heart rate; TAS.
R FRINTS; PRO0237; GPCR.Rhodpsn.
R PROSTTE; PS00237; GPCR.Rhodpsn.
R PROSTTE; PS00237; GPCRENEDPSN.
R PROSTTE; PS002237; GPCRENEDPSN.
R PROSTTE; PS00262; G PROTEIN RECEP FI. 1; 1.
R PROSTTE; PS00262; G PROTEIN RECEP FI. 2; 1.
R PROSTTE; PS00262; G PROTEIN RECEP FI. 2; 1.
R POSTSYNaptic membrane; Ionic channel; Glycoprotein; Transmembrane;
R PLENTAL ACET CHANNEL CHAN
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Gomeza J., Wess J.;

Gomeza J., Wess J.;

Gomeza J., Wess J.;

Isolation, sequence and functional expression of mouse muscarinic
acetylcholine receptor genes.";

Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
-! CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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PHOSPHORYLATION (POTENTIAL)
PHOSPHORYLATION (POTENTIAL)
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY
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66.78;
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Best Local Similarity 66.7-
Best Local Similarity 67.7-
Conservative
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176
446
450
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465 4
466 AA;
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-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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                                                                                                                                                                                                         Pfam; PF00001; /rm 1; 1.

PRINTS; PR00237; GPCRRHODDPSN.

PROSITE; PS00237; GPCRRHODPSN.

PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane; Phostsynaptic membrane; and channel; Glycoprotein coupled receptor.

Phosphorylation; Multigene family; G-protein coupled receptor.

EXTRACELLULAR (POTENTIAL).
                                                                                              [2]
SEQUENCE FROM N.A.
MEDLINE=87206169; PubMed=3107123;
Peralta E.G., Winslow J.W., Peterson G.L., Smith D.H.,
Ashkenazi A., Ramachandran J., Schimerlik M.I., Capon D.J.;
"Primary structure and biochemical properties of an M2 muscarinic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
T., Haga K., Ichiyama A., Kangawa K., Matsuo H., Hirose T.,
S.;
                                       "Primary structure of porcine cardiac muscarinic acetylcholine receptor deduced from the cDNA sequence."; FEBS Lett. 209:367-372(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.1%; Score 52; DB 1; Length 466; 66.7%; Pred. No. 1.3; 0; Indels ive 4; Mismatches 0; Indels
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PHOSPHORYLATION (POTENTIAL)
PHOSPHORYLATION (POTENTIAL)
PHOSPHORYLATION (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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53D089F179789CD9 CRC64;
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EXTRACELLULAR (POTENTIAL)
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EMBL; MAG31; AAA30986.1; -.
RT; A27386; A27386.
InterPro; IPRO00276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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401 APYNVMVLINTF 412
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les 8; Conservative
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TRANSMEM
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Best Local S
Matches 8
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MOD RES
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                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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     THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS ADENTIFATE CYCLASE INHIBITION.
SUBCELLULAR LOCAFION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                            InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS00237; GPROTEIN RECEP F1 2; 1.
PROSITE; PS00262; GPROTEIN RECEP F1 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIŠSUE=Heart;
MEDLINE=87080790; PubMed=3792556;
Kubo T., Maeda A., Sugimoto K., Akiba I., Mikami A., Takahashi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Mezazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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Pred. No. 1.3;
Mismatches 0; Indels
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUTAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLUTAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
PHOSPHORYLATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Moscarinic acetylcholine receptor M2.
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                                                                                                                                                                                                                                              EMBL; AF264049; AAG14343.1; -. MGD; MGI:88397; Chrm2.
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66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.,
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401 APYNVMVLINTF 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 APYNIVLLLNTF 12
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466 AA;
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CARBOHYD CARBOHYD CARBOHYD

MOD_RES SEQUENCE

RES

ACM2 PIG

RESULT 32 ACM2_PIG

8

DOMAIN TRANSMEM

DOMAIN

DOMAIN

DOMAIN TRANSMEM DOMAIN TRANSMEM

TRANSMEM FRANSMEM TRANSMEM

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                 iris.",
J. Smooth Muscle Res. 34:111-122(1998).
J. Smooth Muscle Res. 34:111-122(1998).
J. Smooth Muscle Res. 34:111-122 (1998).

I. SMOOTH MUSCLE RESPONSES, INCLUDING INHIBITION OF PADENYLATE CYCLASE,
BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
BREAKDOWN OF PROSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS
ADENYLATE CYCLASE INHIBITION.

I. SUBCELLULAR LOCATION: Integral membrane protein coupled receptors.

I. SIMILARITY: Belongs to family 1 of G-protein coupled a collabor.

II is produced through a collabor.
                                                                                                                                     katucus norvegicus (rau).
Eukaryota; Megizoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Rammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO001; 7tm 1, 1

PRINTS; PRO01; 7tm 1, 1

PRINTS; PRO01; 7tm 1, 1

PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.

PROSITE; PS00262; GPROTEIN RECEP F1 2; 1.

PROSITE; PS00262; GPROTEIN RECEP F1 2; 1.

POSTSYNADTIC membrane; Ionic channel; Glycoprotein; Transmembrane; DOMAIN

23 45 CATOMAIN

TRANSMEM 23 45 CYTOMAINL).

TRANSMEM 46 59 CYTOMAINL).

TRANSMEM 66 80 CYTOMAINL).

DOMAIN 81 97 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                        Venter J.C.;
"Primary structure of rat cardiac beta-adrenergic and muscarinic
"Primary structure of rat cardiac beta-adrenergic and muscarinic
further gic receptors obtained by automated DNA sequence analysis:
further evidence for a multigene family.";
Proc. Natl. Acad. Sci. U.S.A. 84:8296-8300(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                    Furuta M., Ohya S., Imaizumi Y., Watanabe M.;
"Molecular cloning of m3 muscarinic acetylcholine receptor in rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FOTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

7 (SOTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                       MEDLINE=88066581; PubMed=2825184;
Gocayne J.D., Robinson D.A., Fitzgerald M.G., Chung F.-Z.,
Kerlavage A.R., Lentes K.-U., Lai J., Wang C.-D., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 (POTENTIAL) CYTOPLASMIC (POTENTIAL).
                             P10980; 092221;
01-JUL-1989 (Rel. 11, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
CHRM2 OR CHRM-2.
                 466 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; J03025; AAA40926.1; -.
BEML; ABC17655; BAA56838.1; -.
PIR; S10856; S10856
INTERPRO 1PR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Iris;
MEDLINE=99138467; PubMed=9972520;
                 STANDARD;
                                                                                                                            Rattus norvegicus (Rat)
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242891484444
1890808449
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                       NCBI_TaxiD=10116;
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TRANSMEM
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CARBOHYD
                  RAT
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ACM2 RAT
ID ACM2
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                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
(GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                            Score 52; DB 1; Length 466; Pred. No. 1.3; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Y13775; CAA74106.1; -.

InterPro; IPRO00276; GPCR_Rhodpsn.

FERM; PRO0031; Trm.1; 1.

FRINTS; PRO0037; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G_Protein coupled receptor; Transmembrane.

G_Protein coupled receptor; Transmembrane.

G_Protein coupled receptor; Transmembrane.

FTRANSMEM 35 62 I(POTENTIAL).

FTRANSMEM 35 72 CYTOPLASMIC (POTENTIAL).

FTRANSMEM 73 93 2 (POTENTIAL).

FTRANSMEM 73 94 107 EXTRACELLULAR (POTENTIAL).
                                                                                 (POTENTIAL)
                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                         70ECCD86366A676B CRC64;
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
                                                                               PHOSPHORYLATION (POTENT
PHOSPHORYLATION (POTENT
N -> 5 (IN REF. 1).
VS -> 5A (IN REF. 1).
G -> 10 (IN REF. 1).
C -> Y (IN REF. 1).
C -> Y (IN REF. 1).
I -> V (IN REF. 1).
I -> V (IN REF. 1).
I -> V (IN REF. 1).
                     N-LINKED (GLCNAC
BY SIMILARITY.
PHOSPHORYLATION
    N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C-C chemokine receptor type 3 (CKR3).
                                                                                                                                                                                                                                                                                             51539 MW;
                                                                                                                                                                                                                                                                                                                                   44.1%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ||||:::|:|||
401 APYNVMVLINTF 412
                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    1 APYNIVLLINTF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34
62
72
107
1129
171
    369
466 AA;
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Best Local Similarity
      CERAE
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TRANSMEM
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TRANSMEM
                     CARBOHYD
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MOD_RES
CONFLICT
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P56492;
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CERAE
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us-10-084-813-14.rsp

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DISULFID
CONFLICT
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TRANSMEM
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                                                                                                                            'RANSMEM
                                                                                                                                                                                                                                                                       Query Match
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P56482;
                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute of Bioinformatics and the EMBL outstation on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial continies requires a license agreement (See http://www.isb-sib.ch/announce/corsend an email to license@isb-sib.ch).

EMBL; AF017283; AAAF0527.1; ...

EMBL; SP00273; GPCRHODOPSN.

PRINTS; PR00217; GPCRHODOPSN.

PROSITE; PS00262; GPROTEIN RECEP F1_2; 1.

RPCSITE; P
                                                                                                                                                                                          ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98118446; PubMed=9454694; Sol N., Treboute C., Gomas E., Ferchal F., Shacklett B., Alizon M.; "The rhesus macaque CCR3 chemokine receptor is a cell entry cofactor for HIV-2, but not for HIV-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Virology 240:213-220(1998).

-!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin, MCP-3 MCP-4 and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level.

-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-19998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21354176; PubMed=11461684;
Margulies B.J., Hauer D.A., Clements J.E.;
"Identification and comparison of eleven rhesus macaque chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
                                                                                                                                                                                          7;
                                                                                                                                                        Score 51.5; DB 1; Length 355;
Pred. No. 1.2;
5; Mismatches 3; Indels 1
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                           6 (POTENTIAL).
EXTRACELULAR (POTENTIAL)
7 (POTENTIAL).
                                                                                                                       44F7A5EFEEB978FF CRC64;
                                                                                     CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AIDS Res. Hum. Retroviruses 17:981-986(2001)
                                                                                                                                                                                                                                                                                                                                    355 AA.
                                                                                                                                                                                                                                         254 PYNVAILISTYQSILFGLD 272
                                                                                                                                                                                          . 9
                                                                                                                                                                                                                        2 PYNIVLLINIFQE-FFGLN 19
                                                                                                                                                                                                                                                                                                                                                                                                                                              CCR3 OR CMKBR3.
Macaca mulatta (Rhesus macaque)
                                                                                                                            40830 MW;
                                                                                                                                                            43.68;
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                    STANDARD;
 203
223
223
264
281
355
185
                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                            355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptors."
                                                                                                                                                                                                                                                                                                                                  CKR3_MACMU
P56483;
DOMAIN
TRANSMEM
DOMAIN
TRANSMEM
                                                                                          DOMAIN
DISULFID
SEQUENCE
                                                                              TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALDS RES. HUM. RELTOVITURES 17:981-986(2001).
ALDS RES. HUM. RELTOVITURES A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, 1-FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, RANTES, MCP-3 AND, LESS EFFICIENTLY, TO MIP-1-BETA OR MCP-1 AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL PROLIFERATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 1 (C-C CRR-1) (CC-CRR-1) (CCR1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macaca mulatta (Rhesus macaque).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Margulies B.J., Hauer D.A., Clements J.E.; "Identification and comparison of eleven rhesus macaque chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.6%; Score 51.5; DB 1; Length 355; 47.4%; Pred. No. 1.2; ive 6; Mismatches 3; Indels 1
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
                                                                                                                                  S (POTENTIAL).
CYTOPLASNIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELULAR (POTENTIAL).
7 (POTENTIAL).
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PEfam; PF00001; 7tm 1, 1.
PRINTS; PR00037; GPCRHODDSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN 134
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                              -> E (IN REF. 2).
-> R (IN REF. 2).
E271FIE694970D9F CRC64;
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL). BY SIMILARITY.
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MEDLINE=21354176; PubMed=11461684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 PYNVAILISTYQSVLFGLD 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 PYNIVLLLNTFQE-FFGLN 19
                                                                                                                                                                                                                                                                                                                                                                                                      40805 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cercopithecinae; Macaca.
944
1094
1130
1130
2224
2224
2225
2225
202
1180
355 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9544;
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118-10-084-813-14.18D

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                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jaiol. Chem. 265:2828-2834(1990).

-!- FUNCTION: The muscarinic acetylcholine receptor mediates various cellular responses, including inhibition of adenylate cyclase, breakdown of phosphoinositides and modulation of potassium channels through the action of groteins. Primary transducing effect is inhibition of adenylate cyclase. May couple to multiple functional responses in cell lines.
-!- SUBCELDULAR LOGATION: Integral membrane protein.
-!- SIMILARITY: Expressed in heart and brain.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae;
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                         7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                               .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90153912; PubMed=2154460;
Tietle K.M., Goldman P.S., Mathanson N.M.;
"Cloning and functional analysis of a gene encoding a novel
muscarinic acetylcholine receptor expressed in chick heart and
                                                                                                                                                                                                                                Query Match
43.2%; Score 51; DB 1; Length 355;
Best Local Similarity 45.0%; Pred. No. 1.4;
Matches 9; Conservative 4; Mismatches 7; Indels
                                                     4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                        ' SIMILARITY.
41CAEA7CC19D23D4 CRC64;
    2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL)
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Muscarinic deetylcholine receptor M4.
                                                                                                                                                                                                                                                                                                                                                                                                 490 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP, P02699; IBOJ.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR000237; GPCRRHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP_F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1.
2 (POTENTIAL)
                                                                                                                                                                                                                                                                                                              254 PYNLTELISVFQEFLFTHLC 273
                                                                                                                                                                                                                                                                                             2 PYNIVLLLNTFQEFFGLNNC 21
                                                                                                                                                                                         BY
                                                                                                                                                                                                       MM:
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PIR; A35546; A35546.
                                                                                                                                                                                                       41198
                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken)
11001
1129
1129
1129
1223
1233
1305
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1305
                                                                                                                                                                                         183
                                                                                                                                                                          5
106
355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9031;
 65
92
1130
1147
1147
128
224
224
326
326
306
                                                                                                                                                                                                                                                                                                                                                                                    ACM4_CHICK
ID ACM4_CHICK
AC P17200;
                                          DOMAIN
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                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                      RESULT 37
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STRAIN=VC-16 / DSM 4304 / ATCC 49558;
STRAIN=VC-16 / DSM 4304 / ATCC 49558;
STRAIN=S06494313; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Kletchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Kichardson D.L., Kerlarage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Feterson S., Reich C.I., MoNeil L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Glycoprotein; Transmembrane;
                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
2 SY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                              028255;
28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
41stddinol-phosphate aminotransferase 2 (EC 2.6.1.9) (Imidazole acetol-phosphate transaminase 2).
                                                                                                                                                                                                                                                                                    ö
            receptor
                                                                                                                                                                                                                                                             Score 50, DB 1; Length 490;
Pred. No. 2.8;
4; Mismatches 1; Indels
                                                                         3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                         6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
           Multigene family, G-protein coupled re 42 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
                                                      2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                     342 AA
  membrane; Ionic channel;
                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                          54937 MW;
                                                                                                                                                                                                                                                                42.48;
                                                                                                                                                                                                                                                                            61.5%;
                                                                                                                                                                                                                                                                                                                       |||:::|:|| |
426 PYNVMVLINTFCE 438
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 61...
And 8; Conservative
                                                                                                                                                                                                                                                                                                           2 PYNIVLLLNTFOE 14
                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                        15
20
25
115
490 AA;
             Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=2234;
                                 subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                RESULT 38
HI82 ARCFU
ID HI82 ARCFU
                                                                                                                                                                                                                    CARBOHYD
DISULFID
SEQUENCE
                                                                                                                                                     DOMAIN
TRANSMEM
DOMAIN
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DOMAIN
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CARBOHYD
CARBOHYD
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Score 48; DB 1;
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01-APR-1993 (Rel. 25, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Muscarinio acetylcholine receptor M4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ed. No. 4.3;
Mismatches
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                                                                                                                                                                                                                                                                                                                                              PEAM; PF00001; 7tm.1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Transmembrane.

DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-Ovary;
MEDLINE-95010703; PubMed=7925970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 PYNIVLLINTFQEFFGLNNC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41825 MW;
                                                                                                                                                                                               EMBL; U29677; AAA86118.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8355;
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TRANSMEM
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ACM4_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
      OCCOUNTY SERVICE COCCOUNTY SERVICE COUNTY 
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 41, Last sequence update)
Probable C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR-3) (CCR-3) (CCR3) (CKR3) (Macrophage inflammatory protein-1 alpha receptor-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gao J.-L., Murphy P.M.;
"Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.", J. Biol. Chem. 270:17494-17501(1995).

FINCTION. Receptor for a C-C type chemokine. Binds to ectaxin, MCP-3, MCP-4 and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level.

SUBCELLULAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: Detected in skeletal muscle and in trace amounts in Leukocytes.

SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular characterization of two murine eosinophil beta chemokine
                                                                                                                                                                                                                                                   HAWAP, MF_0103; -; 1.

HARAP, MF_0103; -; 1.

InterPro; IPR004839; Aminotrans_I/II.

InterPro; IPR001917; Aminotrans_II.

InterPro; IPR001917; Aminotrans_II.

InterPro; IPR001917; Aminotrans_II.

InterPro; IPR00185; aminotran 1 2; 1.

IGRFAMS; IGRN; ITGROII41; hisC; 1.

PROSITE; PS00599; Aminotran 1 2; 1.

PROSITE; PS00599; Aminotransferase; Aminotransferase; Pridoxal phosphate; Complete proteome.

Pyridoxal phosphate; Complete proteome.

Pyridoxal phosphate; Complete proteome.

Pyridoxal POSPHATE (BY SIMILARITY).

SEQUENCE 342 AA; 38941 MM; F71DAOFP66191D80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB 1;
Pred. No. 4.1;
5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=129/SvJ;
MEDLINE=95340546; PubMed=7542241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunol. 155:5299-5305(1995).
                                                                                                                                                                        EMBL; AE000963; AAB89229.1; -. PIR; G69502; G69502.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                               HSSP; P06986; 1FG7.
TIGR; AF2024; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MIP-1 alpha RL2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=129/Sv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gerard C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CKR3 MO
P51678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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"Cloning of a Kenopus laevis muscarinic receptor encoded by an intronless gene.", 1000 May 1994).
FEBS Lett. 352:175-179(1994).
-!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS CELLULAR RESPONSES, INTENDING INHIBITION OF ADENYLATE CYCLASE, BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS Gaps Xenopus laevis (African clawed frog). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae, ô Length 359; 8; Indels MGD; MGI:10461b; ucrs.
GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0006935; P:chemotaxis; IDA.
InterPro; IPR000276; GPCR_Rhodpsn. EXTRACELLULAR (POTENTIAL). 2 (POTENTIAL). EXTRACELLULAR (POTENTIAL). 6 (POTENTIAL). EXTRACELLULAR (POTENTIAL). 7 (POTENTIAL). 4 (POTENTIAL). EXTRACELLULAR (POTENTIAL) 5 (POTENTIAL). R -> S (IN REF. 2). AC11ED66E283CEAF CRC64; 1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL). 3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL). S (FOIENTIAL). CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL).

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EMBL; X65865; CAA6694.1; ...

EMBL; X67867, CAACOLTIAL).

ET RANSMEM 33 3 (POTENTIAL).

ET TRANSMEM 108 129 CYTOPLASMIC (POTENTIAL).

ET TRANSMEM 108 CAACOLTIALS.

THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS INHIBATION OF ADENYLAPTE CYCLASS. SUBCELLULAR LOCATION. INTEGRIAL membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.7%; Score 48; DB 1; Length 484; 63.6%; Pred. No. 5.8; 0; Indels ive 4; Mismatches 0; Indels
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Best Local Similarity 63.6
Matches 7; Conservative
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Search completed: September 28, 2004, 09:04:07 Job time : 7.875 secs 420 PYNVMVLINTF 430 g

2 PYNIVLLLNTF 12

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Gaps

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
OM protein - protein search, using sw model
Run on: September 28, 2004, 08:56:16; Search time 35.2 Seconds (without alignments) 197.199 Million cell updates/sec
Title: US-10-084-913-14 Perfect score: 118 Sequence: 1 APYNIVLLINTFQEFFGINNCS 22
Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041
Minimum DB seq length: 0 Maximum DB seq length: 200000000
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database : SPTREMBL 25:* 1: sp_archea:* 2: sp_bacteria:* 3: sp_fungi:* 4: sp_human:* 5: sp_invertebrate:* 6: sp_mammal:* 7: sp_mo:* 8: sp_organelle:* 9: sp_plant:* 10: sp_plant:* 11: sp_rodent:* 12: sp_virus:* 13: sp_virus:* 14: sp_unclassified:* 15: sp_virus:* 16: sp_bacteriap:* 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Ol4694 homo sapien	Q9tuq7 erythrocebu		Q9un26 homo sapien	homod	Q9ubj7 homo sapien	рошо	Q9un27 homo sapien	homo	hylok		Q9tuu9 cercopithec	Q9tuw8 gorilla gor	_	Q9tuw9 hylobates c	Q9tsq1 cercopithec	
SUMMARIES	ΩI	014694	Q9TUQ7	Q9UN24	Q9UN26	Q9UN23	Q9UBJ7	Q9UN25	Q9UN27	Q9UBT9	OMOLGO	Q9TUX1	QUITUO	Q9TUW8	Q9TUT4	Q9TUW9	Q9TSQ1	
	DB	4	9	4	4	4	4	4	4	4	ø	φ	φ	9	φ	9	9	
	Query Match Length DB	333	334	339	339	339	339	339	339	339	339	339	339	339	339	339	339	
ф	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
	Score	118	118	118	118	118	118	118	118	118	118	118	118	118	118	118	118	
	Result No.	-	71	m	4	ហ	φ	7	Ф	σv	10	11	12	13	14	15	16	

Q9tuu8 cercopithec					saguin	macaca f	macaca										Q9tuw7 pan troglod	pongo	papio	macaci	Q9tqv2 papio papio		Q9tuq8 cercopithec				Q9tut6 macaca neme	. Q9tqx2 erythrocebu	
6 Q9TUU8	6 Q9TQW4																	6 Q9TUW3					6 Q9TUQ8					6 Q9TQX2	
339	339	m	339	3	m	m	m	m	3	m	3	m	3	m	m	3	3	m	m	3	339	3	ŝ	339	3	339	339	339	
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
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ALIGNMENTS

RESULT 1 Old694 DC 014694 DC 0
14694 Ol4694 PRELIMINARY; PRT; 333 AA. Ol4694; PRELIMINARY; PRT; 333 AA. Ol-JAN-1998 (TEMBLrel. 05, Created) Ol-JAN-1998 (TEMBLrel. 05, Last sequence update) Ol-JAN-1998 (TEMBLrel. 24, Last annotation update) CCR5 receptor (Fragment). CCR5. Homo sapiens (Human). Eukaryota; Metaza; Chordata; Craniata; Vertebrata; Euteleost Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCB1 TaxID=9606; OCB1 TaxID=9606; INSEL TaxID=9606; ADB2 Res. Hum. Retroviruses 0:0-0(1997). ADB3 Res. Hum. Retroviruses 0:0-0(1997). EMB1, AFO11504; AAB657041. ADB5 Res. Hum. Retroviruses 0:0-0(1997). EMB1, AFO11504; AAB657041. GO; GO:00001587; Frinceptor to membrane; IEA. GO; GO:0001587; Frinceptor activity; IEA. GO; GO:0001587; Frinceptor activity; IEA. GO; GO:0001587; Frinceptor coupled receptor activity; IEA. GO; GO:0001587; Frinceptor coupled receptor activity; IEA. GO; GO:0001587; Frinceptor Coupled receptor protein signalir InterPro; IRRO0276; GPRC Rhodpsn. PROSITE; PS50262; GPRCTEIN RECEP F1 1; 1. PROSITE; PS50262; GPRCTEIN RECEP F1 1; 1. PROSITE; PS50262; GPRCTEIN RECEP F1 2; 1. Receptor. NON TER 333 A3; 38174 MW; AEFBA07A67893AEB CRC64; SECUENCE 333 AA; 38174 MW; AEFBA07A67893AEB CRC64; Duery Match ON 100 100 100; Prec 100; Prec 100; Indels 0; Mismatches 22; Conservative 0; Mismatches 0; Indels 0
14694 O14694 O14694 O1-JAN-1998 (TREMBLrel. 05, La O1-JAN-1998 (TREMBLrel. 24, La CCR5 receptor (Fragment). Homo sapiens (Human). Eukaryota, Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI TaxID=9606; [1] SEQUENCE FROM N.A. Zhang L., Carruthers C.D., He Ho D.D.; "HYV1 subtypes, co-receptor u AIDS Res. Hum. Retroviruses 0: EMBL; ARD11504; AAB65704.1; G0; G0:00016071; C:integral to G0; G0:00016071; C:integral to G0; G0:00016071; C:integral to G0; G0:0001607; C:integral to G0; G0:000180; P:receptor act FRESTOR PROJET; PSS00237; GFRRHODDPSN. PROSITE; PSS00237; GFRRHODDPSN. PROSITE; PSS00237; GFRRHODPSN. PROSITE; PSS00237; GFRRHODPSN. PROSITE; PSS00237; GFRRHONPR. RECEPTOR. NOM TER. S33 333 S33 333 SECUENCE 333 AA; 38174 MM; SURLY MATCH ION.0%; SACCHES 22; CORSERVATIVE 0;
14694 O14694 O14694 O1-JAN-1998 (TREMBLrel. 05, La O1-JAN-1998 (TREMBLrel. 24, La CCR5 receptor (Fragment). Homo sapiens (Human). Eukaryota, Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI TaxID=9606; [1] SEQUENCE FROM N.A. Zhang L., Carruthers C.D., He Ho D.D.; "HYV1 subtypes, co-receptor u AIDS Res. Hum. Retroviruses 0: EMBL; ARD11504; AAB65704.1; G0; G0:00016071; C:integral to G0; G0:00016071; C:integral to G0; G0:00016071; C:integral to G0; G0:0001607; C:integral to G0; G0:000180; P:receptor act FRESTOR PROJET; PSS00237; GFRRHODDPSN. PROSITE; PSS00237; GFRRHODDPSN. PROSITE; PSS00237; GFRRHODPSN. PROSITE; PSS00237; GFRRHODPSN. PROSITE; PSS00237; GFRRHONPR. RECEPTOR. NOM TER. S33 333 S33 333 SECUENCE 333 AA; 38174 MM; SURLY MATCH ION.0%; SACCHES 22; CORSERVATIVE 0;
14694 O14694 O14694 O1-JAN-1998 (TREMBLrel. 05, La O1-JAN-1998 (TREMBLrel. 24, La CCR5 receptor (Fragment). Homo sapiens (Human). Eukaryota, Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI TaxID=9606; [1] SEQUENCE FROM N.A. Zhang L., Carruthers C.D., He Ho D.D.; "HYV1 subtypes, co-receptor u AIDS Res. Hum. Retroviruses 0: EMBL; ARD11504; AAB65704.1; G0; G0:00016071; C:integral to G0; G0:00016071; C:integral to G0; G0:00016071; C:integral to G0; G0:0001607; C:integral to G0; G0:000180; P:receptor act FRESTOR PROJET; PSS00237; GFRRHODDPSN. PROSITE; PSS00237; GFRRHODDPSN. PROSITE; PSS00237; GFRRHODPSN. PROSITE; PSS00237; GFRRHODPSN. PROSITE; PSS00237; GFRRHONPR. RECEPTOR. NOM TER. S33 333 S33 333 SECUENCE 333 AA; 38174 MM; SURLY MATCH ION.0%; SACCHES 22; CORSERVATIVE 0;
14694 O14694 O14694 O1-JAN-1998 (TREMBLrel. 05, La O1-JAN-1998 (TREMBLrel. 24, La CCR5 receptor (Fragment). Homo sapiens (Human). Eukaryota, Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI TaxID=9606; [1] SEQUENCE FROM N.A. Zhang L., Carruthers C.D., He Ho D.D.; "HYV1 subtypes, co-receptor u AIDS Res. Hum. Retroviruses 0: EMBL; ARD11504; AAB65704.1; G0; G0:00016071; C:integral to G0; G0:00016071; C:integral to G0; G0:00016071; C:integral to G0; G0:0001607; C:integral to G0; G0:000180; P:receptor act FRESTOR PROJET; PSS00237; GFRRHODDPSN. PROSITE; PSS00237; GFRRHODDPSN. PROSITE; PSS00237; GFRRHODPSN. PROSITE; PSS00237; GFRRHODPSN. PROSITE; PSS00237; GFRRHONPR. RECEPTOR. NOM TER. S33 333 S33 333 SECUENCE 333 AA; 38174 MM; SURLY MATCH ION.0%; SACCHES 22; CORSERVATIVE 0;
SUL 4691 901 2016 3016

1 APYNIVLLINTFQEFFGLNNCS 22

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Pfam; PF00001; 7tm i; 1.

PRINTS; PR00237; GPCRADOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
C-C chemokine receptor 5 (Fragment).
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InterPro; IPR000276; GPCR_Rhodpsn.
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Best Local Similarity 100.0
Matches 22; Conservative
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                                                                                                            Receptor.
NON TER
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SEQUENCE
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Q9UN26;
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001584; F:G-protein coupled receptor protein signalin. .; IEA.
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GO; GO:0001684; F:receptor activity; IEA.
GO; GO:0001886; F:receptor activity; IEA.
GO; GO:0007186; F:receptor noupled receptor protein signalin. . .; IEA.
InterPro; IPR00027; GPCR_Rhodpsn.
PRINTS; PR00237; GPROTEIN RECEP_F1.1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1.2; 1.
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCR5 genes from diverse simian and prosimian
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                         Erythrocebus patas (Red guenon) (Hussar).
Bukaryota: Metacoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Erythrocebus.
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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0.1.MAY-2000 (TrEMBLrel. 13, Last sequence update)
0.1.UN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                      334 AA.
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       230 APYNIVLLLNTFQEFFGLNNCS 251
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22; Conservative 0
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                                                                                                                      PRELIMINARY;
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09UN24;
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Matches
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kulken C., Marx P., Wolinksy S., Shibata R., Yoder A., Pillai S., Kulken S., Marx P., Wolinksy S., "Sequences of the CCRS genes from diverse simian and prosimian
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:000186; F:receptor activity; IEA.
GO; GO:0007186; F:receptor activity; IEA.
GO; GO:0007186; F:G-protein coupled receptor protein signalin.
InterPro; IRRO0276; GFCR.Rhodpsn.
Pfam; PF00001; 7tm 1: 1.
PRINTS; PR00237; GFCRRHODOPSN.
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100.0%; Score 118; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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339 339
339 AA; 39162 MW; AS6369FE0529F4AB CRC64;
339 AA; 39066 MW; 8BAF02E19423BF79 CRC64;
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Last sequence update)
Last annotation update)
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01-May-2000 (TrEMBLrel. 13, Last sequence update)
01-May-2003 (TrEMBLrel. 24, Last annotation update)
C-C Chemckine receptor 5 (Fragment).
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100.0%; Pred. No. 2.1e-10;
ative 0; Mismatches 0;
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PRELIMINARY;
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SEQUENCE
                                                                                                                                                                                                     Q9UN25
Q9UN25;
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Q9UN27;
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Q9UN27
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Submitted (UTL-1999) to the EMBL/GenBank/DDBJ databases.

REMBL; AF161921; AAD47678.1; -..

RGO; GO:0016021; C:integral to membrane; IEA.

RGO; GO:001681; F:receptor activity; IEA.

RGO; GO:0001584; F:receptor activity; IEA.

RGO; GO:0001584; F:receptor activity; IEA.

RGO; GO:0001186; P:G-propein-like receptor protein signalin. .;

RIGEPPRO; IFR000276; GPCR_Rhodpsn.

R Pfam; PF00001; 7tm 1; 1.

RR PRINTS; PR00237; GFRRADOPSN.

RRSCEP_F1_1; 1.

RRSCITE; PS00237; GFRRENEN_RECEP_F1_2; 1.
                                                                                          Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Stulbata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinkay S.; Stulbata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinkay S.; Species."; United CRS genes from diverse simian and prosimian species."; Junited (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF161920; AAD47677.1; "embrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0001864; F:rhodopsin.like receptor protein signalin. ..; InterPro; IPR000276; GPCR_Rhodpsn.

R GO; GO:00001786; P:GPCRRHODDPSN.

R PRINTS; PRO0237; GPCRRHODDPSN.

R PRINTS; PS00237; G PROTEIN RECEP FI.; 1.

R PROSITE; PS50262; G_PROTEIN_RECEP FI.2; 1.
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K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; "Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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339 339
339 AA, 39128 MW, 9C3369FFF1F2F27A CRC64;
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339
SEQUENCE 339 AA, 39115 MW, 3C6369F922C91AA7 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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Best Local Similarity
Matches 22; Conserv
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tes 22; Conserv
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NON TER
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094947
1D 09498
1D 01-M
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A SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; Subitted (JUL.1999) to the EMBL/GenBank/DDBJ databases.

EMBL: Applies AAD47675.1; Embly GenBank/DDBJ databases.

RR GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:001584; F:receptor activity; IEA.

GO; GO:001584; F:rhodopsin like receptor protein signalin...; InterPro; IPR000276; GPCR_Rhodpsn.

RR GO; GO:0001786; PG-Protein coupled receptor protein signalin...; PRINTS; PR00237; GPROTEIN RECEP_F1_1; 1.

RR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID=9606;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
VCBI_TaxID=9606;
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Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels C
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339 339
339 AA, 39146 MW, 10FE05FE5371D4B3 CRC64;
                                                                                                                                                                             01-WAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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242 APYNIVLLINTFQEFFGLNNCS 263
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EMBL; AF162024; AAD47779.1; --
EMBL; AF162024; AAD47779.1; --
EMBL; AF161889; AAD47779.1; --
EMBL; AF161889; AAD477646.1; --
EMBL; AF161889; AAD47646.1; --
EMBL; AF161889; AAD4779.1; --
EMBL; AF161889; AAD4779.1; --
EGO (GO:0016012); F:receptor activity; IEA.
EGO (GO:0001284; F:rhodopsin-like receptor protein signalin. ..; IEA.
InterPro; IPR000276; GFCR_Rhodopsn.
PROMING; PRO0237; GERRHODOPSN.
PROSITE; PS50262; G-PROTEIN_RECEP_F1_1; 1.
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BMRI, Ap161897, AAD4764.1; -

GO, GO:0016621; C:integral to membrane; IEA.

GO, GO:0016872; F:receptor activity; IEA.

GO, GO:0001884; F:rhodepsin-like receptor activity; IEA.

GO, GO:0001886; P:G-protein coupled receptor protein signalin. .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCR5 genes from diverse simian and prosimian
species.",
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                               Eŭkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hylobatidae, Hylobates.
NCBI_TaxID=29089;
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
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01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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BRNNS; PR00237; GPCRAHOODSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS00262; G PROTEIN RECEP F1 2; 1.
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NON TER
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SEQUENCE
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NON TER
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EMEL; AF161915; AAD47661.1; --
EMEL; AF161915; AAD47661.1; --
EMEL; AF161911; AAD47661.1; --
EMEL; AF161911; AAD47661.1; --
EMEL; AF161912; AAD47669.1; --
EMEL; AF161919; --
EMEL; AAD47669.1; --
EMEL; AF161919; --
EMEL; AAD47669.1; --
EMEL; AAD47669.1; --
EMEL; AF161919; --
EMEL; AAD47669.1; --
EMEL
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186, P:G-potein coupled receptor protein signalin. . .; IEA.
InterPro; IPR000276; PFORTRhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRIMTS; PR00273; GPCRHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 100.0%; Score 118; DB 4; Length 339; 1 Similarity 100.0%; Pred. No. 2.1e-10; 22; Conservative 0; Mismatches 0; Indels
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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339 339
339 AA, 39086 MW, 88AD8B44E2CB4EC2 CRC64;
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339 339
339 AA; 39114 MW; 3C6369F92C29F4A7 CRC64;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemckine receptor 5 (Fragment).
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Matches 22; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibate R., Tohen Z., Fillai S., Kuiken C., Marx P., Wolinksy S.; Shibate R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S.; Shibate R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. GO, GO:0004872; F:receptor membrane; IEA. GO, GO:000186; F:receptor activity; IEA. GO, GO:000186; F:receptor activity; IEA. GO, GO:000186; F:receptor coupled receptor protein signalin. ..; IEA. InterPro; IPRO00276; GPCR_Rhodpsn.
                                                                       species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

B. Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

R. GO; GO:0016021; C:integral to membrane; IEA.

R. GO; GO:0001881; F:receptor activity; IEA.

R. GO; GO:0001884; F:rbeceptor activity; IEA.

R. GO; GO:0001884; F:rbeceptor activity; IEA.

R. GO; GO:0001884; F:rbeceptor activity; IEA.

R. GO; GO:000188; F:rbeceptor coupled receptor protein signalin. . .;

R. PFEMPY; PRO0021; Tum 1; 1.

R. PRINTS; PRO0237; GPCRHHODOPSN.

R. PROSITE; PS00237; GPCRHODOPSN.

R. PROSITE; PS00237; GPCRHODOPSN.

R. PROSITE; PS00237; GPCREIN_RECEP_FI_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca nemestrina (Pig-tailed macaque).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Emmalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy & "Sequences of the CCRS genes from diverse simian and prosimian
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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100.0%; Pred. No. 2.1e-10;
Live 0; Mismatches 0;
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PRINTS; PR00237; GPCRHOODSN.
PROSITE; PS00237; G PROTEIN RECEP P1 1; 1.
PROSITE; PS00262; G PROTEIN_RECEP P1 2; 1.
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hes 22; Conserv
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gorilla gorilla gorilla (Lowland gorilla).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cercopithecus diana (Diana monkey).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bammalia; Dutheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Cercopithecus.
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                                                                                                        Length 339;
                                                                                                        Query Match 100.0%; Score 118; DB 6; Length 3
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels
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                      339 339
339 AA; 39075 MW; 09257FBFB834C4AE CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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OPRAT-2000 (TrEMBLrel. 13, Created)

01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

01-MAY-2003 (TrEMBLrel. 24, Last annotation update)

C-C chemokine receptor 5 (Fragment).
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22; Conservative
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RESULT 15 Q9TUW9

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Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161949; AAD4705.1; ---
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:001884; F:receptor activity; IEA.
GO; GO:001886; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; F:rhodopsin-like receptor protein signalin. .; IEA.
InterPro; IPR000276; GPCR_Rhodopsn.
PROSITE; PS00037; GFCRHODOSN.
PROSITE; PS00037; GFCRHODOSN.
PROSITE; PS00237; GFRHODOSN.
PROSITE; PS00237; GFRHODOSN.
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ammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kulken C., Marx P., Wolinksy S.;
"Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                   Length 339;
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339 339 330 MW; 847E935FA403E52D CRC64;
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339 339
339 AA, 39049 MW; 6D1A93F66270F3ED CRC64;
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01-MAX-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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Last annotation update)
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100.0%; Pred. No. 2.1e-10;
iive 0; Mismatches 0;
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; Pred. No. 2.1e-10;
0; Mismatches 0;
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
Receptor. 1
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SEQÜENCE 339 AA; 39216 MW; 847E935FA40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cercopithecus diana (Diana monkey)
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Best Local Similarity 100.0%;
Matches 22; Conservative 0
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es 22; Conservative
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EMBL; AF161890; AAD4747.1;

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0001884; F:rbodepin-like receptor activity; IEA.

GO; GO:0001886; F:G-Protein coupled receptor protein signalin. .; IEA.
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Submitteed (UUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF162023; AAD47778.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:00018972; F:receptor activity; IEA.
GO; GO:0001894; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001896; F:rhodopsin-like receptor protein signalin. .; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
PFam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
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                                                                                                                                                                                                        Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hylobatidae, Hylobates.
NCBI TaxID=29089;
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K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cerropithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 118; DB 6; Length 339;
; Pred. No. 2.1e-10;
0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          339 339
339 AA; 39024 MW; EC4CE48DEEEF107E CRC64;
                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MXY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEAM; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G-PROTEIN RECEP_F1 1; 1.
PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
                                                                                                                                              C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 APYNIVLLINTFQEFFGLINCS 263
                                                                                                                                                                                           Hylobates concolor (crested gibbon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cercopithecinae, Cercopithecus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 22, Conservative
                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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RESULT 16 Q9TSQ1

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242 APYNIVLLLNTFQEFFGLNNCS 263

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NCBI_TaxID=9598;

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Erythrocebus patas (Red guenon) (Hussar).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Erythrocebus.
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Kunstman R., Chen Z., Pillai S., Kuiken C., Marx P., Wolinksy S.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 118; DB 6; Length 339; 100.0%; Pred. No. 2.1e-10; rive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                339 AA; 39150 MW; 847D5F92BB03E6E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAY-2003 (TrEMBLrel. 24, Last annotation update) C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                        01-MAY-2000 (TYEMBLrel. 13, Created)
01-MAY-2000 (TYEMBLrel. 13, Last sequence update)
01-UJN-2003 (TYEMBLrel. 24, Last amnotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                               Cercopithecus nictitans (white-nosed guenon).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 AA.
                                                                                                                                                                                           339 AA
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PRINTS; PR00237; GPCRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 APYNIVLLINTFQEFFGLNNCS 263
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nes 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                              Q9TQU7
Q9TQU7;
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10 09TU05
10 PUTU06
AC 09TU06
DDT 01-MADDT 01-MADDT 01-MADDT 01-MADDT 01-MADDT 01-MADDT 00-MADDT 00-M
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                              EXPUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;

"Sequences of the CCRS genes from diverse simian and prosimian

species.";

Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; API61901; AAD47662.1; -.

EMBL; AF161901; AAD47662.1; -.

EMBL; AF161901; AAD47662.1; -.

EMBL; AF161901; AAD47661.1; -.

EMBL; AF161901; ALD47661.1; -.

EMBL; ALD47661.1; -.

EMBL; AF161901; ALD47661.1; -.

EMBL; A
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I. Submitter (Jul-1999) to the EmBL/GenBank/DDBJ databases.

EMBL, AF161903; AAD47660.1; C. nembrane; IEA.

GO, GO:0001584; P:rhodopsin-like receptor activity; IEA.

GO, GO:0001586; P:G-protein coupled receptor protein signalin. .; IEA.

InterPro; IPR000276; GPCR_Rhodpsn.

R GO: GO:000237; GPCRHODOPSN.

PRINTS; PR00237; GPRCHENDOPSN.

PROSITE; PS00237; GPROTEIN_RECEP_FI_1; 1.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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339 AA; 39159 MW; 8E699E882BAC0E84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339 AA; 39129 MW; 4A88F8BB601D46A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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100.0%; Score 118; DB 6;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 118; DB 6; 100.0%; Pred. No. 2.1e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22; Conservative
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Best Local Similarity
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EMBL; AF161972; AAD47727.1; ...
EA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:000186; P:Corein coupled receptor protein signalin. ..; IEA.

TherePro; PR000276; GPCR_Rhodopsn.
PROSITE; PS00237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_FI_1; 1.
                                                                                                                                                           Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
mamalia, Butheria, Primates; Catarrhini, Cercopithecidae,
Cercopithecinae; Macaca,
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCR5 genes from diverse simian and prosimian species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF161954; AAD47710.1; -
EMBL; AF161954; AAD47710.1; -
EMBL; AF161952; AAD47706.1; -
EMBL; AF161952; AAD47706.1; -
EMBL; AF161952; AAD47708.1; -
EMBL; AF161952; Preceptor activity; IEA.
GO; GO:0001584; Fracceptor activity; IEA.
GO; GO:000186; Preceptor activity; IEA.
InterPre; IPR000276; GPCR_Rhodpsin...
InterPre; IPR000276; GPCR_Rhodpsin...
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kulken C., Marx P., Wolinksy S.,
"Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 118; DB 6; Length 339; 100.0%; Pred. No. 2.1e-10; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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339 339
339 AA; 39097 MW; CS76E7AA492D7080 CRC64;
               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE, PS00237; G_PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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PRINTS; PR00237; GPCRRHODOPSN.
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22; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                  A PACE OF THE PROPERTY OF THE 
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

BMBL, AR162054; AAD47809.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016021; F:receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001186; F:rhodopsin-like receptor protein signalin. .; IEA.

InterPro; IRR00226; GPCR.Rhodpsn.

PRINTS; PR00021; GGRR.Rhodpsn.

PRINTS; PR00021; GGRR.Rhodpsn.

PROSITE; PS500237; GGRR.HODPSN.

PROSITE; PS500237; GFRR.HODPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
NCBI_TaxID=100754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           r species..;
L Submitted (ULL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF16,2015; AAD47770.1;
R GO; GO:0016021; C:integral to membrane; IEA.
R GO; GO:00164872; F:receptor activity; IEA.
R GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
R GO; GO:0007186; F:rhodopsin-like receptor protein signalin...;
R InterPro; IPR000276; GPCR_Rhodpsn.
R Pfam; PF00001; 7mm 1; 1.
P Ffam; PF00001; 7mm 1; 1.
R PRINTS; PR00237; GPRRHODOPSN.
R PROSTIE; PS00237; GPROTEIN RECEP F1 1; 1.
R PROSTIE; PS00262; G-PROTEIN_RECEP F1 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 118; DB 6; Length 339; 100.0%; Pred. No. 2.1e-10; trive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 339;
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                                                                                                                                                                                                                                                                                                                                                                                              339 339
339 AA; 39048 MW; 1A2E19E3A6A5A52A CRC64;
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339 339
339 AA; 39063 MW; 76BCE7A84B877085 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MYY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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; Pred. No. 2.1e-10;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 APYNIVLLINTFQEFFGLNNCS 263
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ilarity 100.0%;
Conservative 0
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Les 22; Conservative
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nes 22; Conserv
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Matches
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Q9TUR9
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339 AA.

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EMBL; AF162005; AAD47760.1; -.
EMBL; AF162001; AAD47755.1; -.
EMBL; AF162001; AAD47755.1; -.
EMBL; AF162001; AAD47757.1; -.
EMBL; AF162003; AAD47757.1; -.
EMBL; AF162003; AAD47757.1; -.
EMBL; AF162004; Cintegral to membrane; IEA.
GO; GO:00011884; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
FFEAN; PF00001; 7tm 1: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Colobus guereza (Black-and-white colobus monkey).
Bukaryota; Mecazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                                                                                  species..;
Submitted (JUL.1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF162026; AAD47781.1; -.
EMBL, AF162026; AAD47781.1; -.
GO), GO:0016021; C:integral to membrane, IEA.
GO), GO:0004872; F:receptor activity; IEA.
GO), GO:0004812; F:receptor activity; IEA.
GO), GO:000186; P:G-protein coupled receptor protein signalin. .;
InterPro; IPR000276; GPCR_Rhodpsn.
PRINTS, PR00017, 7tm 1; 1.
PRINTS, PR000217; GFCRHUDDPSN.
PROSITE; PS50262; GFORTEIN RECEP_F1_1; 1.
                                SEQUENCE FROM N.A. Korber B., Oprondek J., Stanton J., Agy M., Kunstman K., Chen Z., Korber B., Chrostan R., Wolinksy S.; Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; "Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
Sequences of the CGR5 genes from diverse simian and prosimian
species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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339 AA; 39168 MW; 6A4BF72FBBFF566F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            39178 MW; 9DF2A6F446C55AED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPTOV6;
01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 118; DB 6;
100.0%; Pred. No. 2.1e-10;
ive 0; Mismatches 0;
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PROSITE; PS00237; G PROTEIN RECEP_F1_1;
PROSITE; PS50262; G PROTEIN RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 APYNIVLLINTFQEFFGLNNCS 263
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                                                                                                                                                                                                                                                                                                                                                                    Receptor.
NON_TER 1
NON_TER 339 33
SEQUENCE 339 AA; 3
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MCBI_TaxID=100936;
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NCBI_TaxID=33548;
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Runstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
A Shibara R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
Sequences of the CCR5 genes from diverse simian and prosimian
species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, APIG1953; ApAD4709-1;
RGO; GO:0004872; F:receptor activity; IEA.
RO; GO:00016021; C:integral to membrane; IEA.
RO; GO:000186; P:G-protein coupled receptor protein signalin. .; IEA.
InterPro; IPR00276; GPCR_Rhodpsn.
RPML, PR00217; GFCRRHODDENN.
RRMIS; PR00237; GFCRRHODDENN.
RROSITE; PS00237; GFRRHODDENN.
RROSITE; PS00262; G_PROTEIN_RECEP_FI_2; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCR5.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
NCBI_TaxID=9541;
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                                                                                                                           Length 339;
                                                                                                                                                               Indels
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339 339
339 AA, 39137 MW, 9E626ED3288607C1 CRC64;
                                                                                    SBFCBC5BA96C2F9E CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UJUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment);
                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNAY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                      Match 100.0%; Score 118; DB 6; Local Similarity 100.0%; Pred. No. 2.1e-10; les 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                     339 AA
    PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                                                                                                                                                                                                        1 APYNIVLLINTFORFFGLNNCS 22
                                                                                  339 AA; 39067 MW;
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                                             339
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Q9TSN2;
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CCR5. RESULT 26
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AC Q9TUR
AC Q9TUR
DT 01-MA
DT 01-MA
DT 01-MC
CG
GN CCR5.
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OS EUKAR

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Gaps

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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
NCBI_TaxID=9542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; "Sequences of the CCR5 genes from diverse simian and prosimian
Species.";
Submitted (UTL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161951; AAD47707.1;
GO; GO:0016021; C:Integral to membrane; IEA.
GO; GO:0018622; F:receptor activity; IEA.
GO; GO:0001864; F:rhodopsin-like receptor activity; IEA.
GO; GO:000186; P:GPorotein coupled receptor protein signalin.
InterPro; IPR000276; GPCR_Rhodpsn.
PRINTS; PR000237; GPCRHODOPSN.
PROSITE; PS000237; GPCRHODOPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 118; DB 6; Length 339; 100.0%; Pred. No. 2.1e-10; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                            339 AA; 39098 MW; F0132E8BC44EF829 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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Macaca fuscata (Japanese macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
nes 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          339
                                                                                                                                                                                                                                                                                                                                                         Receptor.
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Best Local
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Matches
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Q9TQV0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecus mona.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCRS genes from diverse simian and prosimian
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K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota; Meretazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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         Length 339;
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                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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339 339
339 AA; 39019 MW; 7176F940AF11F3ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
100.0%; Score 118; DB 6;
100.0%; Pred. No. 2.1e-10;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339 AA.
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                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                     1 APYNIVLLLNIFOEFFGLNNCS 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cercopithecinae, Cercopithecus.
NCBI_TaxID=36226;
                                                             22; Conservative
                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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   Query Match
Best Local Similarity
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NON TER
NON TER
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                                                                                                                                                                                                                                                            RESULT 28
109700
AC 09700
AC 09700
AC 01-MA
DT 01-MA
DE C-C C
GENCA
OC CECCO
OC CECC
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Q9TSN3
                                                             Matches
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF161955; AAD47711.1;

GO; GO:0016201; C:integral to membrane; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0007186; F:rhodopsin-like receptor protein signalin. .; IEA.

InterPro; IFR00027; GPCR_Rhodopsn.

PRAM, FP00001; Thull.

PRINTS; PR00237; GPCRENHODOPSN.

PROSITE; PS00237; GPROTEIN RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                            339 339 34; C576E7AA492D7080 CRC64;
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Gaps

Q9TQV0

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EMBL; AFIG1995; AAA47750.1; ...
GO; GO:00146021; C:integral to membrane; IEA.
GO; GO:00146021; C:integral to membrane; IEA.
GO; GO:000481; F:receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
InterPro; IPRO00276; GPCR Rhodopsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCR5 genes from diverse simian and prosimian
species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCRS.

Papio papio (Guinea baboon).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Mammalia, Butheria, Primates; Catarrhini; Cercopithecidae;

Cercopithecinae, Papio.

NCBI_TaxID=100937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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                                                                                                                                                             Length 339;
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339 339 339 WW, 847F8F936B00E6E2 CRC64;
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339 AA; 39068 MW; 84EB018085DCOA62 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     Q9TUS7;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UMY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-TOW-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 118; DB 6;
100.0%; Pred. No. 2.1e-10;
tive 0; Mismatches 0;
                                                                                                                                                             100.0%; Score 118; DB 6; 100.0%; Pred. No. 2.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                        339 AA
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                                                                                                                                                                                                   0; Mismatches
                   PROSITE; PS00237; G PROTEIN RECEP F1 1; 1. PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                          242 APYNIVLLINTFQEFFGLNNCS 263
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                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                          1 APYNIVLLLNTFQEFFGLNNCS 22
  PRINTS; PR00237; GPCRRHODOPSN
                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
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Les 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                          Receptor.
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SEQUENCE
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SEQUENCE
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Q9TUS7
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EMBL; AF162046; AAD47801.1; -.

EMBL; AF162045; AAAD47801.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001186; F:G-protein coupled receptor protein signalin. ..; IEA.

InterPro; IPR000276; GPCR_Rhodpsn.

PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                         Species."; Submitted (JUL.1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF161989; AAD47743.1; --

R GO; GO:00166021; C:integral to membrane; IEA.

GO; GO:001684; F:rhedoptar activity; IEA.

GO; GO:0001884; F:rhedoptar activity; IEA.

R GO; GO:0001884; F:rhedoptar like receptor activity; IEA.

R GO; GO:000188; F:rhedoptar like receptor protein signalin. .;

R InterPro; IPR000276; GPCR-Rhodpsn.

R Pfam; PF00001; 7tm 1; 1.

R PROSITE; PS00237; GPCR-Rhodpsn.

R PROSITE; PS00237; GPCR-RHODPSN.

R PROSITE; PS00237; GPCR-RHODPSN.

R RECEPTOR II 1.

NON TER 339 339
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Butheria, Primates; Catarrhini, Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                    Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae, Cercopithecinae, Papio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCR5 genes from diverse simian and prosimian species.";
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 339;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) C-C chemokine receptor 5 (Fragment).
                     100.0%; Score 118; DB 6;
100.0%; Pred. No. 2.1e-10;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              339 AA.
  339 AA
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PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                     C-C chemokine receptor 5 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 APYNIVLLINTFQEFFGLNNCS 22
                                                                                                                                              Papio papio (Guinea baboon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similario,
hes 22; Conservative
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  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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RESULT 32

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Gaps

242 APYNIVLLLNTFQEFFGLNNCS 263

SEQUENCE FROM N.A.

SEQUENCE NON TER

Query Match Local

Matches

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Q9TUW3 RESULT 35 Q9TUW3

NCBI_TaxID=9598;

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species.";
submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF161997; AADJ-7752.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:001584; F:receptor activity; IEA.
GO; GO:0001584; F:receptor activity; IEA.
GO; GO:0007186; P:d-protein coupled receptor protein signalin. .; IEA.
InterPro; IFR00027; GPCR_Rhodpsn.
FRMINTS; PR00237; GPCRRHODPSN.
PROSITE; PS00237; GPRRHODPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca mulatta (Rhesus macaque).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia, Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECURICE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kulken C., Marx P., Wolinksy S.,
"Sequences of the CCR5 genes from diverse simian and prosimian
"Species."

Submitted (JUL.1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF161970; AAD47725.1; -.

EMBL, AF161970; Cintegral to membrane, IEA.

GO, GO:0106021; C:integral to membrane, IEA.

GO, GO:010612; F:receptor activity; IEA.

GO, GO:0101884; F:rhodopsin-like receptor activity; IEA.
                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                           Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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339 339
339 AA, 39028 MW; 8C9C978FD880B936 CRC64;
                                                                                      ch 100.0%; Score 118; DB 6; Similarity 100.0%; Pred. No. 2.1e-10; 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339 AA.
                                                  339 AA
                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 APYNIVLLINTFQEFFGLNNCS 263
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                                                                                                                                                                                    Papio papio (Guinea baboon)
                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                 Cercopithecinae, Papio.
                                                                                                                                                                                                                                                                  NCBI_TaxID=100937;
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SEQUENCE FROM N.A.
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Best Local &
                                                  Q9TUS5
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            RESULT 36
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                                 29TUS5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Species.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF161908; AAD47665.1;
GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:001684; F:receptor activity; IEA.

GO; GO:000186; P:receptor activity; IEA.

GO; GO:000186; P:receptor activity; IEA.

GO; GO:000186; P:receptor activity; IEA.

GO; GO:000187; F:receptor activity; IEA.

GO; GO:000187; F:receptor activity; IEA.

FIEA.

FEAR; PF0001; 7tm 1; FEA.

FEAR; FP0001; 7tm 1; FEA.

FEAR; FP0001; 7tm 1; Tm 1; Tm 1; FEA.

FROSITE; PS00237; G-PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                      . .; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCR5 genes from diverse simian and prosimian
species.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pongo pygmaeus (Orangutan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
NCBI_TaxID=9600;
                                                                     species.";
Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF16:1899; AAD47656.1;
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO, GO:0001584; F:rhodopsin-like receptor protein signalin.
InterPro; IPR000276; GPCR_Rhodpsn.
Fam: PF00001; 7tm_1; 1.
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0
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. Pred. No. 2.1e-10;
0; Mismatches 0; Indels 0
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Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels (
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339 339
339 AA; 39157 WW; 4A9EBAD183E8E72D CRC64;
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339 AA; 39103 MW; 4350C4625FB0657C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                            Pfam; PF00001; 7cm 1; 1. —
PRINTS; PR00237; GPCRHODDSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 APYNIVLLINTFQEFFGLNNCS 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 APYNIVLLINTFOEFFGLNNCS 22
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                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                22; Conservative
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Receptor. NON TER NON TER SEQUENCE

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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                     Cercopithecus mona.
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCRS genes from diverse simian and prosimian species.";
                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Papio.
VCBI_TaxID=100937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF161997, AAD47748.1; --

EMBL; AF161997, AAD47745.1; --

EMBL; AF161991, AAD47745.1; --

EMBL; AF161991, AAD47745.1; --

EMBL; AF161991, Cintegral to membrane; IEA.

GO; GO:0016197; F:rreceptor activity; IEA.

GO; GO:001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor protein signalin. .

EMBL; AF1619900275, GPCR. Rhodopsin-like receptor protein signalin.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
InterPro; IPR00276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GFCRHODDESN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
Receptor.
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                                                                                                                                            100.0%; Score 118; DB 6; Length 339; 100.0%; Pred. No. 2.1e-10;
                                                                                                                                                                     Indels
                                                                                             39079 MW; 7176E3EA0E00F3ED CRC64;
                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                         339
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                                                                                                                                                                                                            APYNIVLLINTFQEFFGLNNCS 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 APYNIVLLINTFOEFFGLINICS 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 APYNIVLLINIFQEFFGLNNCS 22
                                                                                                                                                                                              1 APYNIVLLINTFQEFFGLNNCS 22
                                                                                                                                                                                                                                                                                                                                                                                Papio papio (Guinea baboon)
                                                                                                                                                       Local Similarity 100.
tes 22; Conservative
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Q9TQV3
ID Q9TQV
AC Q9TQV
DT 01-MA
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SEQUENCE FROM N.A.

Kunstanan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wollnksy S.;
T sequences of the CCRS genes from diverse simian and prosimian

T species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF162040; AAD47795.1; -.

EMBL; AF162040; AAD47795.1; -.

ROGO: O016021; C:integral to membrane; IEA.

GO: GO: O016021; C:integral to membrane; IEA.

GO: GO: O016021; F:receptor activity; IEA.

GO: GO: O010186; P:G-protein coupled receptor protein signalin. .; III

InterPro; IPR00276; GPCR_Rhodpsn.

PROSITE; PR00237; GPCRRHODOFSN.

PROSITE; PS00237; GPCRRHODOFSN.

PROSITE; PS00237; GPCRRHODOFSN.

PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
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Bukaryota, Metazca, Chordata, Craniata, Vertebrata, Buteleostomi;

Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Cercopithecus.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mamalia, Eutheria, Primates, Cararrhini, Cercopithecidae, Cercopithecinae, Cercopithecinae, VCBI_TaxID=36226,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.
"Sequences of the CCR5 genes from diverse simian and prosimian species.";
Species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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339 339 MW; 7176E3EAOEOOF3ED CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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PROSITE; PS00237; GPROTEIN RECEP F1 1;
PROSITE; PS50262; GPROTEIN_RECEP_F1_2;
Receptor.
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SEQUENCE 339 AA, 39148 MW, 0CA289CDDEEDE831 CRC64;
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100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0

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Search completed: September 28, 2004, 09:06:20 Job time : 36.2 secs

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Aab83354 Human CCR

AAB83354

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        Aab88992 HIV gp120

        Aab88997 HIV gp120

        Aae14757 Human CCR

        Aae14759 Human CCR

        Aae14755 Human CCR

        Aae14755 Human CCR

        Aaw2710144 Human NOV

        Aaw27107 Human Che

        Aaw27103 Human Che

        Aaw27123 Macaque C

        Aaw27123 Human CC

        Aaw27123 Human CC

        Aaw8232 Human CC

        Aaw8232 Human GC

        Aay80128 Human G-P

        Aae07046 Human G-P

        Aae07047 Human G-P

        Aae07048 Human G-P

        Aae07048 Human G-P

        Aae07037 Human G-P

        Aae07038 Human G-P

        Aae07039 Human G-P

        Aae07039 Human G-P

        Aab66858 Human HDG

        Abb56342 Non-endog

                                                                    September 28, 2004, 08:51:21; Search time 42.975 Seconds (without alignments) 118.345 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                    1586107 segs, 282547505 residues
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Maximum Match 100%
Listing first 45 summaries
                                                 OM protein - protein search, using sw model
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AAE14757
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AAW2144
AAW27407
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AAW270000
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                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                   1 YAFVGEKFRNYLLVFFQK 18
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genescqp2000s:*
genescqp2001s:*
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genescqp2003s:*
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Maximum DB seq length: 200000000
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95
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Match
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Aab82948 Human G-D Aau97150 Human G-D Aau97150 Human G-D Aam52829 Human CC Abg70597 Human CC Abg70597 Human G-D Abg70591 Human G-D Abg81054 G-Drotein Abb081054 G-Drotein Abb081054 G-Drotein Abb705540 Human G-D Abr56602 Human G-D Abr6602 Human G-D Abr660343 Human G-C Abu61654 Human G-C Abu61654 Human G-C Abb81031 Human G-C Abb81031 Human G-C Abb810331 Human G-C Abb810331 Human G-C	TIS				glycoprotein 120; gp120; antagonist;								'HIV infection, have homology to receptors CCR5, CXCR4 and STRL33, rical conditions.		ir of peptides which are able to hase are similar to the human 1133, as well as CD4. These are prevent replication of the virus. I peptide of the invention		DB 4; Length 18; 8e-09; .hes 0; Indels 0; Gaps 0;
AABB2948 5 AAU97150 5 AAM52828 5 AAM52828 5 AAM52828 5 AAB692880 5 AAB692880 5 AAB692880 6 AAB692880 6 AAB692880 6 ABB81054 6 ABC5540 6 ABC75540 6 ABC75540 6 ABC75540 6 ABC75540 6 ABC75540 6 ABC75540 6 ABC75540	ALIGNMENT	; 18 AA.		peptide #75.	CD4; HIV; gly CD4; STRL33.			505.	.eo.	HUMAN SERVICES			or treating chemokine r physiolog	English.	describes a number of pen 120 (gpl20). These CR5, CXCR4 and STRL33, nt of HIV, as they previs an example of a pept.		%; Score 95; D %; Pred. No. 8e 0; Mismatches
20000000000000000000000000000000000000		standard; peptide	(first entry)	protein binding	kine receptor;	· w	-A2.	: 2000WO-US0235	99US-01512	рврт неалтн & н		44398/25.	peptides useful fo domains of human to HIV gp120 under	Page 37; 114pp;	nt invention descrive glycoprotein 12 receptors CCR5, Cthe treatment of the sequence is an	AA;	100.0% ilarity 100.0% Conservative
7 7 8 8 9 9 1 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	ULT 1	AAB88982	23-MAY-2001	HIV gp120 pi	Human chemok replication;	Homo sapiens	WO200116182-	08-MAR-2001.	7-AUG-1999	I SO (HSSO)	Saxinger C;	Ŋ	Novel polyperegions of cand binds to	Example 1; E	The present bind to HIV chemokine re useful in th	Sequence 18	Query Match Best Local Simi Matches 18;
	RESULT	XX ID	X E	X E	X & & :	*8\$	\$ E X	OG XX	X &	X & X	ž II X	S X	TA E	Y S X	\$888888\$	os -	Qu Be Ma

YAFVGEKFRNYLLVFFQK

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                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemoxine receptors CRS, CXCR4 and STRL13, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus. The present sequence is an example of a peptide of the invention
                                                                                                                           Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist; replication; CCR5; CXCR4; CD4; STRL33.
                                                                                                                                                                                                                                                                                                                                                                                    have homology to CXCR4 and STRL33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human CCR5 chemokine receptor deletion mutant fragment (aa 295-321).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemokine receptor CCR5; P2 protein; HIV infection; AIDS; human immunodeficiency virus; gene therapy; human; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 95; DB 4; Length 18; 100.0%; Pred. No. 8e-09; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Novel polypeptides useful for treating HIV infection, regions of domains of human chemokine receptors CCR5, and binds to HIV gpl20 under physiological conditions.
                                                                                                                                                                                                                                                                                                      (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                    HIV gp120 protein binding peptide #90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                        AAB88997 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YAFVGEKFRNYLLVFFOK 18
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                                                                                                                                                                                                                                                                              99US-0151270P
                                                                            (first entry)
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Best Local Similarity 100.
Matches 18; Conservative
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Synthetic.
                                                                                                                                                                                                                                                                              27-AUG-1999;
                                                                                                                                                                       Homo sapiens
                                                                           23-MAY-2001
                                                                                                                                                                                                                                                                                                                                   Saxinger C;
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                                                   AAB88997;
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The invention relates to nucleic acid encoding a protein which interacts with the carboxy terminus of the chemokine receptor CCR5 or of other chemokine receptor family members. Molecules of the invention are used to detect, prevent and treat HIV infection and progression to AIDS. Any CCR5 derived peptides, or compounds derived from the protein of the invention (e.g. antagonist or mutants) that disrupt binding of CCR5 to the protein of the invention would block HIV infection. The present sequence is human chemokine receptor CCR5 C-terminal fragment deletion mutant which is incapable of interacting with the protein of the invention
                                                                                                                                                                                                                                         Nucleic acid encoding a protein which interacts with the carboxy terminus of the chemokine receptor CCR5 isolated from a human B cell cDNA library is useful to detect, treat and prevent HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human CCRS chemokine receptor deletion mutant fragment (aa 295-337).
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            /note= "Wild-type Cys replaced by Glx"
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                      Schweneker
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                                                                                                                                                         (MOEL/) MOELLING K.
Misc-difference 27
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Synthetic.
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AAE14756
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John State of State Sta
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                                                                                  Nucleic acid encoding a protein which interacts with the carboxy terminus of the chemokine receptor CCR5 isolated from a human B cell cDNA library is useful to detect, treat and prevent HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to nucleic acid encoding a protein which interacts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor C-terminal mutant fragment (aa 295-352)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                          Example 2; Fig 2A; 28pp; English
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               Schweneker
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                                                WPI; 2002-437464/47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                               Sequence 43 AA;
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               Moelling K,
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with the carboxy terminus of the chemokine receptor CCRS or of other chemokine receptor family members. Molecules of the invention are used to detect, prevent and treat HIV infection and progression to AIDS. Any CCRS-derived peptides, or compounds derived from the protein of the invention (e.g. antagonist or mutants) that disrupt binding of CCRS to the protein of the invention would block HIV infection. The present sequence is human chemokine receptor CCRS C-terminal mutant fragment which is incapable of interacting with the protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding a protein which interacts with the carboxy terminus of the chemokine receptor CCRS isolated from a human B cell cDNA library is useful to detect, treat and prevent HIV infection.
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                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                      Length 58;
                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                                                                                                                                                                                                   ch 100.0%; Score 95; DB 5; I Similarity 100.0%; Pred. No. 2.8e-08; 18; Conservative 0; Mismatches 0;
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Pred. No. 2.8e-08;
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58
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human immunodeficiency vi
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Best Local Similarity
Matches 18; Conserv
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Best Local Similarity
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Binding-site
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The invention relates to novel isolated polypeptides, mature form of the polypeptide, a sequence that is 95% identical to the polypeptide or the polypeptide comprising one or more conservative substitutions. The NOVX polypeptide is useful for treating or preventing a pathology associated with the polypeptide e.g. disorders associated with aberrant expression or activity of the polypeptide, such as cancer, diabetes, obesity, and endocrine, CNS and inflammatory disorders. They can also be used in various detection and screening assays, chromosome mapping, tissue typing and predictive medicine. This sequence corresponds to one of the polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic, antidiabetic, anorectic, cerebroprotective, neuroprotective, antidiammatory; gene therapy, antisenspy, thyronimetic, NOVX; pathology, cancer; diabetes; obesity; endocrine disorder; CNS disorder; inflammatory disorder; chromosome mapping; tissue typing;
                                                                                                                    New isolated NOVX polypeptides and nucleic acid molecules useful for treating, preventing and diagnosing pathological conditions with NOVX-associated disorders, such as cancer, obesity, diabetes and inflammatory or CNS diseases.
Khramtsov NV, Li Liu X, Malyankar UM, Miller CE, Millet I;
Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;
Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK;
Spytek XA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 95; DB 7; Length 268; 100.0%; Pred. No. 1.4e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                            Claim 1; SEQ ID NO 162; 772pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human NOVX polypeptide SEQ ID NO: 164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADC10144 standard; protein; 268 AA.
                           ME, Shenoy SG, Shimker
Stone DJ, Vernet CAM,
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07-UTN-2001, 2001US-0296418P.
11-UTN-2001, 2001US-0297414P.
12-UTN-2001, 2001US-0295573P.
14-UTN-2001, 2001US-0295567P.
14-UTN-2001, 2001US-029858P.
15-UTN-2001, 2001US-029828P.
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04-JUN-2001; 2001US-0295661P.
06-JUN-2001; 2001US-0296404P.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
nes 18; Conservative
                                                      Lepley DM;
                                                                                 WPI; 2003-210149/20.
N-PSDB; ADC10141.
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                                                          Burgess CE,
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     Gaps
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     Indels
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       Mismatches
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2001US-0296404P
2001US-029641BP
2001US-029641BP
2001US-029741BP
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2001US-029828P
2001US-029828P
2001US-029828P
2001US-029828P
2001US-0298230P
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2001US-0322297P.
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2001US-0337477P.
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2002US-0359122P.
2002US-0358978P.
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                                                        3 YAFVGEKFRNYLLVFFOK
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       Conservative
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21-FEB-2002; 2
22-FEB-2002; 2
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15-JUN-2001;
18-JUN-2001;
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22-FEB-2002;
22-FEB-2002;
27-FEB-2002;
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31-JUL-2001;
14-SEP-2001;
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Gaps ; us-10-084-813-15.rag

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Tue Sep 28 15:49:58 2004
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19-JUN-2001; 2001US-0299230P.
22-JUN-2001; 2001US-029949P.
22-JUN-2001; 2001US-029949P.
26-JUN-2001; 2001US-0301530P.
28-JUN-2001; 2001US-0301530P.
28-JUN-2001; 2001US-0301530P.
31-JUL-2001; 2001US-0301550P.
31-JUL-2001; 2001US-0301550P.
31-JUL-2001; 2001US-0301550P.
31-JUL-2001; 2001US-0314669P.
31-FEB-2002; 2001US-035914P.
32-FEB-2002; 2002US-035903P.
34-ARX-2002; 2002US-03693P.
34-AXY-2002; 2002US-03693P.
34-JUN-2002; 2002US-0379444P.
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(CURA-) CURAGEN CORP.

Dipippo VA, Edinger SR, Eisen A, Ellerman K, Catterton E, Gerlach VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA, Gerlach VL, Gorman L, Guo K, Hermann JL, Hjalt T, Ji W, Kekuda R, Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I; Rotramtsov NV, Ei E, Esturajan W, Pena CEA, Rastelli L, Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA, Shithson G, Spaderna SK, Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP; Burgess CE, Lepley DM;

WPI; 2003-210149/20. N-PSDB; ADC10143.

New isolated NOVX polypeptides and nucleic acid molecules useful for treating, preventing and diagnosing pathological conditions with NOVX-associated disorders, such as cancer, obesity, diabetes and inflammatory CNS diseases

Claim 1; SEQ ID NO 164; 772pp; English.

The invention relates to novel isolated polypeptides, mature form of the polypeptide, a sequence that is 95% identical to the polypeptide or the polypeptide compirising one or more conservative substitutions. The NOVX polypeptide is useful for treating or preventing a pathology associated with the polypeptide e.g. disorders associated with aberrant expression or activity of the polypeptide, such as cancer, diabetes, obesity, and endocrine, CNS and inflammatory disorders. They can also be used in various detection and screening assay, chromosome mapping, tissue typing and predictive medicine. This sequence corresponds to one of the polypeptides of the invention

Sequence 268 AA;

Gaps ö Query Match 100.0%; Score 95; DB 7; Length 268; Best Local Similarity 100.0%; Pred. No. 1.4e-07; Matches 18; Conservative 0; Mismatches 0; Indels

213 YAFVGEKFRNYLLVFFQK 230 1 YAFVGEKFRNYLLVFFOK 18

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RESULT 9
AAW26766
ID AAW28

AAW26766 standard; protein; 332 AA

(first entry) 21-MAY-1998 AAW26766;

Human chemokine receptor MMLR-CCR,

Mammalian mixed lymphocyte receptor; chemokine receptor; MMLR-CCR; human; monocyte; macrophage; chemotaxis; haematopoiesis; infection; inflammation; proliferative disease; cardiovascular disease; tumour; rheumatoid arthritis; alveolitis; atherosclerosis; chronic granulomatous disease; asthma; myasthenia gravis; diabetes; inflammatory bowel disease; toxic shock syndrome; septic shock; Chediak-Higashi syndrome; therapy; diagnosis.

Homo sapiens

Location/Qualifiers Peptide

107. .128 /note= "conserved peptide" 121 Misc-difference

/note= "a claimed polypeptide has isoleucine at residue 121"

WO9741225-A2

06-NOV-1997.

97WO-US006993, 25-APR-1997; 96US-00638081. 26-APR-1996;

(INCY-) INCYTE PHARM INC.

Wilde CG; Coleman R, Bandman O, Au-Young J,

WPI; 1997-549729/50. N-PSDB; AAT99542

Polynucleotide encoding MMLR-CCR or MPHG-CCR chemokine receptor - useful to study, diagnose and treat, e.g. infection, inflammation, solid tumour and proliferative and cardiovascular disease.

Claim 8; Page 37-38; 59pp; English

This protein comprises human WMLR-CCR, a novel C-C chemokine receptor associated with monocyte/macrophage infiltration and chemotaxis and haematopolesis. The amino acid sequence was deduced from a cDNA clone (see AAT99542) obtained from a cDNA library made from monomuclear cells collected on day 2 of a mixed lymphocyte culture, i.e. cells associated with inflammation and immunomodulation. Another novel chemokine receptor, MPHG-CCR (see AAN36767), is also claimed. MALR-CCR contains 7 transmembrane spanning segments connected by a serives of intracellular and seriacellular loops. MMLR-CCR and be used to study, diagnose and treat disease states in which normal leukocyte function is perturbed by normal leukopoiesis or inappropriate activation via proliferative disease, tumourigenesis, autoimmune disease, abnormal coll proliferation, solid tumours, cardiovascular disease, abnormal cell arthus, myasthenia gravis, diabetes, inflammatory bowel disease, toxic shock syndrome, septic shock and Chediak-Higashi syndrome

Sequence 332 AA;

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Gaps ö Length 332; 100.0%; Score 95; DB 2; Length 33 100.0%; Pred. No. 1.7e-07; tive 0; Mismatches 0; Indels Local Similarity 100. Query Match Best Local Si Matches 18;

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1 YAFVGEKFRNYLLVFFOK 18

277 YAFVGEKFRNYLLVFFQK 294

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asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy; diagnosis; leukocyte trafficking; G protein coupled receptor; ligand; modulator; antibody; human.

Homo sapiens

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                                                                                                                                                 Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention; inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma; diopathic pulmonary fibrosis; psoriasis; viral infection; cancer; atherosclerosis; autoimmune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Active and inactive forms of human CC chemokine receptor CCR-5 - useful to diagnose, prevent and/or treat inflammatory disorders, autoimmune disease and viral infection.
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                           AAW27407 standard; protein; 352 AA.
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                                                                                       (first entry)
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nes 18; Conservative
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N-PSDB; AAT90117.
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06-AUG-1996;
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                                                                                                                     Human CCR5
                                                          AAW27407;
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be used to modulate receptor activities, particularly ligand and G protein binding, and are potentially potentially useful in the treatment of atheroslerosis, rheumatoid arthritis, tumours, asthma, viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nfection, AIDS, inflammatory conditions, pathological immune response,
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/label= Extracellular_domain
56. .67
/label= Intracellular_domain
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                                                                           cocation/Qualifiers
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/label= E~
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07-JUN-1996;
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RESULT 12

AAW27125

Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;

Human chemokine receptor 88C.

14-DEC-1997 (first entry)

AAW27123;

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Novel human mature G-protein chemokine receptor HDGNRIO (AAW07602) is a 7-transmembrane protein involved in signal transduction. Its amino acid sequence was deduced from a cDNA clone (AAT44042) isolated from a human moncoyte library. Isolation of the cDNA allows prodn. of recombinant HDGNRIO in host, e.g. E. coli, COS or Sf9, cells. The recombinant sceptor can be used to identify agonists or antagonists of the receptor; such cpds. can be used to treat conditions related to the under- and over-expression of G-protein chemokine receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC chemokine receptor 5; CCR5; G-protein coupled receptor; human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.
haematopoiesis; leukaemia; inflammation; rheumatoid arthritis; diagnosis;
                                                                                                                                                                                                                                                                                                    Human G-protein chemokine receptor, HDGNR10 - useful to identify (ant)agonists, for treatment of haematopoiesis, leukaemia, chronic and acute inflammation, rheumatoid arthritis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="extracellular loop-1 (Claim 19)"
143. 171
14bb=1 IV
/note="transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 95; DB 2; L
100.0%; Pred. No. 1.9e-07;
ive 0; Mismatches 0;
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104. .126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human CC chemokine receptor 5 (CCR5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW23835 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 44-46; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 YAFVGEKFRNYLLVFFOK 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YAFVGEKFRNYLLVFFOK 18
                                                                                                                                     95WO-US007173.
                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
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/label= I
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                          WPI; 1997-043072/04.
                                                                                                                                                                                                                                                                         N-PSDB; AAT44042.
                                                                                                                                                                                                                               Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                Homo sapiens.
                                                                           WO9639437-A1
                                                                                                                                     06-JUN-1995;
                                                                                                                                                                  06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JJN-1998
                                                                                                          12-DEC-1996.
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                    therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
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                                                                                                                        Chemokine réceptor 88C; atherosclerosis; rheumatoid arthritis; tumour; setbma, viral infection; AIDS; inflammation; autoimmune disease; therapy; diagnosis; leukocyte trafficking; G protein coupled receptor; ligand; modulator; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This polypeptide sequence comprises macaque chemokine receptor 88C, a G protein coupled receptor that is involved in leukocyte trafficking. Its amno sequence was deduced from a 88C DNA (AAT85163) isolated by PCR amplification. It shows 97% identity to human 88C (AAW27123). 88C receptors and their polypeptide fragments can be produced in transformed host cells. The receptors, peptides comprising one or more of the extracellular or intracellular domains, and anti-receptor antibodies can be used to modulate receptor activities, particularly ligand and G protein binding, and are potentially potentially useful in the treatment of atheroslerosis, inflammatory conditions, pathological immune response, antibody that specifically binds to macaque 88C is claimed antibody that specifically binds to macaque 88C is claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding chemokine receptors 88-2B and 88C - used to modulate leukocyte trafficking, e.g. for treatment of inflammation, tumours, viral infections, auto-immune diseases, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 95; DB 2; Length 352; 100.0%; Pred. No. 1.9e-07; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human G-protein chemokine receptor HDGNR10.
                                                                                                                                                                                                                                                                                                                                                                                                   Raport CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 36; Page 57-58; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW07602 standard; protein; 352 AA
   AAW27125 standard; protein; 352 AA.
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                                                                                             Macaque chemokine receptor 88C.
                                                                                                                                                                                                                                                                                            96WO-US020759
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96US-00661393
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                                                                                                                                                                                                                                                                                                                                                                                                   Gray PW, Schweickart VL,
                                                                (first entry)
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Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 352 AA;
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                                                              14-DEC-1997,
                                                                                                                                                                                                                               WO9722698-A2
                                                                                                                                                                                                                                                                                                                        20-DEC-1995;
07-JUN-1996;
                                                                                                                                                                                                                                                                                            20-DEC-1996;
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                                                                                                                                                                                                                                                              26-JUN-1997
                                                                                                                                                                                                    Macaca sp.
                                   AAW27125;
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AAW07602
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RESULT 16
AAY80128
ID AAY80128 standard; protein; 352 AA.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAV84126
                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 352 AA;
           Homo sapiens.
                                                                                                                                                                                                                                                                        30-MAY-1997;
                                                                                                                                                                                                                WO9854317-A1
                                                                                                                                                                                                                                                     29-MAY-1998;
                                                                                                                                                                                                                                  03-DEC-1998.
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Domain
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                                                                                                                                                                                                                                                                                                                                      This protein sequence comprises of a novel human macrophage-selective CC chemokine receptor that has been designated CGB. The sequence was deduced from an isolated cDNA clone (see AAT76920). An Ala127Leu variant (see W228340 of CCRS was also identified. The susceptibility of human macrophages to HIV infection depends on cell surface expression of CD4 protein coupled cell surface molecules. It plays an essential role in the membrane fusion step of infection by some HIV isolates. The establishment of stable, non-human cell lines and transgenic mammals having cells that coexpress human CD4 and CCR5 provides valuable tools for research of HIV infection. Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding represent potential anti-HIV therapeutics for macrophage tropic strains of HIV
                                                                                                                                                                                                                                                                                           CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 95; DB 2; Length 352; 100.0%; Pred. No. 1.9e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                  Murphy PM;
187. .210
hote= "extracellular loop-2 (Claim 19)"
194. .219
1abel= V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                    'note= "extracellular loop-3 (Claim 19)"
                                                                                                                                                                                                                                  Berger EA, Alkhatib G,
                                      'note= "transmembrane domain"
                                                                  'note≃ "transmembrane domain"
261. .276
                                                                                                                'note= "transmembrane domain"
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                                                                                                                                                                                                                                                                                                     between HIV and a target cell
                                                                                                                                                                          97WO-US009586
                                                                                                                                                                                              96US-0018508P
                                                                                            277. .300
/label= VII
                                                         label= VI
                                              .258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                  C, Feng Y,
Kennedy PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV-1 co-receptor CCR5
                                                                                                                                                                                                                                                              WPI; 1998-032650/03.
N-PSDB; AAT76920.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                  Combadiere C,
                                                                                                                                   WO9745543-A2
                                                                                                                                                                         28-MAY-1997;
                                                                                                                                                                                              28-MAY-1996;
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 Region
                   Domain
                                               Domain
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m HIV-1} infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is the amino acid sequence of wild-type human CCR5, which serves as
                                                                                                                                                                                                                                                                                                    /note= "corresponds to TGT (Cys) in wild-type CCR5, TGA (Stop) in Ccr5m303"
103-124
/note= "transmembrane domain 3"
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100.0%; Pred. No. 1.9e-07;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Braun J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acid encoding a CCR5 variant into the cell, thereby redu
of functional CCR5 molecules present on the cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "transmembrane domain 4"
200. .223
                                                                                                     "transmembrane domain 1"
                                                                                                                                                                                                          'note= "transmembrane domain 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
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Location/Qualifiers
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                                                        32. .56
/note= "
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AAY80128;

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The specification describes an antibody which is specific for an antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN or is exposed upon gp120 binding of DC-SIGN due to concomitant conformational change. DC-SIGN is a receptor that is specifically expressed on dendritic cells and facilitates infection of T lymphocytes with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin. DC-SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes) with high affinity. The antibody of the invention inhibits the trans enhancement of HIV entry into a T cell or macrophage facilitated by dendritic cells. The antibody is useful to treat or prevent HIV infection. The present sequence represents a human CCRS protein, which is a translocation promoting agent that interacts with CD4. This receptor
                                                                                                            dendritic cell; T lymphocyte; HIV; gpl20; entry; T cell; macrophage; HIV infection; CCR5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostatic; immunosuppressive; nootropic; neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    An antibody for the treatment or prevention of HIV-infection comprises a gpl20 portion which binds to DC-SIGN or is exposed upon gpl20 binding of DC-SIGN due to concomitant conformational change.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G-protein chemokine receptor; CCRS; HDGNR10; inflammation; HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 95; DB 4; Length 352; 100.0%; Pred. No. 1.9e-07;
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                                                                   Amino acid sequence of human CCRS protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 118-119; 131pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       functions in HIV-1 entry into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Van Kooyk Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ą.
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                                                                                                                                                                                                                                                                                                                                         28-FEB-2001; 2001WO-US006322.
                                                                                                                                                                                                                                                                                                                                                                                       32-MAR-2000; 2000US-00517605.
                                                                                                                                                                                                                                                                                                                                                                                                                                   UYNY ) UNIV NEW YORK STATE.
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                       (first entry)
                                                                                                                  receptor; DC-SIGN;
lectin; ICAM3; HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kwon D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-602565/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 352 AA;
                                                                                                                                                                                                                                         WO200164752-A2
                                                                                                                                                                                             Homo sapiens.
                       10-DEC-2001
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                                                                                                                                                                                                                                                                                          07-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Littman DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE07046;
                                                                                                                    Human;
                                                                                                                                              C-type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a human G-protein chemokine receptor designated HDGNR10. HDGNR10 polynucleotides are useful in methods of screening for compounds which bind to and either: (1) activate the HDGNR10 polypeptides causing stimulation of haematopolesis, wound healing, coagulation, and angiogenesis; treatment of solid tumours, chronic infections, psoriasis, and to etimulate growth factor activity; or (2) inhibit activation of the HDGNR10 polypeptides which is useful for preventing and/or treating allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histamine and immunoglobulin E-mediated allergic reactions, prostaglandin-independent fever, bone marrow failure, stilosis, sarcoidosis, rheumatoid arthritis shock and hyper-eosinophilia syndrome. The polymucleotides are also useful for diagnostic assays for detecting diseases related to mutations in the altered level of the soluble form of the receptor polypeptides. The polymucleotides are also useful for in vitro purposes related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                     receptor; G-protein chemokine receptor; HDGNR10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid encoding human G-protein chemokine receptor usefu
for diagnostic assays, scientific research and screening for compounds
which bind to and activate or inhibit activation of the receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                       diagnosis, haematopolesis, wound healing; coagulation; angiogenesis; tumour; infection; leukaemia; psoriasis; alerry; T-cell mediated autorimmune disease; atherogenesis; anaphylaxis; inflammation; allergic reaction; silicosis; sarcoidosis; rheumatoid arthritis; hyper-eosinophilia syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polynucleotides are also useful for in vitro purposes related to scientific research, synthesis of DNA and manufacture of DNA vectors
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                                                                                                                    Human G-protein chemokine receptor HDGNR10 SEQ ID NO:2.
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100.0%; Pred. No. 1.9e-07;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 1; 22pp; English.
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                                                                        (first entry)
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Best Local Similarity 100.
Matches 18; Conservative
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N-PSDB; AAZ91481.
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                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                        19-MAY-2000
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Geijtenbeek T;

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Indels

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AAG79089;

RESULT 17 AAG79089

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Sequence 352 AA;
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multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.
                                                                                                                                                                                  /mote= "Segment 2"
                                                                                                                        7. .58
label= Transmembrane_domain
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|label= Transmembrane_domain
|note= "Segment 6"
                                                                                     Extracellular_domain
                                                                                                              Transmembrane domain
                                                                                                                                                            9. .67
|abel= Intracellular_loop_1
                                                                                                                                                                                                                                                   .03. .124
|Tabel= Transmembrane_domain
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/label= Transmembrane_domain
/note= "Segment 4"
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|Tabel= Transmembrane_domain
| note= "Segment 7"
                                                                                                                                                                                                                                     Extracellular_loop_1
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|abel= Extracellular_loop_3
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                                                             Location/Qualifiers
                                                                                                                                                   "Segment 1"
                                                                                                                                                                                                                                                                           note= "Segment 3"
                                                                                                                                                                                                                                                                                                                                                                                                     "Segment 5'
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09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-FEB-2001; 2001WO-US004153
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/label= Ex
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                                                                                                37. .305
/label= T
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'label=
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                                     Homo sapiens
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                                                              Key
Domain
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The invention relates to human G-protein chemokine receptor (CCR5) HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are useful for treating, preventing or ameliorating a disease or disorder

Claim 102; Fig 1; 518pp; English.

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cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's sarroma) or defective or aberrant Total antigen presenting cell interaction. The disease or disorder may also be an infections disease (e.g. a viral infection such as an early stage HIV infection, a autonomensate or disorder may also be an infection, a new compalavirus infection, or a poxvirus infection, an autonoment of disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The disease or disorder may be associated with aberrant CCRS expression, lack of CCRS function. CCRS HOGNRIO protein is used as a food additive or preservative or increase or decrease storage capabilities. CCRS HOGNRIO DNA, cor chromosome identification and in gene therapy. CCRS HOGNRIO DNA, protein, antibodies, agonists and antegonists are also useful in the disorders, agonists and antegonists are also useful in the cland, bone, bone marrow, gastrointestinal tract, liver lung, utodomnume thyroiditis, disbetes mellitus, Crohn's haemolytic anaemia, autoimmune thyroiditis, disbetes mellitus, Crohn's chaemolytic anaemia, autoimmune thyroiditis, disbetes mellitus, Crohn's cadiovascular disorders (myocadial ischaemias) and wound healing. The cyc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV, human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostatic; immunosuppressive; noctropic; neuroprotective; gene therapy; neurodegenerative disorder; Kaposi, s sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 95; DB 4; Length 352; Best Local Similarity 100.0%; Pred. No. 1.9e-07; Matches 18; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE07048 standard; protein; 352 AA.
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09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
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N-PSDB; AAD13299.
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The invention relates to human G-protein chemokine receptor (CCRS)

HDGRRIO polypeptides and polymucleotides. CCRS HDGRRIO antibodies are
useful for treating, preventing or ameliorating a disease or disorder
associated with inflammation, defective or aberrant chemotaxis of immune
cells, HIV inflammation, defective or aberrant chemotaxis of immune
cells, HIV inflammation (such as Pneumcoystis carinii pneumonia or Kaposi's
sarcoma) or defective or aberrant T-cell antigen presenting cell
cinteraction. The disease or disorder may also be an infectious disease
cels, a viral infection such as an early stage HIV infection, a autoimmune
cytomegalovirus infection, or a poxvirus infection), an autoimmune
cytomegalovirus infection, or a poxvirus infection), an autoimmune
cissase (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
disease or disorder may be associated with aberrant CCRS expression, lack
of cCRS function, aberrant CCRS ligand expression, or lack of CCRS ligand
function. CCRS HDGNRIO protein is used as a food additive or preservative
cof curcase or decrease storage capabilities. CCRS HDGNRIO DNA,
cor chromosome identification and in gene therapy. CCRS HDGNRIO DNA,
cor chromosome identification and in gene therapy. CCRS HDGNRIO DNA,
cor chromosome identification and an endomists are also useful in the
content, antibodies, agonists and antegonists are also useful in the
correction, bone marrow, gastrointestinal tract, liver, lung,
curogenital); immune disorders (Addison's disease, altergies, autoimmune
correction or decrease (mycoardial ischaemias) and wound healing. The
correction or decrease (mycoardial ischaemias) and wound healing. The
correction or decrease (mycoardial ischaemias) and wound healing. The
correction or present sequence is human CCRS HDGNRIO protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection; inflammation; autoimmune disease; metastasis; bronchial asthma; lupus; chronic bowel inflammation; rheumatoid arthritis; cytostatic; antiinflammatory; antiasthmatic; immunosuppressive; dermatological; antirheumatic; antiarthritic;
diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.
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                                                                Example 40; Page 504-505; 518pp; English.
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Best Local Similarity 100.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 352 AA;
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Heitland A, Spodsberg N;

Forssmann W, Adermann K,

WPI; 2001-626256/72.

(IPFP-) IPF PHARM GMBH. (FORS/) FORSSMANN U.

02-APR-2001; 2001WO-EP003708, 31-MAR-2000; 2000DE-01016013

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                                                                                                                                                        or prostatio, organ rejection, inflammation and autoimmune diseases. Also inhibitors of (I) are used therapeutically against tumors (and their metastases), inflammation (particularly bronchial asthma or chronic bowel inflammation), or autoimmune diseases (theumatoid asthma or chronic bowel inflammation), or autoimmune diseases (theumatoid arthritis or lupus), where the (cardio) vascular, lymphatic, respiratory, nervous, digestive, endocrine, motor or urogenital systems or skin are affected, and bone marrow diseases. The products of the invention are chemokine derivatives which have cytostatic, antiinflammatory, antiasthmatic, immunosuppressive, dermatological, antirheumatic, antiarthritic. Chemokines act on specific tumor and inflammatory cells through a constellation of chemokine receptors (CR), which control migration and proliferation of these cells. AG880045-AA880128 represent human chemokine fragments used to illustrate the method of the invention
Diagnostic agent containing two or more receptor-specific ligands, useful for detecting tumors, inflammation etc., also therapeutic use of ligand inhibitors.
                                                                                                      This invention describes a novel diagnostic agent (A) comprising at least two different ligands (I) for receptors (II) that are implicated in disease. (A) are used for the diagnosis of tumors (especially colorectal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mammalian cell (I) that contains a CD4 gene, reporter gene for identification of drugs and antibodies for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, transformed mammalian cell; CD4; reporter gene; translocation; human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy; chemokine receptor; CKR; cellular dysfunction; HIV infection; cofactor; CC-CKR-5; envelope glycoprotein; anti-HIV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human chemokine receptor (CKR), CC-CKR-5 related protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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100.0%; Pred. No. 1.9e-07;
ive 0; Mismatches 0;
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                                                                       Disclosure; Page 10; 26pp; German.
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97US-00858660.
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Best Local Similarity 100.0
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19-JUN-1996;
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The present invention relates to a transformed mammalian cell that contains a gene encoding CD4, a construct encoding a reporter gene under the regulation of an human immuno deficiency virus (HIV) long terminal repeat (LTR) and that has been transduced with a vector encoding a human chemokine receptor (CKR) where the CD4 and the CKR are present on the cell surface of transformed mammalian cell. The invention is useful for identifying drugs or antibodies that interfere with the translocation of HIV into transformed mammalian cell or for identifying a human chemokine receptor that facilitates the infection of a particular HIV strain into the transformed mammalian cell. Compounds identified can be used to treat cellular dysfunction and to prevent or combat HIV infection. The present sequence is a human chemokine receptor (CKR), CC-CKR-5 related protein. CC-CKR-5 is the principal cofactor for entry mediated by the envelope glycoproteins of primary macrophage-tropic strains of HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 352;
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100.0%; Pred. No. 1.9e-07;
ive 0; Mismatches 0;
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/label= Transmembrane_domain
/note= "Segment 4"
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/label= Transmembrane_domain
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/label= Transmembrane_domain
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/label= Transmembrane_domain
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Disclosure; Col 47-50; 37pp; English.
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Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostatic; immunosuppressive; nootropic, neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; rheumacoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia. Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.

Claim 102; Fig 1; 495pp; English

Isolated nucleic acid encoding a human G-protein chemokine receptor (CCRS) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders. 224. .235 /label= Intracellular_loop_3 236. .260 /label= Transmembrane_domain 196. .223 /label= Transmembrane_domain 'label= Transmembrane_domain Extracellular_loop_2 Extracellular_loop_3 Li Y, Ruben SM; "Segment 5" note= "Segment 09-FEB-2000; 2000US-0181258P. 09-MAR-2000; 2000US-0187999P. 22-SEP-2000; 2000US-0234336P. 09-FEB-2001; 2001WO-US004152 (HUMA-) HUMAN GENOME SCI INC 167. .195 'label= Ex .274 261. .27 /label= note= Roschke V, WPI; 2001-488965/53. N-PSDB; AAD13181. WO200158915-A2 16-AUG-2001. Rosen CA, Domain Domain Domain Domain Domain Domain Domain

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Gaps

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The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10 protein. CCR5 HDGNR10 cDNA is included in ATCC Deposit No: 97183. CCR5 protein. CCR5 HDGNR10 cDNA is included in ATCC Deposit No: 97183. CCR5 HDGNR10 antibodies are useful for treating, breventing or ameliorating a disease or disorder associated with inflammation, defective or aberrant chemotaxis of immune cells, HIV infection (such as Pneumocystis carini preeming or Raposi's sarcoma) or defective or aberrant T-cell antigen confined in the cation. The disease or disorder may also be an infection, a cytomegalovirus infection, or a poxvirus infection, an infection, a cytomegalovirus infection, or a poxvirus infection, an infection, a cytomegalovirus infection, or a poxvirus infection, or a catofimmune disease or disorder may be associated with aberrant CCR5 disorder. The disease or disorder may be associated with aberrant CCR5 capterssion, lack of CCR5 function. CCR5 HDGNR10 protein is used as a food additive or preservative to increase or decrease storage capabilities. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists are also useful in the diagnosis, treatment and prevention of cancer (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract, cutoimmune haemolytic anaemia, autoimmune thyroidicis, disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroidicis, disease, allitus, colitis); cardiovascular disorders (Myocardial ischaemias) and wound beand the colitis).

Sequence 352 AA;

Gaps ., Query March 100.0%; Score 95; DB 4; Length 352; Best Local Similarity 100.0%; Pred. No. 1.9e-07; Matches 18; Conservative 0; Mismatches 0; Indels

1 YAFVGEKFRNYLLVFFQK 18

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297 YAFVGEKFRNYLLVFFQK 314

AAE07039 standard; protein; 352 AA

AAE07039;

(first entry) 16-0CT-2001 Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.

Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostatic; immunosuppressive; noctropic; neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.

Homo sapiens.

WO200158915-A2.

16-AUG-2001.

09-FEB-2001; 2001WO-US004152.

09-FEB-2000; 2000US-0181258P. 09-MAR-2000; 2000US-0187999P. 22-SEP-2000; 2000US-0234336P.

(HUMA-) HUMAN GENOME SCI INC

Li Y, Ruben SM; Roschke V, Rosen CA,

WPI; 2001-488965/53. N-PSDB; AAD13198.

Isolated nucleic acid encoding a human G-protein chemokine receptor (CCRS) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.

Example 40; Page 486-487; 495pp; English.

The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10 protein. CCR5 HDGNR10 antibodies are useful for treating, preventing or ameliorating a disease or disorder associated with inflammation, and clective or aberrant chemotaxis of immune cells, HIV infection (such as Pheumocystis carinii preumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen presenting cell interaction. The disease or disorder may also be an infectious disease (e.g. a viral infection, or a poxytus infection), an autoimmune disease (e.g. a rheumatoid arthritis) or a neurodegenerative disorder. The disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The disease or disorder may be associated with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5 ilgand euction, aberrant CCR5 ilgand euction. CCR5 HDGNR10 protein is used as a food additive or preservative to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome contification and in gene therapy. CCR5 HDGNR10 DNA, protein, treatment and prevention of cancer (breast, orary, adrenal gland, bone, bone marrow, gastrointestinal tract, liver, lung, urogenital); immune disorders (Addison's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple carders (myocardial ischaemias) and wound healing

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          Length 352;
                            0; Indels
          Score 95; DB 4; I
Pred. No. 1.9e-07;
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cive 0;
Query Match
Best Local Similarity 100...
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Sequence 352 AA;

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RESULT 24 AAB46858

AAB46858 standard; protein; 352 AA

AAB46858;

(first entry) (revised) (revised) 16-AUG-2001 04-MAY-2001

Human HDGNR10 protein.

HDGNR10; human; G-protein chemokine receptor; antiinflammatory; immunomodulatory; anticoagulant; antiallergic; immunosuppressive; cytostatic; antiparasitic; antiparasitic; antiparasitic; antiparasitic; antiparasitic; antiparasitic; anticonsitic; vasotropic; gene therapy; haematopoiesis; wound healing; coagulatic; angiogenesis; solid tumour; infection; leukemia; growth factor activity; T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis; anaphylaxis; malipanacy; inflammation; histamine; IgE; silicosis; shock; immunoglobulin B-mediated allergic reaction; rheumatoid arthritis; prossaglandin-independent fever; bone marrow failure; sarcoidosis; hyper-eosinophilic syndrome; vulnerary.

Homo sapiens.

US2001000241-A1.

12-APR-2001.

29-NOV-2000; 2000US-00725285

95US-00466343. 98US-00195662. 99US-00339912. 06-JUN-1995; 18-NOV-1998;

(LIYY/) LI Y. (RUBE/) RUBEN S M.

25-JUN-1999;

Li Y, Ruben SM;

WPI; 2001-226317/23.

New human G-protein chemokine receptor polypeptides and polynucleotides, useful for identifying (ant)agonists to the G-protein chemokine receptor N-PSDB; AAF26390

Claim la; Page 15; 22pp; English.

This invention describes a novel receptor polypeptide (I) selected from (i) a fully defined 329 amino acid sequence (II) fully disclosed in the specification; and (ii) a polypeptide encoded by the cDNA contained in a plasmid, and fragments, analogs and derivatives of the polypeptide. The products of the invention have antiinflammatory, immunomodulatory, anticoaculant, antiallergic, immunosuppressive, vulnerary, cytostatic, antiportatic, antipheumatic, antiarthritic and vasctropic activity and can be used for gene therapy. The G-protein chemokine activity and can be used for gene therapy. The G-protein chemokine activity and can be used for gene therapy. The G-protein chemokine activate or inhibit activation of (I). The products of the invention can also be used for stimulating haematopoiesis, wound healing, coagulation, and open sees is, treating solid tumours, chronic infections, psortassis, and stimulating growth factor activity. HDGNR10 is useful for treating

RESULT 26

4AB8335

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to G protein-coupled receptors (GPCRs) for which the endogenous ligand has been identified. Non-endogenous constitutively activated versions of known GPCRs are used in the invention for the direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists. Such agonists are useful as therapeutic agents for diseases or disorders associated with GPCRs. The present sequence is a non-endogenous version of a known human GPCR
allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histamine and immunoglobulin E (IgE)-mediated allergic reactions, prostaglandin-independent fever, bone marrow failure, silicosis, sarcoidosis, rheumatoid arthritis, shock and hyperecisinophilic syndrome. (N.B. This record was resubmitted to correct errors in the keyword formatting)
                                                                                                                                                                                        Gaps
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100.0%; Pred. No. 1.9e-07;
ive 0; Mismatches 0;
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N-PSDB; ABI97978.
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es 18; Conser
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Matches
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This sequence represents the human CCRS protein sequence. The invention relates to a method for determining whether an agent is capable of modulating the interaction of chemotractic chemokine receptor 5 (CCRS) with gp120, comprising incubating the agent with CCRS and gp120 and determining whether the agent modulates the interaction, where gp120 and determining whether the agent modulates the interaction, where gp120 is associated with CDR, and where the interaction is a low affinity binding. The method is used to identify an agent capable of modulating the interaction of CCRS with gp120, an agent capable of modulating the comparison of CCRS with gp120 interaction for the treatment of a disease or condition associated with CCRS and gp120 interaction, to treat a subject with a disease or condition associated with CCRS and gp120 interaction, and for preparing a pharmaceutical for treating human immunodeficiency virus (HIV). It can also be treat anti-inflammatory diseases. The method is commercially useful, amenable to high throughput screening, and etects interaction of gp120 with cells expressing only CCRS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determining if an agent can modulate CCRS-gp120 interaction, comprises incubating the agent with CCRS and gp120 and determining if the agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                           Chemotactic chemokine receptor 5; gpl20; CD4; therapy; HIV; CCR5; human immunodeficiency virus; anti-inflammatory disease; human.
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100.0%; Pred. No. 1.9e-07;
Eive 0; Mismatches 0;
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AAB83354 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB82948 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 110; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dobbs S, Perros M, Rickett GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297 YAFVGEKFRNYLLVFFQK 314
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                                                                                                                                                                                                                                                                                                                   03-JAN-2001; 2001EP-00300020.
                                                                                                                                                                                                                                                                                                                                                    12-JAN-2000; 2000GB-00000659.
12-JAN-2000; 2000GB-00000661.
12-JAN-2000; 2000GB-00000663.
                                                                                                            Human CCR5 protein sequence
                                                                      09-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modulates the interaction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-477088/52
N-PSDB; AAF87099.
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                             (PFIZ ) PFIZER LTD (PFIZ ) PFIZER INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 352 AA;
                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                           25-JUL-2001.
                                     AAB83354;
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Gaps

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297 YAFVGEKFRNYLLVFFQK 314

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1 YAFVGEKFRNYLLVFFOK 18

Conservative

Local Similarity les 18; Conserv

Best Loca Matches

Query Match

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Human, G-protein chemokine receptor; CCR5; HDGNR10; inflammation; fimune cell chemotaxis; autoimmine disease; rheumatoid arthritis; neurodegeneration; viral infection; Kaposi sarcoma; cancer; hyperproliferative disease; neurological disease; receptor.
            Human G-protein chemokine receptor (CCR5) HDGNR10 #1.
                                                                                                                                                                                   09-FEB-2001; 2001US-00779879.
                                                                                                                              US2002048786-A1
                                                                                                        Homo sapiens.
                                                                                                                                                         25-APR-2002.
                                                                                                                                                                                                                                                                                      (LIYY/) I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of human HIV-1 co-receptor CCR5. Amino acids 2-18 in the N-terminal region of CCR5 comprise an HIV-1 gp120-binding site that determines the specificity of the interaction between CCR5 and HIV-1 gp120. Post-translational sulfation of the tyrosine residues in the CCR5 N-terminus is required for gp120 binding and may critically modulate the susceptibility of target cells to HIV-1 infection in vivo. The invention provides claimed sulfated peptides (see AAB82947) that are based on the CCR5 N-terminal region and which are effective for inhibiting HIV-1 binding to CCR5. These peptides are used in claimed methods of inhibiting HIV infection of CO4+ cells, of preventing CD4+ cells from becoming infected with HIV, of tracating a subject whose CD4+ cells are infected with HIV, and of identifying an agent which inhibits building of a CCR5 ligand to a CCR5 receptor. The methods may be carried out in a subject, especially a human, infected (therapeutic method), not infected with HIV (prophylactic method), or in a subject who is not infected with, but has been exposed to, HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                  CCR5; chemokine; co-receptor; human immunodeficiency virus type 1; HIV-1; infection; therapy; vaccine; anti-HIV-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          Novel compounds comprising specific amino acids within CCRS (HIV 1 ocreceptor) amino terminal domain including negatively charged and two sulfated tyrosine residues is useful for treating HIV infection in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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                                                                                                                                 2. .18
/note= "binds to HIV-1 gp120"
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(AARO-) AARON DIAMOND AIDS RES CENT.
                                                                                                                   Location/Qualifiers
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19-MAY-2000; 2000US-0205839P.
07-FEB-2001; 2001US-0267231P.
                                                                                                                                                                                                                          28-FEB-2001; 2001WO-US006699.
                          Human HIV-1 co-receptor CCR5
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(first entry)
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                                                                                                                                                                                                                                                                                                                                           Olson WC;
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N-PSDB; AAH26903.
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                       WO200164710-A2
                                                                                                                     Key
Binding-site
                                                                                           Homo sapiens
                                                                                                                                                                                                07-SEP-2001.
21-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       humans.
                                                    CCR5;
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AAU97150
ID AAU97
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AC AAU97
XX
DT 13-AU
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The present invention relates to the isolation of a novel human G-protein chemokine receptor (CCRS) designated HDGNR10, and polynucleotide chemokine receptor (CCRS) HDGNR10 and polynucleotide sequences encoding it. The invention also describes antibodies that bind human G-protein chemokine receptor (CCRS) HDGNR10 and polynucleotide chuman G-protein chemokine receptor (CRS) HDGNR10 and polynucleotide cor preventing inflammation, defective or aberrant chemotexis of immune colls and T-cell/antigen-presenting cell interactions, infections of immune cells and T-cell/antigen-presenting cell interactions, infections of immune cells and T-cell/antigen-presenting cell interactions, infections of immune cells and polynucleotide strong-cells interaction viral correspondations of the conditions associated with aberrant or deficient expression of the CCRS receptor or its ligands. The antibodies are also useful to determine CCRS expression, ce.g. for diagnosis, prognosis and monitoring of cancer and other compinant receptor, and in the treatment of a wide range of diseases such as infectious diseases (e.g. influenza) neurological diseases (e.g. HDGNR10 the receptor (CCRS) HDGNR10 and produce the receptor (CCRS) HDGNR10 and singer receptor (CCRS) HDGNR10 the receptor (CCRS) the HDGNR10 th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding an antibody specific for the G-protein chemokine receptor CCRS, useful for treatment and diagnosis of e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
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100.0%; Pred. No. 1.9e-07;
ive 0; Mismatches 0;
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09-FEB-2000; 2000US-0181258P.
09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li Y,
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N-PSDB; ABK51853.
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                  (ROSE/) ROSEN C A. (ROSC/) ROSCHKE V.
                                                                                                                                                                                                                                                                                                                                          RUBEN S M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammation.
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CCR5, CC chemokine receptor 5; human; HIV infection; human immunodeficiency Virus; AIDS; acquired immunodeficiency syndrome; drug screening; identification; variant.

(first entry)

22-FEB-2002

AAM52829;

Human CCR5 Gln 55 variant

Location/Qualifiers

Homo sapiens

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The present invention relates to the isolation of a movel human G-protein chemokine receptor (CCR5) designated HDGNR10, and polymucleotide sequences encoding it. The invention also describes antibodies that bind human G-protein chemokine receptor (CCR5) HDGNR10 and polymucleotide sequences encoding the antibodies. The antibodies are useful for treating or preventing inflammation, defective or aberrant chemotaxis of immune cells and T-cell/antigen-presenting cell interactions, infections and autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral infections (especially early-stage human immune deficiency virus (HIV), cytomegalovitus or pox virus infections, Kaposi sarcoma, or conditions associated with aberrant or deficient expression of the CCR5 expression, its ligands. The antibodies are also useful to determine CCR5 expression, e.g. for diagnosis, prognosis, and monitoring of caneer and orher hyperproliferative diseases. The polymucleotide sequences encoding human G-protein chemokine receptor (CCR5) HDGNR10 can be used to produce the receptor, and in the treatment of a wide range of diseases such as infections diseases (e.g. influenza), neurological diseases (e.g. cancer). The present sequence represents human G-protein chemokine receptor (CCR5) HDGNR10 chemokine receptor (CCR5) TDGNR10 chemokine receptor (CCR5) TDGNR10 chemokine receptor (CCR5) TDGNR10 chemokine 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding an antibody specific for the G-protein chemokine receptor CCR5, useful for treatment and diagnosis of e.g. inflammation.
                                                                                                                                                  immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;
neurodegeneration; viral infection; Kaposi sarcoma; cancer;
hyperproliferative disease; neurological disease; receptor.
                                                                                                                             G-protein chemokine receptor; CCRS; HDGNR10; inflammation;
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                                                                            Human G-protein chemokine receptor (CCR5) HDGNR10 #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Page 165-166; 180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Li Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-FEB-2000; 2000US-0181258P.
09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
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                           13-AUG-2002 (first entry)
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Best Local Similarity 100.
Matches 18; Conservative
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N-PSDB; ABK51870.
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                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (LIYY/)
(RUBE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROSE/)
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The invention relates to a method for identifying a binding compound for a chemokine receptor 5 (CCR5). The method involves screening a library of test molecules (particularly peptides) with immobilised CCR5, and then identifying those molecules which bind. The invention also relates to cors.-binding molecules identified using the method of the invention. The transfer vector encoding tagged CCR5, a computer-aided methods for transfer vector encoding tagged CCR5, a computer specifies, a computer aided drug screening assay that utilises the three-dimensional a computer aided drug screening assay that utilises the three-dimensional structure of CCR5. Compounds identified using the methods for structure of CCR5. Compounds identified using the methods of the invention are useful for treating or preventing HTV (human immunodeficiency virus) infection or AIDS (acquired immunodeficiency syndrome) in a patient. The methods of the invention may also be used to identify agonists or antagonists of the interaction of CCR5 with its natural ligand, and to determine a binding motif for CCR5. The present is equence represents a naturally occurring variant of human of the control of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying CC chemokine receptor 5 binding compound for treating AIDS, comprises binding a molecule from library to a molecule having binding property corresponding to CCRS and identifying bound molecule.
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                                                                                                                                                                                                                                                                                                                                                           'note= "Glu replaces wild-type Leu; encoded by CTG'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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100.0%; Pred. No. 1.9e-07;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Encoded by AGC"
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21-MAR-2000; 2000US-0191299P.
21-MAR-2001; 2001US-0191299P.
20-MAR-2001; 2001US-00813448.
20-MAR-2001; 2001US-00813653.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CONS-) CONSENSUS PHARM INC
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Best Local Similarity
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Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
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297 YAFVGEKFRNYLLVFFQK 314

1 YAFVGEKFRNYLLVFFOK 18

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Gaps

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AAM52829 standard, protein; 352 AA.

RESULT 30 AAM52829 ID AAM5

1 YAFVGEKFRNYLLVFFQK 18

297 YAFVGEKFRNYLLVFFQK

haematopoiesis, wound healing, coagulation; angiogenesis; solid tumcunichronic infection; leukaemia; T-cell mediated autoimmune disease; parasitic infection; psoriasis; growth factor activity; allergy; parasitic infection; psoriasis; growth factor activity; allergy; atherogenesis; anaphylaxis; malignancy; inflammation; histamine; immunoglobulin B; IgE-mediated allergic reaction; sarcoidosis; prostaglandin-independent fever; bone marrow failure; shock; rheumatoid arthritis; hyper-eosinophilic syndrome; cytostatic; antianteriosclerotic; antiparasitic; antipsoriatic; antiallergic; antipyretic; receptor.

99US-00339912. 95US-00466343

25-JUN-1999; 36-JUN-1995; (LIYY/) LI Y.

25-JUL-2002.

JS2002099176-A1.

Homo sapiens.

Human; G-protein chemokine receptor; HDGNR10; CCR5 receptor;

Human G-protein chemokine receptor, HDGNR10.

(first entry)

03-DEC-2002

ABG70597;

ABG70597 standard; protein; 352 AA.

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The invention relates to a method for identifying a binding compound for CC chemokine receptor 5 (CCR5). The method involves screening a library of test molecules (particularly peptides) with immobilised CCR5, and then identifying those molecules which bind. The invention also relates to CCR5-binding molecules identified using the method of the invention, methods for identifying consensus motifs for CCR5-binding peptides, a transfer vector encoding tagged CCR5, a computer-aided methods for determining the relative binding asfainity of a test molecule to CCR5 and a computer aided drug screening assay that utilises the three-dimensional structure of CCR5. Compounds identified using the methods of the invention are useful for treating or preventing HIV (human immunodeficiency virus) infection or AIDS (acquired immunodeficiency syndrome) in a patient. The methods of the invention may also be used to seduence in a determine a binding motif for CCR5. The present sequence represents human CCR5.
                                                                                                                                                                      CCR5; CC chemokine receptor 5; human; HIV infection; human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome; drug screening; identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying CC chemokine receptor 5 binding compound for treating AIDS, comprises binding a molecule from library to a molecule having binding property corresponding to CCR5 and identifying bound molecule.
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                                                                                                                                          Human CC chemokine receptor 5 (CCR5)
                              AAM52828 standard; protein; 352 AA
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                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2000; 2000US-0190996P.
21-MAR-2000; 2000US-0191299P.
20-MAR-2001; 2001US-00813448.
20-MAR-2001; 2001US-00813651.
20-MAR-2001; 2001US-00813653.
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                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nestor JJ, Wilson CJ,
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N-PSDB; ABA02317.
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                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                     22-FEB-2002
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                                                                     AAM52828;
RESULT 31
                   AAM5282
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The present invention relates to the isolation of human G-protein chemokine receptor, HDGNR10 (CCR5 receptor), and the polymucleotide sequence encoding it. HDGNR10 polymeptide and polymucleotide sequences or useful for diagnosing a disease or a susceptibility to a disease related to underexpression of HDGNR10. They are useful for identifying modulators for stimulating haematopoiesis, wound healing, coagulation, angiogenesis, to treat solid tumours, chronic infections, psoriasis, or for stimulating growth factor activity. The sequences are also useful for preventing and/or treating allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histamine and immunoglobulin E (IgB)-mediated allergic reactions, prostaglandin-independent fever, bone marrow failure, sarcoidosis, rheumatoid arthritis, shock and hypercessinophilic syndrome. Polymucleotide sequences encoding HDGNR10 can be used in gene therapy to treat conditions related to underexpression of HDGNR10. The present sequence represents human G-protein chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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les 18; Conservative
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Matches
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100.0%; Score 95; DB 5; Length 352; larity 100.0%; Pred. No. 1.9e-07; Conservative 0; Mismatches 0; Indels

Query Match Best Local Similarity Matches 18; Conserv

RESULT 32 ABG70597

Novel human G-protein chemokine receptor polypeptide useful for identifying modulators for stimulating hematopoiesis, wound healing, leukemia, for treating allergy, rheumatoid arthritis, shock and as

WPI; 2002-690494/74. N-PSDB; ABS54272.

RUBE/) RUBEN S M.

Li Y, Ruben SM;

Claim 7; Fig 1; 22pp; English.

research agents.

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Immunoglobulin, variable heavy chain, variable light chain, human, G-protein chemokine receptor; CCR5, HDGNR10; cancer; inflammation; mimunologic deficiency syndrome; blood protein disorder; nephritis; at at a telangiectasia; endoctoxin lethality; inflammatory bowel disease; histiocytosis; chemotaxis; infectious disease; autoimmune disease; hastiocytosis; chemotaxis; infectious disease; allergy; neurodegenerative disorder; viral infection; poxvirus infection; human immunodeficiency virus; cytomegalovirus; Raposi's sarcoma; pheumocystis carnii infection; cardiovascular disorder; atherosclerosis;
                                                                                     Human immunoglobulin variable heavy domain #1.
                     ABG92883 standard; protein; 352 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Ruben SM;
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12-OCT-2001; 2001US-0328447P.
21-DEC-2001; 2001US-0341725P.
                                                                                                                                                                                                                                                                                                                               2001WO-US004153.
2001US-0297257P.
                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                 08-FEB-2002; 2002WO-US003634
                                                                                                                                                                                                                                                                                                                      2001US-00779880
                                                               19-NOV-2002 (first entry)
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N-PSDB; ABS68606.
                                                                                                                                                                                                             lymphocytopenia
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                                           ABG92883;
RESULT 33
           ABG92883
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The invention describes an isolated polynucleotide encoding a first antibody at least 95-100% identical to a second antibody consisting of an amino acid sequence comprising at least one, three CDR regions of a wariable heavy (VH) or variable light (VL) domain of the antibody expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8, XF27/28.1885, XF27/28.3F1, XF11.1F8, XF27/28.1885, XF27/28.3F2.0F2, XF27/28.3F2.0F2, XF27/28.3F2.0F2, XF27/28.1885, XF27/28.3F2.0F2, XF27/28.3F2, XF
New human G-protein Chemokine Receptor gene (HDGNR10) useful for treating, preventing, ameliorating or monitoring diseases or disorders associated with aberrant expression of HDGNR10 e.g. cancer.
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against HDGNR10
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                                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin; variable heavy chain; variable light chain; human; G-protein chemokine receptor; CCRS, HDGNR10; cancer; inflammation; immunologic deficiency syndrome; blood protein disorder; nephritis; ataxia telanglectasia; endotoxin lethality; inflammatory bowel disease; histiocytosis; chemotaxis; infectious disease; autoimmune disease; Addison's disease; dermatitis; rheumatoid arthritis; allergy; neurodegenerative disorder; viral infection; poxvirus infection; HIV; human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma; pneumocystis carnii infection; cardiovascular disorder; atherosclerosis;
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                                                                  Gaps
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                            100.0%; Score 95; DB 5; Length 352; 100.0%; Pred. No. 1.9e-07;
                                                                0; Indels
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                                                                Mismatches
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                                                                                                                                                                                                                                 ABG92880 standard; protein; 352 AA.
                                                                                                                            297 YAFVGEKFRNYLLVFFQK 314
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                                                                                                      1 YAFVGEKFRNYLLVFFQK 18
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2001US-0310458P.
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                                                                    18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-643455/69.
N-PSDB; ABS68553.
                                Query Match
Best Local Similarity
Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lymphocytopenia
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12-JUN-2001; 2
08-AUG-2001; 2
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                                                                      Matches
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expression of CCR5 or their ligands. They are also used for the

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The invention relates to human G-protein chemokine receptor (CCR5), HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5 defectives are used for the treatment or prevention of inflammation, defective or aberrant chemotaxis of immune cells or T cell antigenpresenting cell interaction, viral infections (specifically human immune deficiency (including its early stages), cytomegalo or pox viruses), autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis carinii infection, Kaposi's sarcoma or any condition associated with
                                                                                                                                                                                                                                                                        ö
certain haematopoietic cells such as histiocytosis, defective or aberrant chemotaxis of immune cells or T-cell antigen presenting cell interaction, an infectious disease, an autoimmune disease such as Addison's disease, dermatitis and rheumatoid arthritis, allergies, a neurodegenerative disorder, a viral infection e.g. HIV infection, cytomegalovitus or poxvirus infection, a Pneumocystis carnii infection, Kaposi's sarcoma, cardiovascular disorders such as atherosclarosis, lymphocytopenias, or a disease or disorder associated with aberrant expression of novel human G-protein chemokine receptor (CCRS) HDGNR10. This is an amino acid sequence of Human G-protein chemokine receptor (CCRS) HDGNR10. #1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer; inflammation; viral infection; autoimmune disease; neurodegeneration; rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma;
                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                      Length 352;
                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                                                                                                      100.0%; Score 95; DB 5; I
                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hyperproliferative disease; receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE25808 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                             297 YAFVGEKFRNYLLVFFOK 314
                                                                                                                                                                                                                                                                                                           1 YAFVGEKFRNYLLVFFOK 18
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09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
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es 18; Conservative
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ROSCHKE V.
LI Y.
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                                                                                                                                                                                                      Sequence 352 AA;
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The invention relates to human G-protein chemokine receptor (CCR5), HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5 antibodies are used for the treatment or prevention of inflammation, defective or aberrant chemotaxis of immune cells or T cell antigenpresenting cell interaction, viral infections (specifically human immune deficiency (including its early stages), cytomegalo or pox viruses), autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis carinii infection, kaposi's sarcoma or any condition associated with detection, diagnosis, prognosis and monitoring of cancers or other hyperproliferative diseases. The present sequence is human G-protein chemokine receptor (CCR5), HDGNR10 DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding antibodies to the human CCRS receptor HDGNR10, useful for treatment, prevention and diagnosis of e.g. cancer, also
                                                                                                                                                                                                                                                                                                                                                                                                       Human, G-protein chemokine receptor; CCR5, HDGNR10 protein; cancer; inflammation; viral infection; autoimmune disease; neurodegeneration; rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma; hyperproliferative disease; receptor.
                                                                                                                                    Gaps
           detection, diagnosis, prognosis and monitoring of cancers or other hyperproliferative diseases. The present sequence is human G-protein chemokine receptor (CCRS), HDGNR10 DNA
                                                                                                                                    0
                                                                                                    Length 352;
                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                          Human G-protein chemokine receptor (CCR5), HDGNR10 #2.
                                                                                                      100.0%; Score 95; DB 5; I
100.0%; Pred. No. 1.9e-07;
                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                   AAE25811 standard; protein; 352
                                                                                                                                                                                                    297 YAFVGEKFRNYLLVFFOK 314
                                                                                                                                                                    1 YAFVGEKFRNYLLVFFOK 18
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09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
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                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                        Similarity 100.
18; Conservative
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N-PSDB; AAD42426.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                   AAE25811;
                                                                                                        Query Match
Best Local S
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                                                                                                                                        Matches
                                                                                                                                                                                                                                                     RESULT 36
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Human chemokine C-C motif receptor 5; CCR5; haplotype pair; isogene; single nucleotide polymorphism; SNP; human immunodeficiency virus 1; HIV-1 infection; acquired immunodeficiency syndrome; AIDS; antiviral; genotype; polymorphic variant; transgenic; drug screening; gene therapy;

chromosome 3p21

Homo sapiens

Human chemokine (C-C motif) receptor 5 polypeptide.

(first entry)

18-JUN-2002

ABB08343;

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ABB08343 standard; protein; 352

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G-protein chemokine receptor; haematopoietic; immunosuppressant; antiparasitic; antipsoriatic; antiallergic; antiinflammatory; cytostatic; antirheumatic; antiarthritic; gene therapy; human; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel human 7-transmembrane receptor, HDGNR10, which has been identified as a G-protein chemokine receptor. The GPCR HDGNR10 polypeptide can be expressed by standard recombinant methodology. Compounds that activate or inhibit the receptor polypeptide, optionally expressed from DNA in gene therapy vectors, are used to treat diseases that require: (a) activation of the receptor (e.g. stimulation of haematopoises; treatment of solid tumours, T-cell mediated autoimmune diseases, parasitic infections, psoriasis etc.); or (b) inhibition of the receptor (e.g. allergy, inflammation, rheumatoid arthritis, silicosis etc.). The present sequence represents the human HDGNR10 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotide encoding a human G protein chemokine receptor HDGNR10, useful e.g. for treating tumors.
                                Gaps
                                                                                                                                                                                                                                                                                          7-transmembrane receptor; G-protein coupled receptor; GPCR; HDGNR10;
                                ;
0
100.0%; Score 95; DB 5; Length 352; 100.0%; Pred. No. 1.9e-07;
                           0; Indels
                           Mismatches
                                                                                                                                                                                                                                                             G-protein chemokine receptor, HDGNR10
                                                                                                                                                                     A.
                                                                                                                                                                  ABB81054 standard; protein; 352
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                                                                                     297 YAFVGEKFRNYLLVFFOK 314
                                                            1 YAFVGEKFRNYLLVFFOK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Fig 1; 22pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-00195662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-00466343
                                                                                                                                                                                                                            05-NOV-2002 (first entry)
                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002-598724/64.
              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ABN86542
                                                                                                                                                                                                                                                                                                                                                                                                US2002076745-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LIYY/) LI Y.
(RUBE/) RUBEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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Query Match
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                Best Loc
Matches
                                                                                                                                     RESULT 37
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The present sequence is that of a polypeptide encoded by the human chemokine (C-C motif) receptor 5 (CCR5) gene of the invention (see ABA97318, ABA97319). The specification describes haplotyping the CCR5 ABA97319. The specification describes haplotyping the CCR5 can individual by determining if the individual has one of the CCR5 haplotypes or haplotype pairs fully defined in the specification of the specification also describes an isolated polymucleotide comprising a nucleotide sequence which is a polymorphic variant of the reference CCR5 gene sequence and comprises an isolated by a haplotype described in the specification and its encoded polypeptide. The methods of the invention are useful to diagnose and develop treatment for diseases associated with abnormal expression or function of the gene. The CCR5 isogenes and the screened compounds are useful for treating human immunodeficiency vitua (HIV)-1 infection and the progression to acquired immunodeficiency syndrome (AIDS). The invention has antiviral applications. The specification describes genotyping the CCR5 gene of an individual; predicting a haplotype pair for the CCR5 gene of an individual; identifying an association expense a trait and a haplotype or haplotype pair of the CCR5 gene. The specification describes a composition comprising a general areas and an antivity of an analyzaber or haplotype pair of the CCR5 gene. The specification describes a composition comprising a general areas and an antivity of a composition comprising a general areas and a standard and a s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New haplotypes of the human chemokine (C-C motif) receptor 5 gene, useful to diagnose and treat diseases associated with its abnormal expression or function, including human immunodeficiency virus-1 infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polymorphism; a recombinant non-human organism transformed with CCRS bylynucleotide expressing a CCRS protein encoded by the variant sequence; an isolated antibody specific for the CCRS polypeptide and a method for screening drugs targeting the CCRS polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 29; Fig 3; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENA-) GENAISSANCE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-APR-2000; 2000US-0194361P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-APR-2001; 2001WO-US010708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  label= Leu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Phe,
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N-PSDB; ABA97318, ABA97319.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200177125-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Choi JY,
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Score 95; DB 5; Length 352; Pred. No. 1.9e-07;

100.0%;

Query Match Best Local Similarity

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Gaps

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100.0%; Score 95; DB 5; Length 352; 100.0%; Pred. No. 1.9e-07; ive 0; Mismatches 0; Indels

VAFVGEKFRNYLLVFFQK 314

297

RESULT 38 ABB08343

1 YAFVGEKFRNYLLVFFQK 18

Conservative

Query Match Best Local Similarity Matches 18; Conserv

Sequence 352 AA;

us-10-084-813-15.rag

Sequence 352 AA;

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Novel human G-protein chemokine receptor polypeptide useful for diagnostic purposes and for identifying modulators of the polypeptide useful for treating leukemia, autoimmune diseases, psoriasis and allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; receptor; G-protein chemokine receptor; 7-transmembrane receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HDGNRio; signal transduction; gene therapy; haematopoiesis; wound healing; coagulation; angoidgenesis; tumour; chronic infection; pleukaemia; T-cell mediated auto-immune disease; parasitic infection; psoriasis; growth factor; allergy; atherogenesis; anaphylaxis; mallagnancy; inflammation; histemine; IgE-mediated; prostaglandin-independent fever; bone marrow failure; silicosis; practicidis; shock; hyper-eosinophilic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human G-protein chemokine receptor, HDGNR10, protein.
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Mismatches
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                                                                                                                                                                                                                                                                          ABG75540 standard; protein; 352
                                                                                                 297 YAFVGEKFRNYLLVFFOK 314
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                                                       1 YAFVGEKFRNYLLVFFQK 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-FEB-2000; 2000US-00502783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-208944/20.
N-PSDB; ABX10635.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2002132269-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                  16-APR-2003
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The invention discloses a G-protein chemokine receptor (sometimes referred to as a 7-transmembrane receptor) polypeptide, HDGNR10, and the polymucleotide encoding it. G-protein chemokine receptors are involved in signal transduction pathways. The polymucleotide and polypeptide can be useful to identify compounds which activate or inhibit activation of the protein and these compounds are useful for treating a patient having need to activate or inhibit a G-protein chemokine receptor. The compound is doministered by providing to the patient DNA encoding the agonist or antagonist and expressing them in vivo (gene therapy). The polymucleotides and polypeptide are also useful for for diagnosing a disease or susceptibility to a disease related to an under-expression of the protein for chromosome identification or as immunogens for producing antibodies. Agonists are useful in strimulating haematopoiesis, wound haltagonists are useful in the prevention and treatment of allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, hastamine and igE-mediated allergic reactions, proversilation, angingenesis, succidesis, rheumatoid arthritis, shock and hyper-eosinophilic syndrome. The sequence presented is the human HDGNRIO protein
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The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down-regulated in specific cancers (e.g. about 1031 genes up-regulated in regulated in specific cancers (e.g. about 1031 genes up-regulated in cacute lymphocytic leukemia). ACC75641 to ACC72860 represent cancer related gene nucleotide sequences which encode the proteins given in ABR58521 to ABR58709. Also described: (1) determining the presence or abence of a pathological cell in a patient; (2) an expression vector comprising the vector; (4) an isolated polypeptide, which is encoded by comprising the vector; (4) an isolated polypeptide, which is encoded by comprising the vector; (4) an isolated polypeptide, which is encoded by comprising the vector; (5) an antibody that specifically binds the polypeptide of (4); (6) specifically trargeting a compound to a pathological cell in a complete by administering to the patient the antibody above; and (7) a companient by administering to the patient the antibody above; and (7) a companient of the patient the nucleic acid is useful for therapeutic targets. In particular, the nucleic acid is useful for atheroselex, brain, breast, cervix, colon/rectum, kidney, lung, ovary, companient produces, patient and uterue), wounds, ischaemia, heart diseases, and content of any screening, particularly for identifying agents for treating these contents.

Claim 12; Page 745; 767pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                    New genes that are up-regulated or down-regulated in cancers, useful a markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.
                                                                                                                                                                               Human, cancer; diagnosis; screening; modulator; leukaemia; ischaemia; heart disease; atherosclerosis; endometriosis.
                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                           Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
100.0%; Score 95; DB 6; Length 352; 100.0%; Pred. No. 1.9e-07;
                                                                                                                                                               Human cancer related protein SEQ ID NO:259.
                    0; Mismatches
                                                                                                         ABR58602 standard; protein; 352 AA
                                                   297 YAFVGEKFRNYLLVFFQK 314
                                      1 YAFVGEKFRNYLLVFFOK 18
                                                                                                                                                                                                                                                                                                          2001US-0350666P.
2002US-035145P.
2002US-0355257P.
                                                                                                                                                                                                                                                                                                                                                           (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                       17-SEP-2002; 2002WO-US029560.
                                                                                                                                                                                                                                                                                         2001US-0323469P.
2001US-0323887P.
                                                                                                                                                                                                                                                                                                                                        2002US-0372246P
                                                                                                                                              (first entry)
  Query Match
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-354600/33.
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                                                                                                                                                                                                                                  WO2003025138-A2.
                                                                                                                                                                                                                                                                                                                      08-FEB-2002;
08-FEB-2002;
                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                           17-SEP-2001;
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                                                                                                                                              09-JUL-2003
                                                                                                                                                                                                                                                     27-MAR-2003
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Zlotnik A;
                                                                                                                           ABR58602;
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XX SQ Sequence 352 AA;

0; Gaps Query Match
100.0%; Score 95; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels

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Search completed: September 28, 2004, 09:03:39 Job time : 43.975 secs

Sequence 4, Appli Sequence 7, Appli Sequence 56, Appl Sequence 56, Appl Sequence 8, Appli Sequence 48, Appli Sequence 48, Appli Sequence 5, Appli Sequence 5, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 6, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli

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100.0%; Score 95; DB 3; L
100.0%; Pred. No. 8.2e-09;
ive 0; Mismatches 0;
US-08-720-565-4
US-08-567-882-7
US-09-645-184-2
US-09-045-583-56
US-09-534-185-56
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US-09-045-583-48
US-09-045-583-48
US-09-045-583-48
US-09-045-383-48
US-09-234-988A-2
US-08-410-393A-2
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US-08-410-393A-2
US-09-239-938-1
US-09-239-938-1
US-09-239-938-1
US-09-239-938-1
US-09-239-938-1
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US-09-153-848-28
US-08-15-65-6
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nes 18; Conservative
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MOLECULE TYPE: protein
  US-08-466-343D-2
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                                                              September 28, 2004, 09:00:23 ; Search time 16.2 Seconds (without alignments) 57.362 Million cell updates/sec
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Sequence
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2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-087-232A-13
US-08-575-967A-2
US-09-554-185-52
US-09-554-185-52
US-09-554-185-52
US-09-524-185-52
US-09-796-202-1
US-08-73-752-5
US-09-796-202-1
US-08-745-294A-2
US-08-745-294A-2
US-08-745-294A-2
US-08-745-294A-2
US-08-745-294A-2
US-09-196-202-1
US-09-534-185-50
US-09-534-185-50
US-09-534-185-50
US-09-534-185-51
US-09-534-185-51
US-09-534-185-51
US-09-534-185-51
US-09-534-185-51
US-09-645-583-51
                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -08-720-565-2
                                                                                                                                                            389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                              protein search, using sw model
                                                                                               US-10-084-813-15
95
1 YAFVGEKFRNYLLVFFQK 18
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match
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Perfect score:
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No.
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Gaps

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Length 352; Indels

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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REPERECHE/DOCKET NUMBER: 1049-1-004 NI
TELECOMUNICATION INFORMATION:
TELEPHONE: 201487-5600
TELEPHONE: 201487-5600
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 626184and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32918
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297 YAFVGEKFRNYLLVFFQK 314
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TYPE: amino acid
STRANDEDNESS: single
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
        COMPUTER READABLE FORM:
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ORGANISM: Hom
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Sequence 13, Application US/09087232A
Patent No. 6153431
GENERAL INFORMATION:
APPLICANT:
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Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels
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COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/087,232A
FILING DATE: 28 MAY 1998
CLASSIFICATION DATA:
APPLICATION UNBER: 60/048,057
FILING DATE: 30 MAY 1997
APPLICATION NUMBER: 60/048,057
RIGHT SAPLICATION NUMBER: 35,225
REGISTRATION NUMBER: 35,225
REGISTRATION NUMBER: 35,225
REFERENCE/DOCKET NUMBER: AP 31115
TELEPONE() 1212, 408-2628
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APPLICANT: DING, HONGKUI
APPLICANT: BLIMEIER, WILFRIED
APPLICANT: BLIMEIER, WILFRIED
APPLICANT: LANDAU, NATHANIEL R.
APPLICANT: LANDAU, NATHANIEL R.
TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WI.
TITLE OF INVENTION: MACROPHAGE-TROPHIC HIV, AND DIAGNO, TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVIG A. Jackson, Esq.
STREET: Floor
CITY: Hackensack
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 YAFVGEKFRNYLLVFFQK 314
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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Gaps
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US-08-575-967A-2

US-08-575-967A-2

Sequence 2, Application US/08575967A

Patent No. 6265184

GENERAL INFORMATION:

APPLICANT: Gray et al.

TITLE OF INVENTOR: Chemokine Receptor Materials and Methods NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Mirray & Borun STRET: closego

CITY: Chicago

STRET: closego

STRET: 11110018

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: LEATHING SYSTEM: PC-DOS/WS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,105
FLING DATE: US/08/861,105
FLING APPLICATION AJA:
APPLICATION NUMBER: US 08/666,020
CLASSIFICATION: 436
PRIOR APPLICATION: 436
PRIOR APPLICATION: 436
PRIOR APPLICATION NUMBER: US 08/227,319
FILING DATE: 13-APR-1994
ATTORNEY AGENT INFORMATION:
NUMBE: Jackson Esq., David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/575,967A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 95; DB 3; I
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0;
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ORGANISM: Homo sapiens
US-09-517-605-5
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US-09-045-583-52
Sequence 52, Application US/09045583
Sequence 52, Application US/09045583
Patent No. 6287805.
APPLICANT: Graham, Gerard J. et al.
APPLICANT: Graham, No. 6287805el Molecules of the G Protein-Coupled NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE! LAHIVE & COCKFIELD, LLP
ATREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels
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ZIP: 02109

ZIP: 02109

COMPUTER READABLE FORM:
MEDLING TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
FILING DATE: 20-MAR-98
FILING DATE: 20-MAR-98
FILING DATE: TILING DATA:
APPLICATION NUMBER: RIPORMATION:
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MI-044
TELECOMMUTCATION INFORMATION:
TELEFHONE: (617)742-7104
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERICATIOS:

SEQUENCE CHARACTERICATIOS

SEQUENCE CHARACTERICATION

SEQUENCE CHARACTERICATION

SECUENCE CHA
                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature; OTHER INFORMATION: /= "88C amino acid sequence" US-08-575-967A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 95; DB 3; I ilarity 100.0%; Pred. No. 8.2e-09; Conservative 0; Mismatches 0;
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           TELEFAX: 206-485-1662
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH 352 amino acids TYPE: amino acid TOPDIOSY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YAFVGEKFRNYLLVFFOK 18
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206-485-1900
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                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 18; Conservat
TELEPHONE:
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Gaps

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Sequence 2. Application US/08724984A

Sequence 2. Application US/08724984A

Patent No. 6388055

GENERAL INFORMATION:
APPLICANT: Derk Bergsma, Mary Brawner, and Usman Shabon
APPLICANT: Derk Bergsma, Mary Brawner, and Usman Shabon
TITLE OF INVENTION: CRRS Receptor
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-796-202-1

| Sequence 1, Application US/09796202
| Patent No. 6548616
| Farent No. 6548616
| GENERAL INFORMATION |
| APPLICANT: Disagic, Tatjana |
| APPLICANT: Olson, William |
| TITLE OF INVENTION: William |
| FILE REFERENCE: 2048/61,010/JPW/SHS |
| CURRENT APPLICATION NUMBER: US/09/796,202 |
| NUMBER OF SEQ ID NOS: 17 |
| SOFTWARE: PatentIn version 3.0 |
| SEQ ID NO 1 |
| LENGTH: 352
                                                                                                                                                                                                                                                                                           100.0%; Score 95; DB 4; Length 352; 100.0%; Pred. No. 8.2e-09; ive 0; Mismatches 0; Indels
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ZIF: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MD STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 95; DB 4; L
100.0%; Pred. No. 8.2e-09;
iive 0; Mismatches 0;
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OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: MICROSOFT WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,984A
FILING DATE: October 3, 1996
CURRENT APPLICATION NUMBER: US/09/502,783A
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
LENGTH: 352
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Best Local Similarity 100.0%;
Matches 18; Conservative C
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                  ; TYPE: PRT; ORGANISM: Homo sapiens US-09-502-783A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: human
US-09-796-202-1
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US-08-724-984A-2
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Sequence 2, Application US/09502783A

Sequence 2, Application US/09502783A

Sequence 2, Application US/09502783A

GENERAL INFORMATION:

APPLICANT: Li, Yi

APPLICANT: Li, Yi

APPLICANT: Li, Yi

TITLE OF INVENTION: HGGNL10

TITLE OF INVENTION: HGGNL10

FILE REFERENCE: 1488.1150006
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Patent No. 6448375

GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: SAMSON, MICHEL
APPLICANT: MASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                             Length 352;
                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTE: SACON
COMPUTE: SACON
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
                                                                                                                          Ouery Match 100.0%; Score 95; DB 4; 1
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                              ; FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
03-09-534-185-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 9-APR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: ALLWAN, DANIEL E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                          297 YAFVGEKFRNYLLVFFQK 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297 YAFVGEKFRNYLLVFFQK 314
                                                                                                                                                                                                                         1 YAFVGEKFRNYLLVFFQK 18
       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-833-752-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U
ZIP: 92660
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US-08-833-752-5
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Sequence 4, Application US/08450393A
; Sequence 6, Application US/08450393A
; Sequence 6, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
APPLICANT: Charch, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: PROTEIN RECEPTORS
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto Square
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08446669
; Patent No. 613287
; GENERAL INFORMATION:
    APPLICANT: Charo, Israel
    APPLICANT: Coughlin, Shaun
    TITLE OF INVENTION: PROTEIN RECEPTORS
    NUMBER OF SEQUENCES: 14
    CORRESPONDENCE ADDRESS:
    ADDRESSE: ADDRESS:
    STREET: 5 Palo Alto Square
    CITY: Palo Alto
    STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.2%; Score 79; DB 1; Length 360;
83.3%; Pred. No. 5.4e-06;
tive 1; Mismatches 2; Indels
       Indels
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ZIP: 94306-2155

COUNTEY: USA

ZIP: 94306-2155

COMPUTER READABLE FORM:
MEDIUM TYPE: FILPOPY disk

COMPUTER: IBM PC COMPATIble
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIL Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,393A
FILING DATE: May 25, 1995
CLASSITEATION THORMATION:
NAME: CSETY: LUANN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-237/02US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 145-843-5165
       5
       1; Mismatches
                                                                                                                                          292 YAFVGEKFRYLSVFFRK 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 YAFVGEKFRRYLSVFFRK 322
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                                                                        1 YAFVGEKFRNYLLVFFQK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-802, TELEX: 380816COOLeyPA
INFORMATION FOR SEQ ID NO: 4:
SEQUEBNCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.3
Matches 15, Conservative
       15; Conservative
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                                                                                                                                                                                                                                                RESULT 13
US-08-450-393A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-08-446-669-4
          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 79; DB 1; Length 347; Pred. No. 5.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Soppet, Daniel R.
APPLICANT: Yi, Li
APPLICANT: Yi, Li
APPLICANT: Ruben, Steven M.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32
NUMBER OF SEQUENCES: 7
CORRESSONDENCE ADDRESS:
ADDRESSEE: GARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STREET: 6 Becker Farm Road
STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION WHERE: US/08/461,244 FILING DATE: 05-JUN-1995 CLASSIPICATION: 536
PRIOR APPLICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: William T. Han
REGISTRATION NUMBER: 34,344
REPERENCE/COCKET NUMBER: ATG50023
TELEPHONE: 610 270 5090
TELEPHONE: 610 270 5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACIERISTICS:
LENGTH: 354
TYPE: Amino Acid
TYPE: Amino Acid
TYPE: Amino Acid
TYPE: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPATIBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08461244
Patent No. 5776729
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R.
APPLICANT: Yi, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 3256
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-170
TELEFAX: 201-994-174
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 YAPVGEKFRSYLSVFFRK 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YAFVGEKFRNYLLVFFOK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36,134
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 347 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-724-984A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-461-244-3
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COMPUTER READBELE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BY SYTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION DATA:
APPLICATION DATE: CURROWN>
PRIOR APPLICATION NUMBER: 09/045,583
FILING DATE: CURROWN>
ATTORNEY/AGENT INFORMATION:
NAME: MANDITAGENCE/CAST NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
TELEPHONE: (617)227-7400
INFORMATION FOR SEQ ID No: 50:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 360;
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                                                                                                                                                                                                                                                                                              Query Match

83.2%; Score 79; DB 3; 1
Best Local Similarity 83.3%; Pred. No. 5.4e-06;
Matches 15; Conservative 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) MOLECULE TYPE: peptide
; FRACMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-534-185-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/09131827A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305 YAFVGEKFRRYLSVFFRK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 YAFVGEKFRKLISVFFRK 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative 1
                                                                                        ) MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-50
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 17
US-09-131-827A-2
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Patent No. 6287805

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TORRESPONDENCE ADDRESS:

ADDRESSE:

ADDRESSE
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                                 CUNTATION OF THE CONTROL OF TELETRAL AND TELETRAL OF T
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MEDIUM TYPE: Floppy disk
COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CONFUTER: IBM PC compatible
CONFUTER: PATENTIN PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FLING DATE: 20-MAR-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTOMBER APPLICATION NUMBER ATTOMBER APPLICATION NUMBER ATTOMBER APPLICATION NUMBER ATTOMBER ATTOMBER APPLICATION NUMBER ATTOMBER ATTOMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 79; DB 3; I
Pred. No. 5.4e-06;
1; Mismatches 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 YAFVGEKFRYLSVFFRK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YAFVGEKFRNYLLVFFQK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)42-4214
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 83.3
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-446-669-4
     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
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Gaps

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Sequence 7, Application US/08833752
Sequence 10. 6448375
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: SAMSON, MICHEL
APPLICANT: PREMENTIER, MARC
APPLICANT: PREMENTIER, MARC
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOXINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: KLODDE, MATTENS, Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Knobbe, Martens, Olson & Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach STATE: 62 Newport Center Drive 16th Floor STATE: 62 COUNTRY: U.S.A.

COUNTRY: U.S.A.

COUNTRY: U.S.A.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.2%; Score 79; DB 5; Length 360;
83.3%; Pred. No. 5.4e-06;
iive 1; Mismatches 2; Indels
                                                                                                            ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: FIPOPPO disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BA PC compatible
COMPUTER: PATEMIN PC-DOS/MS-DOS
SOFTWARE: PATEMIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00476
FILING DATE:
CLASSIFICATION:
                201 N. Figueroa Street, 5th Floor
                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 555-291
TELECHONE: 310-977-1001
TELEPHONE: 310-977-1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 YAFVGEKFRYLSVFFRK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YAFVGEKFRNYLLVFFQK 18
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REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
STREET: 201 W. CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US95-00476-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-833-752-7
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US-09-131-827A-20
IS-09-131-827A-20
Sequence 20, Application US/09131827A
Sequence 20, Application US/09131827A
Sequence 20, Application US/09131827A
Sequence 20, Application
Sequence 20, Application To Alds
TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
FILE REFERENCE: 14014.033
CURRENT APPLICATION NUMBER: 08/09/131,827A
CURRENT PILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 20
SEQ ID NO 20
INMEDIATE: 1997-08-14
NUMBER OF SEQ ID NOS: 20
SEQ ID NO 20
INMEDIATE: 360
INMEDIATE: 360
INMEDIATE: 360
INMEDIATE: 360
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NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
     | Patent No. 6600030
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Dean, Stephen J.
| APPLICANT: Smith, Michael
| APPLICANT: Carrington, Mary
| TITLE OF INVENTION: DELAKED PROGRESSION TO AIDS BY A
| TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
| FILE REFERENCE: 14014.0333
| CURRENT APPLICATION NUMBER: US/09/131,827A
| CURRENT APPLICATION NUMBER: 60/055,659
| PRIOR APPLICATION NUMBER: 60/055,659
| PRIOR APPLICATION NUMBER: 1997-08-14
| NUMBER OF SEQ ID NOS: 20
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .4e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application PC/TUS9500476 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 YAFVGEKFRYLSVFFRK 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 15; Conserv
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PCT-US95-00476-4
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                 Sequence 51, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: No. 6287805e1 Molecules of the G Protein-Coupled NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                  Gaps
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                                                                                                                            Length 360;
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                                                                                                                           Query Match

81.1%; Score 77; DB 4; Length 360
Best Local Similarity 77.8%; Pred. No. 1.2e-05;
Matches 14; Conservative 2; Mismatches 2; Indels
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MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURENT APPLICATION NUMBER: US/09/045,583

FILING DATE: 20-MAR-98

CLASSIPICATION: 435

PRIOR APPLICATION: 435

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 76; DB 3; I
Pred. No. 1.8e-05;
2; Mismatches 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MANDAGGOURS, AMY
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)742-4214
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHAPACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 22
US-09-534-185-51
; Sequence 51, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
                                                                                                                                                                                                                              305 YAFVGEKFRRYISVFFRK 322
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77.8%;
                                                   TOPOLOGY: linear

MOLECULE TYPE: No. 6448375e

US-08-833-752-7
360 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                360 amino acids
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Best Local Similarity 77.8'
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-51
                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Massachusetts
COUNTRY: USA
                 TYPE: amino acid
STRANDEDNESS: siz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02109
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                                                                                                                                                                                                                                                                                                 RESULT 21
US-09-045-583-51
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APPLICANT: Graham, Gerard J. et al.

TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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US-08-575-967A-4

Sequence 4, Application US/08575967A

Sequence 4, Application US/08575967A

Parent No. 6A561B-4

GENERAL INFORMATION:

APPLICANT: Gray et al.

TITLE OF INVENTION: 16

MUBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                            COMPUTER NEARDLE FORTH

MEDIUM TYPE: FLORDY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/534,185

FILING DATE: 24 Mar-2000

CLASSIFICATION OATA:

APPLICATION NUMBER: 09/045,583

FILING DATE: CURKNOWN-

PRIOR APPLICATION NUMBER: 09/045,583

ATTORNEY/AGENT INFORMATION:

NAME: MANDE: MANDERER: 36,207

REFERENCE/DOCKET NUMBER: 36,207

REFERENCE/DOCKET NUMBER: MAI-0444

TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.0%; Score 76; DB 4; Length 360; 77.8%; Pred. No. 1.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/575,967A
FILING DATE:
                                                                                       NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: peptide; PRACHENT TYPE: internal; SEQUENCE DESCRIPTION: SEQ ID NO: 51: US-09-534-185-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFRA: (617) 742-4214
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 YAFVGEKFRRYLSMFFRK 322
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                                                                                                                                                                                        CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
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STREET: 6300
CITY: Chicago
STATE: Illinois
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WESUTI 25
US-09-045-583-54
Sequence 54, Application US/09045583
Fatent No. 6287805:
Applications:
Application US/09045583
Fatent No. 6287805:
GENERAL INFORMATION:
APPLICATION:
APPLICATION:
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
COUNTY:
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTY: USA
ZIP: 03109
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PerentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION DATA:
APPLICATION NUMBER: #36,207
FILING DATE: APPLICATION: #35
RICHARD ADDRESS: MNI-044
TELECOMMUNICATION NUMBER: MNI-044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Heptahelical Receptor Superfamily and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                   Length 355;
                                                                   Query Match 68.4%; Score 65; DB 3; Best Local Similarity 66.7%; Pred. No. 0.0015; Matches 12; Conservative 2; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 54: SEQUENCE CHARACTERISTICS: LENGTH: 355 amin.
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                                                                                                                                                                             301 YAFVGERFRKYLRHFHR 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YAFVGEKFRNYLLVFFQK 18
                                                                                                                                          1 YAFVGEKFRNYLLVFFQK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 66.73
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-847-296B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 26
US-09-534-185-54
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                                                                                                                                                                                                                                                                                                                                            68.4%; Score 65; DB 3; Length 355; 66.7%; Pred. No. 0.0015; tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) NAME/KRY: misc feature
; OTHER INFORMATION: /= "88-2B amino acid sequence"
US-08-575-967A-4
             ATTORNEY AGENT INFORMATION:
NAME: No. 6265184and, Greta E.
REGISTRATION NUMBER: 32,302
REFERENCE/DOCKET NUMBER: 32918
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-485-1960
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Thies, J. Eric
REGISTRATION NUMBER: 35,382
REFERENCE/DOCKET NUMBER: 1963
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3904
TELEFAX: 908-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                             301 YAFVGERFRKYLRHFFHR 318
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                      MOLECULE TYPE: protein
   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-847-296B-1
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Gaps
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APPLICANT: Gerard, No. 6537764ma P.
APPLICANT: Gerard, No. 6537764ma P.
APPLICANT: Gerard, No. 6537764ma P.
APPLICANT: Ponath, Paul D.
APPLICANT: Poneth, Paul D.
APPLICANT: Pot, Theodore W.
APPLICANT: Pot, Theodore W.
APPLICANT: Pot, Theodore W.
APPLICANT: Pot, Theodore W.
APPLICANT: Gin, Shixin
TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND TITLE OF INVENTION: ANTAGONISTS THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,565
FILING DATE: 30-SEP-1996
CLASSIFICATION: 530
               CURKENT AFFLICATION DATA:

CLASSIFICATION NUMBER: US/08/720,565
FILING DATE: 30-SEP-1996
CLASSIFICATION SATA:
APPLICATION NUMBER: PCT/US96/00608
FILING DATE: 19-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375,199
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BLOOK, DAVIG E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS94-05A2
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION INFORMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIORA APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00608
FILING DATE: 19-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375,199
FILING DATE: 19-JAN-1995
ATTORNEY AGENT INFORMATION:
NAME: Brook, David E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 28
US-06-720-565-4
; Sequence 4, Application US/08720565
; Patent No. 6537764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 355 amino acids TYPE: amino acid
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-720-565-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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APPLICANT: Gerard, No. 6537764ma P.
APPLICANT: Mackay, Charles R.
APPLICANT: Mackay, Charles R.
APPLICANT: Post, Theodore W.
APPLICANT: On. Shixin
TITLE OF INVENTION: GROUPLED RECEPTOR GENE CCR3 AND TITLE OF INVENTION: ANTAGONISTS THEREOF CORRESPONDENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible

COMPUTER: IEM PC compatible

COMPUTER: IEM PC compatible

COMPUTER: IEM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/534,185

FILING DATA:

APPLICATION NUMBER: 09/045,583

FILING DATE: CUNKNOWN-

PRIOR APPLICATION NUMBER: 09/045,583

FILING DATE: CUNKNOWN-

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

RESPERENTS/DOCKET NUMBER: MI-044

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617),247-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 68.4%; Score 65; DB 4; Length 355; Best Local Similarity 66.7%; Pred. No. 0.0015; Matches 12; Conservative 2; Mismatches 4; Indels
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COMPOTER: IBM PC Compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                  NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STRET: 28 State Street
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGNENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-09-534-185-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 2, Application US/08720565; Patent No. 6537764; GENERAL INFORMATION:
   Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 355 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 YAFVGERFRKYLRHFFHR 318
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Lexington STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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RESULT 31
US-09-045-583-56

US-09-045-583-56

Sequence 56, Application US/09045583

Patent No. 6287805

GENERAL INFORMATION:

APPLICANT: Graham, Gerard J. et al.

TITLE OF INVENTION: No. 6287805e1 Molecules of the G Protein-Coupled

TITLE OF INVENTION: S6

CORRESPONDENCE: 56

CORRESPONDENCE ADDRESS: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

CITY: Boston

CITY: Massachusetts

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.3%; Score 63; DB 1; Length 355; 66.7%; Pred. No. 0.0034;
                                                                                                             APPLICANT: Soppet, Daniel R.
APPLICANT: Soppet, Daniel R.
APPLICANT: Yi, Li,
APPLICANT: Rosen, Steven M.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSEE: GREELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBN PC comparatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,244
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                        RESULT 30
US-08-461-244-2
; Sequence 2, Application US/08461244
; Patent No. 5776729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 YAFVGEKFKKHLSEIFQK 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGIGSTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YAFVGEKFRNYLLVFFQK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 66.3'
Best Local Similarity 66.7'
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                      Length 355;
                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dairaghi, Daniel J.
APPLICANT: Miyalima, Takahiko
APPLICANT: Miyalima, Atsushi
APPLICANT: Schall, Thomas J.
APPLICANT: Woshimura, Atsushi
APPLICANT: Woshimura, Akihiko
ITITLE OF INVENTION: MANMALIAN CHEMOKINE REAGENTS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
ZIP: 940°.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 65; DB 4;
Pred. No. 0.0015;
2; Mismatches 4
22,592
FR: LKS94-05A2
REGISTRATION NUMBER: 22,592
REPERSNEW POCKET NUMBER: LKSS
TELECOMMUNICATION INPORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                   301 YAFVGERFRKYLRHFFHR 318
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Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein US-08-567-882-7
                                                                                                                                                                         TOPOLOGY: linear; MOLECULE TYPE: protein US-08-720-565-4
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APPLICANT: SAMSON, MICHEL
APPLICANT: PARENTIER, MAC
APPLICANT: PARENTIER, MAC
APPLICANT: UASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEWOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                    66.3%; Score 63; DB 4; Length 355; 66.7%; Pred. No. 0.0034; ive 2; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSEE: Knobbe, Martens, Olson & Bear
T: 620 Newport Center Drive 16th Floor
Newport Beach
                       MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/09503219B; Patent No. 6645491; GENERAL INFORMATION: APPLICANT: Oldham, Elizabeth R. APPLICANT: Homey, Bernhard; APPLICANT: Dieu-No. 6645491jean, Marie C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 33
US-08-833-752-8
Sequence 8, Application US/08833752
; Patent No. 6448375
                                                                                                                                                                                                                                                                                                                                                                 300 YAFVGEKFKKHLSEIFQK 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 355 amino acids
amino acid
                                                                                                                                                                                           Query Match
Best Local Similarity 66.7°
Matches 12; Conservative
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-503-219B-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Sequence 56, Application US/09534185
Batent No. 6403767
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled TITLE OF INVENTION: Heptahelical Receptor Superfamily and Uses
Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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MEDIUM TYPE: Flopew;

MEDIUM TYPE: Flopew;

MEDIUM TYPE: Flopew;

COMBUTER: IEM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/534,185

FILING DATE: 24-Mar-2000

CLASSIFICATION: -Unknown>

PRIOR APPLICATION PATA:

APPLICATION NUMBER: 09/045,583

FILING DATE: -Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISCHARINO NUMBER: 36,207

REFERENCE/DOCKET NUMBER: MNI-044

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 63; DB 3; Length 355
Pred. No. 0.0034;
2; Mismatches 4; Indels
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                       20-MAR-98
N: 11
                                                                                                                                                                                                                                                                                                                                                          MNI-044
                                                                                                                                                                                                                                                                                                                                         REFERENCE DOCKET NUMBER: MNI-TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 742-7400
TELEPAX: (617) 742-4214
INFORMATION FOR SEO ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 YAFVGEKFKKHLSEIFOK 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617)742-4214 INFORMATION FOR SEQ ID NO: 56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YAFVGEKFRNYLLVFFOK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy ERGISTRATION NUMBER: 36,5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 355 amino acids
amino acid
GY: linear
                              CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-56
                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 32
US-09-534-185-56
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Sequence 48, Application US/09534185
Patent No. 6403767
GENERAL INFORMATION:
GENERAL STORM Gerard J. et al.
TITLE OF INVENTION: Ho. 640376761 Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                             Gaps
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Macrophage Inflammatory Protein-1 alpha (MIP-1
alpha)/RANTES Receptor
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      76.9%; Pred. No. 0.0081;
tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02109
COMPUTER READABLE FORM:
MUTER PRENDABLE FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RILING DATE: 24-Mar-2000
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,583
FILING DATE: CURROWN:
ATTORNEY AGENT INFORMATION:
NAME: MANCHAGOURAS, AMY E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
INFORMATION POR SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESSES
ADDRESSES: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-06-012-988A-2; Application US/08012988A; Sequence 2, Application US/08012988A; Patent No. 5652133 GENERAL INFORMATION:
APPLICANT: Murphy, Philip M.
TITLE OF INVENTION: Macrophage Infl; TITLE OF INVENTION: alpha)/RANTES R; NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 374 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                        Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 YAFIGOKFRNYFL 328
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316 YAFIGQKFRNYFL 328
                                                                    1 YAFVGEKFRNYLL 13
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      Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 76.9
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                                                                                                                                                                                                    US-09-534-185-48
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Matches
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Patent No. 6287805
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSER:
ADDRESSER:
ARREFT: 28 State Street
CITY:
Boston
STATE:
Massachusetts
CONTRY:
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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APPLICANT: Caux, Christophe
APPLICANT: Zlotnick, Albert
TITLE OF INVENTION: CHEMOKINE USES, COMPOSITIONS, METHODS;
FILE REPERENCE: DX0394K1
CURRENT PILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: US 60/118,335
PRIOR PELICATION NUMBER: 1999-02-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 365
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 64.2%; Score 61; DB 4; Length 365; Best Local Similarity 76.9%; Pred. No. 0.0079; Matches 10; Conservative 2; Mismatches 1; Indels
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ZIF: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION HATA:
PILING DATE: #15.0-MAR-98
PRICATION NUMBER: #15.207
REPERENCE/DOCKET NUMBER: #16.207
REFERENCE/DOCKET NUMBER: MAI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)22-1-400
TELEPHONE: (617)22-1-400
TELEPHONE: (617)242-421
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: #374 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
; LOCATION: (579)...(579)
; OTHER INFORMATION: unknown nucleotide
US-09-503-219B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307 YAFIGOKFRNYFL 319
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                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 35
US-09-045-583-48
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                                                                                                                                                                                                                                                                 TYPE: PRT
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64.2%; Score 61; DB 3; Length 374;

Query Match

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Gaps
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Sequence 5, Application US/08446669

Patent No. 613287

GENERAL INFORMATION

GENERAL INFORMATION

TITLE OF INVENTION: MANMALIAN MONOCYTE CHEMOATTRACTANT

TITLE OF INVENTION: MANMALIAN

STREET: 5 Palo Alto Square

COUNTRY: GSA

CONTRY: GSA

CONTRY: GSA

CONTRY: GSA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PALOATION DATA:

APPLICATION NUMBER: 30,092

REGISTRATION NUMBER: 30,092

REGISTRATION NUMBER: 30,092

REGISTRATION NUMBER: 30,092

REGISTRATION NUMBER: 30,092

REFERENCE/DOCKET NUMBER: UCAL-237/01US

TELECOMOTNICATION INFORMATION:

TELECOMOTNICATION INFORMATION:

TELECOMOTNICATION NUMBER: 30,092
                                                                                                                                                                                                                                                        Query Match 63.2%; Score 60; DB 1; Length 355; Best Local Similarity 61.1%; Pred. No. 0.011; Matches 11; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.2%; Score 60; DB 3; Length 355; 61.1%; Pred. No. 0.011; ive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                    301 YAFVGERFRKYLROLFHR 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 YAFVGERFRKYLRQLFHR 318
                                                                                                                                                                                                                                                                                                                                                         1 YAFVGEKFRNYLLVFFQK 18
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                                                                        : 355 amino acids
amino acid
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 355 amino acids
amino acid
GY: linear
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Best Local Similarity 61.1.
Best 10 Conservative
The Conservative
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TELEX: 380816CooleyPA
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TELEX: 380816CooleyPA
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein uvporterICAL: NO
                                                                                                                                                               HYPOTHETICAL: N
HYPOTHETICAL: N
HATI-SENSE: NO
US-08-450-393A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: P
ANTI-SENSE: NO
US-08-446-669-5
                                                                                                                  TOPOLOGY:
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US-08-446-669-5
                                                                          LENGIH:
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Sequence 5, Application US/08450393A
Batent No. 5707815
GENERAL INFORMATION:
APPLICANT: Chart, Israel
APPLICANT: Congolin, Shaun
TITLE OF INVENTION: PROTEIN RECEPTORS
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 63.2%; Score 60; DB 1; Length 355; Best Local Similarity 61.1%; Pred. No. 0.011; Matches 11; Conservative 2; Mismatches 5; Indels
                        ADDRESSEE: Townsend and Townsend Khourie and Crew STREFT: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DESYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Rclease #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: MAY 25, 1995
CLASSIFICATION: 424, 1995
                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 19930128
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: CSET, LUANN
REGISTRATION NUMBER: 31,822
REPERENCE/DOCKET NUMBER: UCAL-237/02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5165
TELEFAX: 415-8857-0663
                                                                                                                                                                                                                                                                                                                                                                                                                                                          15280-118
                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFRENCE/DOCKET NUMBER: 1528/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YAFVGEKFRNYLLVFFQK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFRAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 355 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 38
US-08-450-393A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-012-988A-2
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                                                                                                                         COUNTRY:
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RESULT 40

US-09-239-308-1

US-09-239-308-1

US-09-239-308-1

Sequence 1, Application US/0923938

Patent No. 632510

GENERAL INFORMATION:

APPLICANT: Oth, Shixth

APPLICANT: Masman, Walter

APPLICANT: Leukcôite, Inc.

TITLE OF INVENTION: THEREFOR

CURRENT FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 1

SOFTWARE: FastSEQ for Windows Version 3.0

SOFTWARE: FastSEQ for Windows Version 3.0

SOFTWARE: PRT

ORGANISM: Homo sapien

US-09-239-938-1

ORGANISM: Homo sapien

US-09-239-938-1

ORGANISM: Homo sapien

US-09-239-938-1

ORGANISM: Homo sapien

US-09-239-938-1

OURTH STEPPER ORGENERRYLLUVFFOR 18

Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps

OY 1 YARVGERFRRYLLUVFFOR 18

Db 301 YARVGERFRRYLRQLFHR 318

Search completed: September 28, 2004, 09:21:33

JOB time: 16.2 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

3 ; Search time 59.625 Seconds (without alignments) 97.074 Million cell updates/sec September 28, 2004, 09:06:23 Run on:

US-10-084-813-15 95 Title:

1 YAFVGEKFRNYLLVFFQK 1'8 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1349238 seqs, 321558718 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:*

| Cgn2 6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
| Cgn2 6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
| Cgn2 6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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| Cgn2 6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| Cgn2 6/ptodata/1/pubpaa/US00_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 15, Appl	Sequence 105, App	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 22, Appl	Seguence 2, Appli	Sequence 22, Appl	Sequence 15, Appl	Sequence 17, Appl	Sequence 1, Appli	Seguence 2, Appli	Sequence 2, Appli	Sequence 5, Appli
	QI	US-10-084-813-15	US-10-084-813-105	US-10-095-876A-2	US-09-725-285-2	US-09-759-841-2	US-09-779-879A-2	US-09-779-879A-22	US-09-779-880A-2	US-09-779-880A-22	US-09-813-653-15	US-09-813-653-17	US-09-796-202-1	US-09-195-662A-2	US-09-339-912A-2	US-09-938-719-5
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	Score	95	95	9	95	95	95	95	95	95	95	95	95	95	95	95
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ALIGNMENTS

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Sequence 15, Application US/10084813
; Sequence 15, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICAMY: SAXINGER:
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; TILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; PRIOR FILING DATE: 1999-08-27
; NUMBER: OF SEQ ID NOS: 1242
; SOPTWARE: PATENTIN VETSION 3.1
; SEQ ID NO 15
! LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: binding peptide US-10-084-813-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 18, Conservative
US-10-084-813-15
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RESULT 2 US-10-064-813-105 ; Sequence 105, Application US/10084813 ; Publication No. US20030068615A1 1 YAFVGEKFRNYLLVFFQK 18 요

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CURRENT APPLICATION NUMBER: US/09/725,285
                                            09/339,912
              CURRENT FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 09/339,
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1998-06-15
PRIOR FILING DATE: 1998-11-18
PRIOR FILING DATE: 1998-11-18
PRIOR RILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTING DATE: 1995-06-06
LENGTH: 352
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; ORGANISM: Homo sapiens
US-09-759-841-2
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US-09-779-879A-2
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US-09-759-841-2
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Patent No. US20010000241A1
Batent No. WORNATION:
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven, M.
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10
FILE REFERENCE: 1488.1150003
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              APPLICANT: SXXINGER, CARL
TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USS
FILE REPERENCE: 21.8875
CURRENT PELING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US/10/084,813
PRIOR APPLICATION NUMBER: PCT/US00/23505
PRIOR FILING DATE: 2000-08-25
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 1242
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; CTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Au-Young, Janice; Bandman, Olga
APPLICANT: Au-Young, Janice; Bandman, Olga
APPLICANT: Coleman, Roger; Wilde, Craig G.
TITLE OF INVENTION: DNA ENCODING NOVEL CHEMOKINE RECEPTORS
FILE REFERENCE: PP-0060-1 CON
CURRENT APPLICATION NUMBER: US/10/095,876A
CURRENT APPLICATION NUMBER: US 08/638,081
PRIOR FILING DATE: 1996-04-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PERL Program
SOFTWARE: PERL Program
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"NAME/KEY: misc feature

"OTHER INFORMATION: Incyte ID No. US20030148294A1 478861
US-10-095-876A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 95; DB 14;
Pred. No. 3.5e-08;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%;
Matches 18; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                SEQ ID NO 105
LENGTH: 18
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Gaps
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APPLICANT: Rosen, Craig A.
APPLICANT: Roschke, Viktor
APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNRIO
FILE REFERENCE: 1488.115000A
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; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-725-285-2
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Petent No. US20010039026A1

GENERAL INFORMATION:

APPLICANT: Rickett, Graham A

APPLICANT: Dobbs, Susan

APPLICANT: Derros, Manoussos

TILLE REFERENCE: PC10348APME

CURRENT APPLICATION NUMBER: US/09/759,841

CURRENT APPLICATION NUMBER: GB 0000661.9

PRIOR APPLICATION NUMBER: GB 0000661.9

PRIOR FILING DATE: 2001-01-12

PRIOR APPLICATION NUMBER: GB 0000663.5

PRIOR FILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-01-12
                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence: Genomic
09/195,662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09779879A Patent No. US20020048786A1
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Sequence of Application US/09813653
Sequence No. US20020064770A1
GENERAL INFORMATION:
APPLICANT: Nestor, John
APPLICANT: Wilson, Carol
APPLICANT: Tan Hehir, Christina
TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
TITLE OF INVENTION: Binding Compounds
TITLE OF INVENTION: Binding Compounds
CURRENT APPLICATION NUMBER: US/09/813,653
CURRENT FILING DATE: 2001-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-9-//9-MENDALE

Sequence 22, Application US/09779880A

Patent No. US2020061834A1

GENERAL INFORMATION:

APPLICANT: Rosen, Craig A.

APPLICANT: Li, Yi steven, M.

APPLICANT: Li, Yi steven, M.

APPLICANT: Li, Yi steven, M.

TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10

FILE REPERENCE: 1488.11500C

CURRENT APPLICATION NUMBER: US/09/779,880A

CURRENT PLICATION NUMBER: US 60/181,258

FRIOR FILING DATE: 2000-02-09

FRIOR FILING DATE: 2000-02-09

FRIOR FILING DATE: 2000-03-09

FRIOR PRICE FILING DATE: 2000-03-09

FRIOR PRICE FILING DATE: 2000-03-09

FRIOR FILING DATE: 2000-03-09
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Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 95; DB 9; Length 352; Best Local Similarity 100.0%; Pred. No. 7.4e-07; Matches 18; Conservative 0; Mismatches 0; Indels
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,258
PRIOR PILING DATE: 2000-02-09
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-03-2
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PATENTIN VETSION 3.0
LENGTH: 352
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                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT; ORGANISM: Homo sapiens
US-09-779-880A-2
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ORGANISM: Homo sapiens
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US-09-779-880A-22
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US-09-813-653-15
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US-09-779-879A-22

US-09-779-879A-22

Sequence 22, Application US/09779879A

Patent No. US2002048786A1

GENERAL INFORMATION:

APPLICANT: Roschke, Viktor

APPLICANT: Roschke, Viktor

APPLICANT: Ruben, Steven, M.

TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10

FILE REPRENCE: 1488 115000A

CURRENT FILING DATE: 2001-02-09

PRIOR PILING DATE: 2000-02-09

PRIOR PILING DATE: 2000-02-09

PRIOR PILING DATE: 2000-02-09

PRIOR FILING DATE: 2000-02-09

PRIOR FILING DATE: 2000-02-09

PRIOR FILING DATE: 2000-02-09

PRIOR FILING DATE: 2000-03-09

PRIOR FILING DATE: 2000-03-09

PRIOR FILING DATE: 2000-03-09

PRIOR FILING DATE: 2000-03-09

SPRIOR FILING DATE: 2000-03-05

NUMBER OF SEQ ID NOS: 58

SOC ID NO 22

LENGTH: 352
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Patent No. US20020061834A1
GENERAL INFORMATION:
APPLICANT: Roschke, Viktor
APPLICANT: Roschke, Viktor
APPLICANT: Roschke, Viktor
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven, M.
TITLE OF INFORTION: Human G-protein Chemokine Receptor (CCRS) HDGNRIO FILE REFERENCE: 1488.115000C
CURRENT APPLICATION NUMBER: US/09/779,880A
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Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
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100.0%; Score 95; DB 9; I
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0;
       CURRENT APPLICATION NUMBER: US/09/179,879A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,258
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/187,999
PRIOR PLING DATE: 2000-03-09
PRIOR FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 58
SEQ ID NOS: 58
SECTRARE: PATENTIN VERSION 3.0
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CRGANISM: Homo sapiens
US-09-779-879A-2
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US-09-779-880A-2
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Tue Sep 28 15:49:59 2004

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Sequence 2, Application US/0933912A;
Sequence 2, Application US/0933912A;
Patent No. US20020099176A1
GENERAL INFORMATION:
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10;
TITLE OF INVENTION: (CCES Receptor);
TITLE OF INVENTION: (CCES Receptor);
TITLE OF INVENTION: (CCES Receptor);
TITLE OF INVENTION: 0/09/339, 912A;
CURRENT FILING DATE: 1999-06-25;
PRIOR PELING DATE: 1999-06-25;
PRIOR PELING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR PELING DATE: 1995-06-06;
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2. Application US/09195662A

Sequence 2. Application US/00006745A1

GENERAL INFORMATION:
APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Li, Yi
TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGNR10 (CCR5 Receptor)
FILE REFERENCE: 1488.1150002
CURRENT APPLICATION NUMBER: US/09/195,662A
CURRENT PILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR PLING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
SEQ ID NO 2. Patentin version 3.0
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100.0%; Pred. No. 7.4e-07;
iive 0; Mismatches 0;
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100.0%; Score 95; DB 9; 1
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0;
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; CTHER INFORMATION: Deduced Amino Acid Sequence US-09-339-912A-2
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ORGANISM: Artificial Sequence: Genomic
FEATURE:
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ORGANISM: Artificial Sequence: Genomic
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Matches 18; Conserv
                                                         , ORGANISM: human
US-09-796-202-1
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US-09-195-662A-2
        LENGTH: 352
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LENGTH: 352
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| Patent No. US2002064770A1
| GENERAL INFORMATION:
| APPLICANT: Nestor, John
| APPLICANT: Mestor, John
| APPLICANT: Wilson, Carol
| APPLICANT: Tan Hehir, Christina
| FILE REPRENCE: CNS-0.05
| CURRENT APPLICATION NUMBER: US 60/190,946
| PRIOR APPLICANTON NUMBER: US 60/190,996
| PRIOR FILING DATE: 2000-03-21
| PRIOR APPLICATION NUMBER: US 60/191,299
| PRIOR FILING DATE: 2000-03-21
| NUMBER OF SEQ ID NOS: 44
| SOSTWARE: Patentin version 3.0
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Patent No. US20020068813A1
GENERAL INFORMATION:
APPLICANT: Dragio, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCRS PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010/JPW/SHS
CURRENT APPLICATION NUMBER: US/09/796,202
CURRENT FILING DATE: 2001-02-28
NUMBER: OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
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PRIOR APPLICATION NUMBER: US 60/190,946
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/190,996
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/191,299
PRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Version 3.0
SEQ ID NO 15
LENGTH: 352
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ORGANISM: Homo sapiens
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US-09-813-653-17
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SEQ ID NO 17
LENGTH: 352
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US-09-813-653-17
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PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOXINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: CACOUNTRY: U.S.A.

COUNTRY: U.S.A.

ZIP: 9260A

ZIP: 9260A

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/938,703
                                                                                                                       COMPUTER READABLE FORM:
MEDTION TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
RAPLICATION DATA: US/09/939,226
FILING DATE: 24-Nug-2001
CLASSIFICATION: <UNknown>
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CORRESPONDENCE ADDRESS:
ADDRESSE: Kartens, Olson & Bear
ADDRESSE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
             ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 95; DB 9; Sest Local Similarity 100.0%; Pred. No. 7.4e-07; Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFRENCE/DOCKET NUMBER: «Unknown>
INFORWATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTER.STICS:
LENGTH: 352 amino acids
TYPE: amino acid
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CLASSIFICATION: «Unknown»
PRIOR APPLICATION NDATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
RAPPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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GENERAL INFORMATION:
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  CORRESPONDENCE ADDRESS:
                                                                                                       U.S.A.
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US-09-938-703-5
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Patent No. US20020110805A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                           Gaps
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRING APPLICATION NUMBER: US/09/938,719
FILING DATE: 24-Aug-2001
CLASSIFICATION: «Unknown»
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                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSER: KNObbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
Local Similarity 100.0%; Pred. No. 7.4e-07; nes 18; Conservative 0; Mismatches 0;
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REGIGTRATION NUMBER: 34,115
REGIGTRATION NUMBER: 401/snown>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:

APPLICATION WURBER: 09/626,939

FILING DATE: 27-ULLY-2000

ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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Best Local Similarity 100.
Matches 18, Conservative
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US-09-939-226-5
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Gaps

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Sequence 477, Application US/09826509

Sequence 477, Application US/09826509

Publication No. US20030204073A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Protein-Coupled Receptors
FILE REFERENCE: AREN 207
CURRENT APPLICATION NUMBER: US/09/826,509
CURRENT FILING DATE: 2001-04-05

FRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2001-04-07
PRIOR PILING DATE: 1998-10-13
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100.0%; Score 95; DB 11; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0
  ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/734,221A
FILING DATE: 11-Dec-2000
CLASSIFCATION: CURROWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                               APPLICATION DATE:

APPLICATION NUMBER: US 08/666,020
FILING DATE: 19-JUN-1996
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-004 NZ
TELEPHONE: 201-487-5800
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 95; DB 10; Best Local Similarity 100.0%; Pred. No. 7.4e-07; Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Homo sapiens
) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-734-221A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 352 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 589
SOFTWARE: Patentin Version 2.1
SEQ ID NO 477
LENGTH: 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CORGANISM: Homo sapiens
US-09-826-509-477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
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US-09-826-509-477
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Patent No. US20020132269A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven M.
ITILE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS TITLE OF INVENTION: HDGNR.0
FILE REFERENCE: 1488 115006
CURRENT APPLICATION NUMBER: 08/96502,783A
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR PLING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
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LIU, ROUG
LIU, ROUG
TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
MACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
USES THEREOF
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CORRESPONDENCE ADDRESS:
ADDRESSE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
                                                                                                                                                      TOPOLOGY: linear ; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 5: US-09-938-703-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DENG, HONGKUI
ELLMEIER, WILFRIED
LANDAU, NATHANIEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 19
US-09-734-21A-14
Sequence 14, Application US/09734221A
Publication No. US20030096221A1
                                                                                                                                                                                                                                                                                                                                                                                                                                           297 YAFVGEKFRNYLLVFFOK 314
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APPLICANT: LITTMAN, DAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New Jersey
COUNTRY: USA
                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CORGANISM: Homo sapiens
US-09-502-783A-2
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US-09-502-783A-2
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LENGTH: 352
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Gaps
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                                                                                                                                                                                                                                                Length 352;
                                                                                                                                                   NAME/KEY: misc_feature
OTHER INFORMATION: /= "88C amino acid sequence"
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
                                                                     LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                    297 YAFVGEKFRNYLLVFFQK 314
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               TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                         1 YAFVGEKFRNYLLVFFOK 18
                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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                                                                                                                                            FEATURE
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                                                                                                                   Sequence 5, Application US/10151274

Publication No. US20030064071A1

GENERAL INFORMATION:

APPLICANT: Littman, Dan R.

APPLICANT: Kwon, Douglas S.

APPLICANT: Wan Kooyk, Yvette

APPLICANT: Geijtenbeck, Tneo

TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY

TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY

TITLE OF INVENTION: ELLS

FILE REPRENCE: 1049-1-017

CURRENT APPLICATION NUMBER: US/10/151,274

CURRENT APPLICATION NUMBER: US/09/517,605

PRIOR FILING DATE: 2000-03-02

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 5

MANDER OF SEQ ID NOS: 17

MANDER OF SEQ ID NOS: 17

SEQ ID NO 5

MANDER OF SEQ ID NOS: 17
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; Publication No. US2002015088A1
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 6606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/106,623
FILING DATE: 26-MAI-2002
CLASSICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/771,276
FILING DATE: -CURROWN-
APPLICATION NUMBER: 08/771,276
FILING DATE: -CURROWN-
ATTORNEY/AGENT INFORMATION:
NAME: NO. US20020150888A1ANG Greta E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 95; DB 12; Best Local Similarity 100.0%; Pred. No. 7.4e-07; Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33670
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297 YAFVGEKFRNYLLVFFQK 314
                                297 YAFVGEKFRNYLLVFFQK 314
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     1 YAFVGEKFRNYLLVFFQK 18
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STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CRGANISM: Homo sapiens
US-10-151-274-5
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US-10-106-623-2
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JUNEARADA LINCHARATION:

APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Steven, M.
APPLICANT: Rosen, Steven, M.
APPLICANT: Ruben, Steven, M.
APPLICANT: Ruben Steven, M.
APPLICANT: Ruben G.
TITLE OF INVENTION: Human G.
FILE REPERENCE: 1488.115001
CURRENT PAPLICATION NUMBER: US/10/067,800
CURRENT FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: 60/297,257
PRIOR FILING DATE: 2001-06-12
PRIOR FILING DATE: 2001-06-12
PRIOR FILING DATE: 2001-06-12
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-12-21
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                                      Human G-protein Chemokine Receptor (CCR5) HDGNR10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 95; DB 14; Length 352; 100.0%; Pred. No. 7.4e-07; ive 0; Mismatches 0; Indels (
                            FILE REPERENCE: 1488.115001
CURRENT APPLICATION: Human G-protein Chemokine
FILE REPERENCE: 1488.1150001
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 02/10/04/153
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-06-12
PRIOR PILING DATE: 2001-08-08
PRIOR PILING DATE: 2001-10-12
PRIOR PILING DATE: 2001-10-12
PRIOR PILING DATE: 2001-110-12
PRIOR PILING DATE: 2001-110-13
PRIOR PILING DATE: 2001-110-13
PRIOR PILING DATE: 2001-110-13
PRIOR PILING DATE: 2001-112-21
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PATENTIN VERSION 3.1
SOFTWARE: PATENTIN VERSION 3.1
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; Sequence 22, Application US/10067800
; Beduence 12, Application US/00058A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               297 YAFVGEKFRNYLLVFFOK 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YAFVGEKFRNYLLVFFQK 18
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Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-10-067-800-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; CRGANISM: Homo sapiens
US-10-067-800-22
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                                                                                                                                                                                                                                                                                   APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Li, Yi
TILE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10
FILE REFERENCE: 1488.115000N
CURRENT FILING DATE: 2002-09-03
FURRENT FILING DATE: 2002-09-03
FRIOR PILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-01-15
PRIOR FILING DATE: 1998-11-18
PRIOR PLING DATE: 1998-11-18
PRIOR PLING DATE: 1998-11-18
PRIOR PLING DATE: 1998-06-06
SOFTWARE: PALENTING DATE: 1998-06-06
SOFTWARE: PALENTING DATE: 1998-06-06
SOFTWARE: PALENTING DATE: 1995-06-06
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Publication No. US2030092632A1

GENERAL INFORMATION:

APPLICANT: Dragic, Tatjana

APPLICANT: Dragic, Tatjana C.

TITLE OF INVENTION: SULFATED CCR5 FEPTIDES FOR HIV-1 INFECTION

FILE REFERENCE: 61010-AB-1;

CURRENT APPLICATION NUMBER: US/10/086,814

CURRENT FILING DATE: 2002-02-28

NUMBER OF SEQ ID NOS: 38

SOFTWARE: Patentin version 3.1

SEQ ID NO 1

LENTH: 352
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100.0%; Pred. No. 7.4e-07;
ative 0; Mismatches 0;
                                                                                                                           RESULT 24
US-10-232-686-2
'Sequence 2, Application US/10232686
'Publication No. US20030023044A1
'GENERAL INFORMATION:
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Publication No. US20030100058A1
GENERAL INFORMATION:
APPLICANT: ROSCHKE, VIKTOR
APPLICANT: ROSCHKE, Craig A.
297 YAFVGEKFRNYLLVFFQK 314
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Best Local Similarity lov..
Best 18; Conservative
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; ORGANISM: Homo sapiens US-10-232-686-2

US-10-086-814-1

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297 YAFVGEKFRNYLLVFFOK 314

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; ORGANISM: Homo sapiens US-10-086-814-1

TYPE: PRT

RESULT 26 US-10-067-800-2

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Squence 1. Application US/10072301
| Sequence 1. Application VS/10072301
| Publication No. US20030152913A1
| GENERAL INFORMATION:
| APPLICANT: Hua, Shao-bing
| APPLICANT: Pauling, Michelle H.
| APPLICANT: Pauling, Michelle H.
| TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNOBER]
| TITLE OF INVENTION: VIRUS
| TITLE OF INVENTION: VIRUS
| FILE REFERENCE: 25636-718
| CURRENT APPLICATION NUMBER: US/10/072,301
| CURRENT APPLICATION NUMBER: 2002-02-08
| NUMBER OF SEQ ID NOS: 54
| SOFTWARE: Patentin version 3:1
| SEQ ID NO. 1.
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WINDER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSES: LAHIVE & COCKFIELD, LLP

STREET: 28 State Sireet

CITY: Boston

STARE MASSACHERED

CONTEXT: USA

CONTEXT: USA

CONTEXT: USA

CONTEXT: USA

CONTEXT: USA

COMPUTER: PROPABLE FORM:

WESTON 7.5

WESTON 4.6

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFFWARE: Patentin Release #1.0, Version #1.25
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100.0%; Pred. No. 7.4e-07;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                         Query Match 100.0%; Score 95; DB 14; Best Local Similarity 100.0%; Pred. No. 7.4e-07; Matches 18; Conservative 0; Mismatches 0;
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RAPLICATION NUMBER: US/10/164,649
FILING DATE: 07-UUN-2002
CLASSIFICATION: <Unknown>
CURRENT APPLICATION NUMBER: US/10/323,314
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 1
LENGTH: 352
                                                                                                                                                                                                                                                                                                                                                                                    297 YAFVGEKFRNYLLVFFQK 314
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Matches 18; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                              TYPE: PRT
ORGANISM: human
US-10-323-314-1
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US-10-072-301-1
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US-10-225-567A-352

Sequence 352, Application US/10225567A

Publication No. US20030113798A1

GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: BIOWN, JOSEPh P.
APPLICANT: BIOWN, JOSEPh P.
APPLICANT: BOUSH, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: 05/257,144

PRIOR APPLICATION NUMBER: 60/257,144

PRIOR PILING DATE: 2000-12-19
PRIOR PILING DATE: 2000-12-19

NUMBER OF SEQ ID NOS: 2292

SOFTWARE: Patentin version 3.1

SEQ ID NO 35.2

SEQ ID NO 35.2
                                                                                        ; Sequence 6, Application US/10290058A
; Publication No. US20030104455A1
; Cantence 6, Application No. US20030104455A1
; Cantence 6, Application No. US2030104455A1
; APPLICATT. Silos Santiago, Inmaculada
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Without 10 US/10/290,058A
; TITLE OF INVENTION: WITHOUT US/10/290,058A
; FILE REFERENCE: MPIOL-289PIRM
; CURRENT FILING DATE: 2002-11-07
; PRIOR PELING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 6
; LENGTH: 352
; TYPR: PATES
; TYPR: PATES
; ORGANISM: Homo Sapien
US-10-290-058A-6
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US-10-323-314-1
Sequence 1, Application US/10323314
Publication No. US20030139571A1
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010-1/JPW/MAP/DJK
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100.0%; Score 95; DB 14;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0;
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US-10-225-567A-352
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Best Local Similarity
Matches 18; Conserv
                                                                                 US-10-290-058A-6
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Sequence 67, Application US/10239423
Publication No. US20300186889A1
Publication No. US20300186889A1
GENERAL INFORMATION:
APPLICANT: FORSSMANN, Wolf-Georg; FORSSWANN, Ulf; ADERMANN, Knut;
APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikolaj
TITLE OF INVENTION: Disgnostic Agent and Medicament for Examining the
TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells and
TITLE OF INVENTION: For Treating Tumor Diseases and Inflammation Cells and
TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine
TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction
FILE REFERENCE: 022217us
CURRENT APPLICATION NUMBER: US/10/239,423
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Publication No. US2003166024A1
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Rosenke, Viktor
APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven, M.
TITLE REFERENCE: 1488.11500A
CURRENT APPLICATION NUMBER: US/10/135,839
CURRENT FILING DATE: 2002-05-01
FRICA APPLICATION NUMBER: US/09/779,879A
FRICA PAPLICATION NUMBER: US 60/187,999
FRICA FILING DATE: 2000-02-09
FRICA RILING DATE: 2000-03-09
FRICA RILING DATE: 2000-03-05
FRICA RILING DA
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Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0;
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100.0%; Score 95; DB 14;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/187,999
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 58
SSEYTARRE: Patentin version 3.0
LENGTH: 352
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ORGANISM: Homo sapiens
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US-10-135-839-22
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US-10-135-839-22
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US-10-239-423-67
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Publication No. US2003016598A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hua, Shao-bing
APPLICANT: Pauling, Michelle H.
APPLICANT: Zhu, Li
TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST
TITLE OF INVENTION: PRAGMENTS DERIVED FROM MEMBRANE PROTEINS
FILE REPERENCE: 25636-117
CURRENT APPLICATION NUMBER: US/10/071,866
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 1.
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Publication No. US20030166024A1
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Roschke, Viktor
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
FILE REFERENCE: 1488.115000A
CURRENT APPLICATION WUMBER: US/10/135,839
CURRENT FILING DATE: 2002-05-01
PRIOR APPLICATION NUMBER: US/09/779,879A
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100.0%; Score 95; DB 14;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0;
                                 APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MI-044
TELECOMUNICATION INFORMATION:
TELEPHONE: (617)227-740
TELEFRAX: (617)227-740
TELEFRAX: (617)227-741
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
SEQUENCE TYPE: peptide
SEQUENCE TYPE: peptide
SEQUENCE TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-164-649-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 YAFVGEKFRNYLLVFFOK 314
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           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 33
US-10-071-866-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-071-866-1
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USA
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ZIP: 92037
                                                                                                                                                                                                                                                                                                               CITY: La J
STATE: CA
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US-10-360-828-1
                                                                                                     US-10-439-845-4
                                                                                 RESULT 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                        Length 352;
                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/439,845
FILING DATE: May 28, 1997
APPLICATION NUMBER: Provisional 60/018,508
FILING DATE: May 28, 1996
CLASSIFICATION:
MAPPLICATION NUMBER: 38,347
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
TELEFRANCE/DOCKET NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 38,347
TELEFRANCE 619/678-5070
TELEFRANCE 619/678-5070
TELEFRANCE 619/678-5070
TELEFRANCE 619/678-5070
TELEFRANCE CARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: mino acid
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: DE10016013.1
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 67
LENGTH: 352
                                                                                                                                                                                                                                                                                                                                                               297 YAFVGEKFRNYLLVFFQK 314
                                                                                                                                                                                                                                                                                                                                   1 YAFVGEKFRNYLLVFFQK 18
                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
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US-10-439-845-2
                                                                                                                                                              FEATURE:
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1 YAFVGEKFRNYLLVFFQK 18

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US-SOUR 48

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Sequence 5, Application US/10661798

Publication No. US20040110127A1

GENERAL INFORMATION:
APPLICANT: Samoon, Michael
APPLICANT: Parmentier, Marc
APPLICANT: Parmentier, Marc
APPLICANT: Parmentier, Marc
APPLICANT: Prederic, Libert
ITILE OF INVENTION: Screening Methods for Identifying Compounds which Decrease HIV ET
ITILE OF INVENTION: A Cell
FILE FERENCE: 9409/2027F
CURRENT APPLICANTON NUMBER: 09/938,703
PRIOR APPLICANTON NUMBER: 09/938,703
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 1209-0-27
PRIOR APPLICANTON NUMBER: 09/833,752
PRIOR FILING DATE: 1997-04-09

PRIOR FILING DATE: 1997-04-09

PRIOR FILING DATE: 1997-03-01

PRIOR FILING DATE: 1996-03-01

PRIOR PRIOR FILING DATE: 1996-03-01

PRIOR FILING DATE: 1996-03-01

PRIOR FILING DATE: 1996-03-01

PRIOR FILING DATE: 1996-03-01

PRIOR PRIOR FILING DATE: 1996-03-01

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 95; DB 16; Length 352; Best Local Similarity 100.0%; Pred. No. 7.4e-07; Matches 18; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: September 28, 2004, 09:44:42 Job time : 59.625 secs
PRIOR APPLICATION NUMBER: US 10/072,301
PRIOR FILING DATE: 2002-08-08
PRIOR FILING DATE: 2002-04-25
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297 YAFVGEKFRNYLLVFFQK 314
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                                                                                                                                                                                                                                                                                                                     TYPE: PRT
; ORGANISM: Homo sapiens
US-10-360-828-1
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CRGANISM: Homo sapiens
US-10-661-798-5
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein September 28, 2004, 08:57:36; Search time 9.675 Seconds (without alignments) 178.961 Million cell updates/sec Run on:

US-10-084-813-15 95 score:

1 YAFVGEKFRNYLLVFFQK 18 Perfect sc Sequence: 283366 seqs, 96191526 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Total number of hits satisfying chosen parameters:

seg length: 0 seg length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		•			SUMMERTES	
Result		Query				
No.	Score	Match	Length	BB	CI .	Description
Н	95	100.0	352	7	A43113	chemokine (C-C) re
7	79	83.2	360	~	JC2443	chemokine (G-C) re
m	65	68.4	355	7	G02436	kine (C-C)
4	64		359	N	I49341	MIP-1 alpha recept
വ	63	66.3	355	Ŋ	90	
9	62		383	N	9	
7	61		369	7	90	G protein-coupled
80	9	m.	355	7	A45177	m
6	58	61.1	354	7	158186	probable G protein
10	57	0.09	355	(1)	JC4304	ď
11	57	0.09	360	(7	A57160	ž
12	53	55.8	355	7	I49339	macrophage inflamm
13	53	'n.	356	7	149340	ha r
14	52	54.7	360	Ŋ	JC4587	
15	52	4.	378	0	B55735	lymphocyte-specifi
16	20	ď	356	Ŋ	S42096	interleukin-8 rece
17	20	52.6	359	N	A48921	interleukin-8 rece
18	20	ď	360	N	A53611	interleukin-8 rece
19	20	52.6	378	7	A45680	G protein-coupled
20	49	ä	76	~	E95247	hypothetical prote
21	49	ä	16	0	B98112	cal
22	49	ä	374	7	10	ò
23	48	50.5	367	7	JE0349	interferon-inducib
24	47	•	358	7		interleukin-8 rece
25	47	•	378	7	A55735	G protein-coupled
26	46	•	354	7	99	interleukin-8 rece
27	46	48.4	355	~		interleukin-8 rece
28	45.5		377	N	$\overline{}$	glycosyltransferas
29	45	47.4	350	7	JN0621	G protein-coupled

angiotensin II rec	angiotensin II rec	angiotensin II rec	angiotensin II rec	H	angiotensin II rec	angiotensin II rec	angiotensin II rec	angiotensin II rec	IL8-related recept	G protein-coupled	hypothetical prote	hypothetical prote	hypothetical prote	sugar transport pr	G protein-coupled
JC1104	844425	JC1194	A48857	A42656	JQ1516	S15403	JH0621	JC2134	G02670	JC5069	C81207	E64514	T03883	C90270	165989
~	N	(7	Ŋ	~	N	N	~	(1	N	~	7	7	N	~	N
359	359	359	359	359	359	359	359	359	358	375	119	259	293	297	333
4	4.	4.	4.	4.	4.	4.	4.	4.4	.3	۳.	۳.	۳,	45.3	6.3	۳.
47.4	47	47	47	47	4	47	47	4	4	4	45	4.5	4	4	4
	45 47		45 47	45 47	45 47	45 47	45 47	45 47	44 46	44 46	43 45	43 45	43 45	43 45	43 45

ALIGNMENTS

-1		
5	A43113	
RESI	A43	

chemokine (C-C) receptor 5 - human N;Alternate names: C-C CKR-5; CCR5

N. Alecanate names: C-C CRR-5; CRR5

(Species: Homo sapiens (man)
(C) Edet: 12-701-1996 #sequence revision 12-701-1996 #text_change 20-70n-2000
(C) Edet: 12-701-1996 #sequence revision 12-701-1996 #text_change 20-70n-2000
(C) Accession: All113; \$71808; Acs8832; G02653; As58833
(E) Semeon, M. 1 Labbe. O.; Molleraau, C.; Vassart, G.; Parmentier, M.
(E) Ederence number: All13; MUID:9241590; PMID:8639485
(A) Title: Molecular cloning and functional expression of a new human CC-chemokine receptor A; Resterence number: A3113; MUID:9241590; PMID:8639485
(A) Accession: A3113; MUID:9241590; PMID:8639485
(A) Title: Resterence (BEX39492; NID:91262810; PIDN:CAA62796.1; PID:91262811
(A) Inai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Dome, R.W.; Vassart, G.; Parmentier, M.; Imbert, F.; Doran, B.; Yii, Y.; Smyth, R.J.; Collman, R.G.; Dome, R.W.; Vassart, G.; Parmentier and A; Reterence number: S71809; MUID:96345670; PMID:8751444
(A) Reterence number: S71809; MUID:96345670; PMID:8751444
(A) Reterence number: S71809; MUID:96345670; PMID:8751444
(A) Reterence number: MASSARACHGHILLGANPKNSAVSKY (SAM3)
(A) Accession: A58834
(A) Accession: A58832
(A) Accession:

R,Combadiere, C. submitted to the EMBL Data Library, May 1996

A,Reference number: H01541
A,Accession: G2653
A,Accession: G2653
A,Accession: G2653
A,Accession: G2653
A,Accession: G2653
A,Accession: G2653
A,Accession: G270
A,Accession: G270
A,Cross-references: EMB1.U570
B,Residues: 1-89,'L', 91-352
A,Cross-references: EMB1.U570
B,Resport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
A,Title: Molecular cloning and functional characterization of a novel human CC chemokine A,Reference number: A58833; WUID:96291862; PMID:8663314

Gaps

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Length 360;

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A/Gene: GDB:CMKBR3
A/Gene: GDB:CMKBR3
A/Gene: GDB:CMKBR3
A/Gene: GDB:CMKBR3
A/Gene: GDB:CMCBR3
A/Gene: GDB:CMCBR3
C/Superfamily: vertebrate rhodopsin
C/Superfamily: vertebrate rhodopsin
C/Superfamily: vertebrate rhodopsin
C/Superfamily: vertebrate receptor; glycoprotein; phosphoprotein; transmembrane #status predicted <TML>
F)36-60/Domain: transmembrane #status predicted <TML>
F)10-11/Domain: transmembrane #status predicted <TML>
F)147-11/Domain: transmembrane #status predicted <TML>
F)205-223/Domain: transmembrane #status predicted <TMC>
F)205-233/Domain: transmembrane #status predicted <TMC>
F)240-261/Domain: transmembrane #status predicted <TMC>
F)241-273,106-183/Disulfide bonds: #status predicted
F)345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1998
C;Accession: 149341
C;Accession: 149341
J; Murphy, P.M.
J; Murphy, P.M.
J; Biol. Chem. 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokin.
A;Reference number: 149339; MUID:95340546; PMID:7542241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-106, N',108-275,'S',277-280,'R',282-355 <COM>
A;Cross-references: GB:U28694; NID:g1199579; PIDN:AACS0469.1; PID:g1199580
A;Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AACS0469.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: G22436
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-155 < PON>
A;Residues: 1-155 < PON>
A;Cross-references: EMBL:U49727; NID:G1477560; PIDN:AAB09726.1; PID:g1477561
A;Crombadiere, C.; Ahuja, S.K.; Murphy, P.M.
J. Biol. Chem. 270, 16491-16494, 1995
A;Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.
A;Reference number: A57237
A;Accession: A57237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 04-Mar-2000 C;Accession: G02436; A57237 ExPonath, P.D. submitted to the EMBL Data Library, February 1996 A;Reference number: H01272 A;Reference number: H01272
carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 65; DB 2; Length our Pred. No. 0.0035;
                                                                                                    Score 79; DB 2; Les
Pred. No. 1.6e-05;
                                                                                                                                                                                                                                  1; Mismatches
F;14/Binding site: carbohydrate (Asn) (covale
F;113-190/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A_iStatus: nucleic acid sequence not shown A_iMolecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                        305 YAFVGEKFRRYLSVFFRK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 YAFVGERFRKYLRHFFHR 318
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MIP-1 alpha receptor like-2 - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chemokine (C-C) receptor 3 - human
N;Alternate names: C-C CKR-3
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.4%;
66.7%;
                                                                                                                                        Query Match 83.2%;
Best Local Similarity 83.3%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 66.7
Matches 12; Conservative
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S. Superfamally: vertebrate rhodopsin

C; Superfamally: vertebrate rhodopsin

C; Superfamally: vertebrate rhodopsin

C; Superfamally: vertebrate splicing, G protein-coupled receptor; glycoprotein; transmembrane #status predicted <TM1>
F; 43-70/Domain: transmembrane #status predicted <TM2>
F; 11-6.136/Domain: transmembrane #status predicted <TM3>
F; 115-136/Domain: transmembrane #status predicted <TM4>
F; 1507-226/Domain: transmembrane #status predicted <TM5>
F; 2007-26/Domain: transmembrane #status predicted <TM6>
F; 2807-309/Domain: transmembrane #status predicted <TM6>
F; 287-309/Domain: transmembrane #status predicted <TM7>
                                                                                                                                             A;Cross-references: GB:U54994; NID:g1457945; PIDN:AAC50598.1; PID:g1457946
C;Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see
C;Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A) Description: G protein-coupled receptor for chemokines MIP-lalpha, MIP-lbeta and RANTE A) Note: probably acts to control granulocyte proliferation and differentiation C;Superfamily: vertebrate rhodopsin C;Superfamily: vertebrate rhodopsin C;Superfamily: vertebrate rhodopsin C;Xeywords: AlDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane #status predicted <TM1> F;32-56/Domain: transmembrane #status predicted <TM2> F;03-124/Domain: transmembrane #status predicted <TM3> F;103-124/Domain: transmembrane #status predicted <TM4> F;135-256/Domain: transmembrane #status predicted <TM6> F;236-257/Domain: transmembrane #status predicted <TM7> F;236-257/Domain: transmembrane #status predicted <TM6> F;236-257/Domain: transmembrane #status predicted <TM7> F;236-257/Domain: transmembrane #status predicted <TM7> F;236-257/Domain: transmembrane #status predicted <TM6> F;236-257/Domain: transmembrane #status predicted <TM7> F;236-257/Domain: transmembrane #status predicted <TM6> F;236-257/Domain: transmembrane #status predicted <TM7> F;236-257/Domain: transmembrane #status predicted <TM6> F;236-257/Domain: transmembrane #status predicted <TM7> F;236-257/Domain: transmembrane #
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R;Charo, I.F.; Myers, S.J.; Hernan, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. US.A. 91, 2752-2756, 1994
A;Title: Molecular cloning and functional expression of two monocyte chemoattractant pro
A;Reference number: A53477; MUID:94195821; PMID:8146186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chemokine (C-C) receptor 2, splice form B - human
N'Alternate names: C-C CRR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1995 #sequence revision 05-Apr-1995 #text_change 20-Jun-2000
C;Accession: JC2443; I38463
E;Aramagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
A;Title: CDNA cloning and functional expression of a human monocyte chemoattractant prot
A;Reference number: JC2443; MUID:94324942; PMID:8048929
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A,Molecule type: mRNA
A,Molecule type: mRNA
A,Kesidues: 1-360 <RES>
A,Cross-references: EMBL:U03905; NID:g472557; PIDN:AAA19120.1; PID:g472558
C,Genetics:
A,Gene: GDB:CMKBR2
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F;268/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
F;340,343/Binding site: phosphate (Thr) (covalent) #status predicted
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100.0%; Pred. No. 3.2e-08;
rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                  A)Gene: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CKR5; ChemR13
A;Cross-references: GDB:1230510; OMIM:601373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GDB:337364; OMIM:601267
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                                                                                                                                                                                                                                                                                                                                                                                                                             A, Map position: 3p21-3p21
C; Function:
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Best Local Similarity
                                                  A; Molecule type: mRNA
A; Residues: 1-352 <RAP>
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A; Residues: 1-360 < YAM>
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          A; Accession: A58833
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Gaps

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Length 355;

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Chemokine (C-C) receptor 1 - human
NyAlternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
Cypecies: Homo sapiens (man)
Cypecies: Assorting (man)
Cypecies: Assorting (man)
Cypecies: Assorting (man)
Cypecies: 
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: 31-Jan 1997 #sequence_revision 31-Jan 1997 #text_change 21-Jul 2000
C;Accession: J05068
R;Zaballos, A; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A;Title: Molecular cloning and RNA expression of two new human chemokine receptor-like ge A;Reference number: J05067; MUID:97040707; PMID:8886020
A;Accession: J05068
A;Molecule type: DNA
A;Residues: 1-369 - ZABA>
A;Residues: 1-360 - ZABA>
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C;Species: equine herpesvirus 2
C;Date: 10-Apr_1196 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
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                                                                                                               Cyaces in S55594
R;Telford, B.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
Cyacession: S55594
Bill: 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Telference number: S55594; MUID:95302501; PMID:7783207
A;Accession: S55594
A;Accession: S55594
A;Cession: S55594
A;Cession: S55594
A;Cetus: preliminary; nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-383 <TELDA
A;Cross-references: GB:U20824; NID:g695172; PIDN:AAC13788.1; PID:g695173
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor
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A;Cross-references: GDB:5370639; OMIM:601835
A;Map Position: 6427-6427
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
F;42-68/Domain: transmembrane #status predicted <TM1>
F;12-68/Domain: transmembrane #status predicted <TM2>
F;115-136/Domain: transmembrane #status predicted <TM3>
F;15-136/Domain: transmembrane #status predicted <TM3>
F;12-233/Domain: transmembrane #status predicted <TM4>
F;212-233/Domain: transmembrane #status predicted <TM5>
F;250-271/Domain: transmembrane #status predicted <TM5>
F;292-315/Domain: transmembrane #status predicted <TM5>
F;292-315/Domain: transmembrane #status predicted <TM5>
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Matches 12, Conservative
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A.Accession: G02776
A.Status: translated from GB/EMBL/DDBJ
A,Status: translated from GB/EMBL/DDBJ
A,Residues: 1-355 «NAP»
A,Gross-references: EMBL:U62556; NID:g1468978; PID:g1468979
R,Repsidues: 1-355 «NAP»
A,Accession: G02387
A,Accession: G02387
A,Accession: G02387
A,Accession: G02387
A,Accession: G02387
A,Accession: G02387
A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-355 «SON»
A,Gross-references: EMBL:U45983; NID:g1245056; PID:g1245057
C,Comment: This protein belongs to the family of beta chemokine receptors.
C,Genetics: GDB:G053733; OMIX:601834
A,Gross-references: GDB:G053733; OMIX:601834
A,Map position: 3p21-3p21
C,Superfamily: vertebrate thodopsin
C,Reywords: G protein-coupled receptor; transmembrane protein
F,36-63/Domain: transmembrane #status predicted «TM1»
F,36-63/Domain: transmembrane #status predicted «TM1»
F,36-63/Domain: transmembrane #status predicted «TM2»
F,00-106/main: transmembrane #status predicted «TM2»
F,00-106/main: transmembrane #status predicted «TM2»
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                                                                                                                                                                                                                                                                                                                                                                                                                   Length 359
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 67.4%; Score 64; DB 2; Length 355
Best Local Similarity 61.1%; Pred. No. 0.0052;
Matches 11; Conservative 4; Mismatches 3; Indels
                                                                                   A;Molecule type: DNA
A;Residudes 1.359 «RES.
A;Cross-references: EMB:U28406; NID:9881551; PID:9881552
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;108-129/Domain: transmembrane #status predicted <TM3>F;147-171/Domain: transmembrane #status predicted <TM4>F;202-222/Domain: transmembrane #status predicted <TM5>F;239-260/Domain: transmembrane #status predicted <TM5>F;239-260/Domain: transmembrane #status predicted <TM5>F;281-304/Domain: transmembrane #status predicted <TM7>
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G protein-coupled receptor El - equine herpesvirus 2
                    preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 YAFVGEKFKKHLSEIFQK 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 YAFVGERFRKHLRLFFHR 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YAFVGEKFRNYLLVFFQK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YAFVGEKFRNYLLVFFQK 18
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Matches 12; Conserv
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us-10-084-813-15.rpr

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A;Accession: JC4304
A;Molecule type: mRNA
A;Residues: 1-355 cRAP>
A;Cross-references: GB:U20350; NID:g665580; PIDN:AAA91783.1; PID:g665581
A;Cross-references: GB:U20350; NID:g665580; DIDN:AAA91783.1; PID:g665581
C;Comment: This protein is a cell-surface receptor which recognizes extracellular signals:
C;Comment: This protein is a key regulator of many immune and homeostatic responses, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Circumstry.

Fig. 65/Domain: transmembrane #status predicted <TM1>

Fig. 65/Domain: transmembrane #status predicted <TM3>

Fil2-133/Domain: transmembrane #status predicted <TM3>

Fil2-137/Domain: transmembrane #status predicted <TM3>

Fil2-137/Domain: transmembrane #status predicted <TM5>

Fil2-26/Domain: transmembrane #status predicted <TM6>

Fil2-26/Domain: transmembrane #status predicted <TM6>

Fil2-376/Domain: transmembrane #status predicted <TM6>

Fil2-376/Domain: transmembrane #status predicted <TM7>

Fil2-376/Domain: transmembrane #status predicted <TM7>

Fil2-376/Domain: transmembrane #status predicted <TM7>

Fil2-376/Jonain: stansmembrane (Ser) (covalent) (by casein kinase II) #status predicted Fil2-314/Rainding site: phosphate (Ser) (covalent) #status predicted Fil3-194/Rainding site: carbohydrate (Asn) (covalent) #status predicted Fil3-194/Rainding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted Fil2-31/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted Fil2-31/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted Fil2-31/Binding site: phosphate (Thr) (covalent) (covalent) (by protein kinase C) #status predicted Fil2-31/Binding site: phosphate (Thr) (covalent) (Thr)
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R,Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Froudfoot, A.E.I.; We Biol. Chem. 270, 19495-19500, 1995
A,Title: Molecular cloning and functional expression of a novel CC chemokine receptor cDA; Reference number: A57160; MUID:95370289; PMID:7642634
A,Accession: A57160
                                                                                                 C;Accession: JC4304
R;Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Gene 163, 295-299, 1995
A;Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related
A;Reference number: JC4304; MUID:96011651; PMID:7590284
C;Species: Homo sapiens (man)
C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chemokine (C-C) receptor 4 - human
NjAlternate names: C-C CKR4-4
C.Species: Homo sapiens (man)
C.Spacie: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Superfamily: vertebrate rhodopsin
C,Superfamily: vertebrate rhodopsin
C,Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
C,St-5-57/Domain: transmembrane #status predicted <TM1>
F;66-88/Domain: transmembrane #status predicted <TM2>
F;104-125/Domain: transmembrane #status predicted <TM3>
F;146-165/Domain: transmembrane #status predicted <TM4>
F;197-217/Domain: transmembrane #status predicted <TM6>
F;230-254/Domain: transmembrane #status predicted <TM6>
F;235-254/Domain: transmembrane #status predicted <TM7>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 57; DB 2;
Pred. No. 0.078;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 YAFAGEKFRRYLYHLYGK 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YAFVGEKFRNYLLVFFQK 18
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C; Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 60.0%;
Best Local Similarity 61.1%;
Matches 11; Conservative
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A;Cross-references: GDB:677463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Map position: 3pter-p21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Note: source clone K5-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: v28
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Affille: Structure and functional expression of the human macrophage inflammatory 1 alph
A;Reference number: 155671; MUID:93240122; PMID:7683036
A;Accession: 155671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      다
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A/Cross-references: GDB:138446; CMIN:601159
A/Map position: 3p21-3p21
C/Superfamily: vertebrate rhodopsin
C/Superfamily: vertebrate
C/Superfamily: ve
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Neurosci. Lett. 169, 85-89, 1994
A;Tetle: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and A;Reference number: IS8186; MUID:94323113; PMID:8047298
A;Recession: IS8186
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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C.Species: Rattus norvegicus (Norway rat)
C.Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C.Accession: 158186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Residues: 1-354 <RES>
A,Cross-references: EMBL:U04808, NID:g2558635, PIDN:AAB87093.1, PID:g439861
C,Superfamily: vertebrate rhodopsin
C,Superfamily: ortebrate rhodopsin
C,Keywords: G protein-coupled receptor
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                                                                                                                                                                                             A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
A;Experimental source: HL60 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:124876)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
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61.1%; Pred. No. 0.024;
iive 2; Mismatches
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61.1%; Pred. No. 0.053;
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                                           A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-355 <NEO>
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Matches 11, Conservative
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Best Local Similarity
Matches 11; Conserv
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A; Residues: 1-355 < RES>
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DB 2; Length 360;

60.0%; Score 57;

Query Match

orphan G protein-coupled receptor - human N;Alternate names: V28 protein

RESULT 10 JC4304

YAFAGEKFRRYLRHLYNK 311

g 8

1 YAFVGEKFRNYLLVFFQK 18

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lymphocyte-specific G protein-coupled receptor EB11 - human

NyAlternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
C;Accession: B55735; S25443
R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B., Genneics 23, 643-650, 1994
A;Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor A;Reference number: A55735; MUID:95154835; PMID:7851893
A;Sctatus: preliminary
A;Molecule type: mRNA
A;Residues: 1-378 <SCH>
A;Cross-references: GB:131581; NID:9468319; PIDN:AAA74231.1; PID:9468320
A;Residues: 1-378 <SCH
A;Burgstahler, R.; Kempkes, B.; Staeube, K.; Lipp, M.
Submitted to the EMBL Data Library, February 1995
A;Reference number: S52443
A;Reference number: S52443
A;Reference number: S52443
A;Residues: 21-378 <BURN>
A;Residues
A;Cross-references: EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g1167852
A;Experimental source: thymus
C;Genetics:
A;Genetics:
A;Genetics:
C;Crystamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhosphoprotein; receptor; thymus
F;2,183,194/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F;72,202,350/Binding site: phosphate (Ser) (covalent) (by protein kinase II) #status predicted
F;72,202,350/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
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A;Cross-references: GDB:342065; OMIM:600242
A,Map position: 1742-17421.2
G;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor
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Best Local Similarity 58.8%;
Matches 10; Conservative
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C;Species: Mus musculus (house mouse)
C;Date: 02-Uul-1996 #sequence_revision 02-Uul-1996 #text_change 13-Aug-1999
C;Accession: 149940
C;Accession: 149940
B;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemoki A;Title: Cloning and differential tissue-specific expression of three mouse beta chemoki A;Title: Cloning and differential tissue-specific expression of three mouse beta chemoki A;Title: Cloning and differential tissue-specific expression: 149340
A;Accession: 149340
A;Accession: 149340
A;Accession: DNA
A;Accession: 1-356 cRES
A;Cose-references: EMBL:U28405; NID:g881549; PIDN:AAA89154.1; PID:g881550
C;Superfamily: vertebrate rhodopsin
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chemokine (C-C) receptor 4 - mouse

chemokine (C-C) receptor 4 - mouse)

c;Species Mus musculus (house mouse)

c;Species Mus musculus (house mouse)

c;Accession: JC4587

R;Hoogwearf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.

Biochem. Biophys Res. Commun. 218, 337-343, 1996

A;Reference mumber: JC4587; Mulb:96136324; PMID:8573157

A;Accession: JC4587

A;Accession: JC4587

A;Reference mumber: JC4587

A;Residues: 1-360 <-HOO>
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                                          Pred. No. 0.079;
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Pred. No. 0.37;
2; Mismatches
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Pred. No. 0.37;
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301 YVPVGERFWKYLRQLFQR 318
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Best Local Similarity 55.6%;
Matches 10; Conservative
                                          58.8%;
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52.6%; Score 50;
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313 YAFIGOKFRHGLL 325
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Best Local Similarity 69.2
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A,Molecule type: DNA
A,Residues: 6-360 <SPR>
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Aritle: Identification, chromosomal location, and genome organization of mammalian G-pr A;Reference number: A48909; MUID:94116980; PMID:8288218
A;Accession: H48909
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text change 05-Nov-1999
C;Accession: A48921; A53677; I49348; I55421; H48009; I53774
R;Cerretti, D.P.; Nelson, N.; Kozlosky, C.J.; Morrissey, P.J.; Copeland, N.G.; Gilbert, Genomics 18, 410-413, 1993
A;Title: The murine homologue of the human interleukin-8 receptor type B maps near the iA;Accession: A48921; MUID:94117014; PMID:8288247
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R;Bozic, C.R.; Gerard, N.P.; von Uexkull-Guldenband, C.; Kolakowski, L.F.
J. Biol. Chem. 269, 29355-29358, 1994
A;Title: The murine interleukin 8 type B receptor homologue and its ligands. Expression A;Feference number: 155421; MUID:95050766; PMID:7961909
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A; Residues: 1-359 <CERN-
A; Richard, M.; Prado, G.N.; Wilkinson, N.; Navarro, J.
J. B; Cl. Chem. 269, 18263-18266, 1994
A; Title: The W terminus of interleukin-8 (IL-8) receptor confers high affinity binding A; Title: The winder: A53677, MUID:94308043; PMID:7518426
A; Accession: A53677
A; Reference number: A53677
A; Referen
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A;Residues: 145-258 <WIL>
A;Cross-references: GB:L20337; NID:g438800; PIDN:AAA16853.1; PID:g438801
R;Harada, A.; Kuno, K.; Nomura, H.; Mukaida, N.; Murakami, S.; Matsushima, K. Gene 142, 297-300, 1994
A;Tele: Cloning of a CDNA encoding a mouse homolog of the interleukin-8 receptor. A;Reference number: I53774; MUID:94252584; PMID:8194768
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A)Residues: 1-359 < 8002>
A)Cross-references: GB:L26549
A;Note: sequence extracted from NCBI backbone (NCBIP:149812)
A;Note: sequence extracted from NCBI backbone (NCBIP:149812)
B;Lee, J; Cacalano, G.; Camerato, T.; Toy, K.; Moore, M.W.; Wood, W.I.
J. Immunol. 155, 2158-2164, 1995
A;Title: Chemokine binding and activities mediated by the mouse IL-8 receptor.
A;Reference number: 149348; MUID:95363183; PMID:7636264
A;Accession: 149348
A;Accession: 149348
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
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A;Residues: 1-359 <RE2>
A;Cross-references: GB:L13239; NID:g293665; PIDN:AAA62109.1; PID:g293666
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                                                                                                                                                                                                                                                                                           Length 356;
                                         A,Residues: 1-356 <GOB>
A,COSs-references: BMBL:X77797
C,Superfamily: vertebrate rhodopsin
C,Superfamily: vertebrate rhodopsin
C,Keywords: G protein-coupled receptor; transmembrane protein
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                                                                                                                                                                                                                                                                                Score 50; DB 2;
Pred. No. 1.2;
3; Mismatches
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YAFIGQKFRHGLL 322
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Matches 9; Conserv
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A; Molecule type: mRNA
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interleukin-8 receptor type B - human (5) periods (7) 
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A, Residues: 1-15 cRE2-
A, Kresidues: 1-15 cRE2-
A, Cross-references: EMBL:U11872; NID:9511808; PIDN:AAA64380.1; PID:9511809; EMBL:U11873;
11876; NID:9511816; PID:9511817; EMBL:U11877; NID:9511818; PID:9511819; EMBL:U11878; NID:
R, Sprenger, H.; Lloyd, A.R.; Lautens, L.L.; Bonner, T.I.; Kelvin, D.J.
B ±01-Chem. 269, 11065-11072, 1994
A, Title: Structure, genomic organization, and expression of the human interleukin-8 receptive number: A53611; MUID:94209273; PMID:7512557
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A.Cross-references: GB:M73969
C.Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8, inc
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R;Murphy, P.M.; Tiffany, H.L.
Science 233, 1280-1283, 1991
A;Title: Cloning of complementary DNA encoding a functional human interleukin-8 receptor.
A,Reference number: A39446; MUID:91368200; PMID:1891716
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*Residues: 1-360 «RES>
A;Cross-references: EMBL:U11869; NID:g511801; PIDN:AAB60656.1; PID:g511803
A;Accession: 138712
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A;Molecule type: mRNA
A;Residues: 1-359 <RE3>
A;Cross-references: GB:D17630; NID:g493671; PIDN:BAA04536.1; PID:g493672
C;Genetics:
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G Superfamily: vertebrate rhodopsin
G Superfamily: vertebrate rhodopsin
G Keywords: G protein-coupled receptor; glycoprotein; tri
F 49-74/Domain: transmembrane #status predicted <TM1>F 84-106/Domain: transmembrane #status predicted <TM2>F) 120-141/Domain: transmembrane #status predicted <TM3>F) 163-182/Domain: transmembrane #status predicted <TM3>F) 234/Domain: transmembrane #status predicted <TM5>F) 21-271/Domain: transmembrane #status predicted <TM5>F) 21-271/Domain: transmembrane #status gredicted <TM5-F) 21-271/Domain: transmembrane #status gredicted <TM5-F) 328/Domain: transmembrane #status gredicted <TM
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Pred. No. 1.2;
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                                       A; Cross-references: GDB:127868; OMIM:146928
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C, Superfamily: vertebrate rhodopsin
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Length 360;

DB 2;

8 g

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Chemokrate (C-C) receptor 2, splice form A - human
Chemokrate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemocytes: Homo sapiens (man)
C;Date: 16-Peb-1996 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999
C;Accession: I38450
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proco. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A;Title: Molecular cloning and functional expression of two monocyte chemoattractant prot A;Reference number: A53477; MulD:94195821; PMID:8146186
A;Accession: I38450
A;Accession: I38450
A;Accession: I38450
A;Accession: Selection of two monocyte chemoattractant prot A;Residues: 1-374 <RES>
A;Cross-references: EMBL:U03882; NID:9472555; PIDN:AAA19119.1; PID:9472556
C;Genetics:
A;Genetics:
A;Genetics:
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A/Amap position: 3p21-3p21
C|Suberfamily: vertebrate rhodopsin
C|Suberfamily: vertebrate rhodopsin
C|Suberfamily: vertebrate rhodopsin
C|Suberfamily: vertebrate rhodopsin
F|44-68/Domain: transmembrane #status predicted <TM1>
F|79-99/Domain: transmembrane #status predicted <TM2>
F|115-136/Domain: transmembrane #status predicted <TM3>
F|14-178/Domain: transmembrane #status predicted <TM3>
F|154-178/Domain: transmembrane #status predicted <TM5>
F|28-226/Domain: transmembrane #status predicted <TM5>
F|29-309/Domain: transmembrane #status predicted <TM6>
F|29-309/Domain: transmembrane #status predicted <TM6>
F|29-309/Domain: transmembrane #status predicted <TM6>
F|34-465/Domain: transmembrane #status predicted <TM7>
F|34/Binding site: carbohydrate (Asn) (covalent) #status predicted
F|32-277,113-190/Disulfide bonds: #status predicted
C.Accession: B98112
R,Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Es e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Mc y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A,Authons: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A,Accession: B98112
A,Genetics: preliminary
A,Genetics: C.; Genetics: C.; GSPDB:GN00174
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C;Species: Mus musculus (house mouse)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
C;Accession: JE0349
R;Tamaru, M.; Tominaga, Y.; Yatsunami, K.; Narumi, S.
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Pred. No. 1.8;
1; Mismatches
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90.0%;
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Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
Matches 9; Conserv
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C;Genetics:
A;Gene: SP2115
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G protein-coupled peptide receptor EBI 1 - human
C,Specials: Homos aspiens (man)
C,Specials: Homos aspiens (man)
C,Specials: Homos aspiens
C,Date: 21.56p-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C,Accession: A45680
C,Accession: A45680
A,Fitle: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled )
A,Fitle: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled )
A,Reference number: A45680; MUD:93188173; PMID:8383238
A,Accession: A45680
A,Status: preliminary
A,Molecule type: nucleic acid
A,Residues: 1-378 kBIR>
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hypothetical protein SP2115 [imported] - Streptococcus pneumoniae (strain TIGR4)
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hypothetical protein spr1925 [imported] - Streptococcus pneumoniae (strain F
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:L08176; NID:g183484; PID:g183485
A;Experimental source: B-lymphocytes
A;Note: sequence;extracted from NCBL backbone (NCBIN:127094, NCBIP:127095)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
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                 Pred. No. 1.2; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YAFIGVKFRNDIFKLFK 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YAPVGEKFRNYLLVFFQ 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YAFVGEKFRNYLLVFF 16
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                    69.2%;
                                                                                                                                 |||:|:|||:
314 YAFIGOKFRHGLL 326
                                                                                                  1 YAFVGEKFRNYLL 13
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Best Local Similarity 62.5
Matches 10; Conservative
                 Best Local Similarity 69.2
Matches 9; Conservative
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V.; Lyman, S.; Gerard
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A; Residues: 1-355 <BBC>
A; Residues: 1-355 <BBC>
A; Crease Teferences: GE:M74240; NID:g165438; PIDN:AAA31375.1; PID:g165439
B; Lee, J: Kuang, WJ.; Rice, G.C.; Wood, W.I.
J. Immunol. 148, 1261-1264, 1992
A; Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor.
A; Reference number: A46483; MUID:92148149; PMID:1737938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycosyltransferase [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Dates: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: B97185
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
                                               Interleukin-8 receptor, high affinity - rabbit
Nylternate names: fMLP receptor
C)species: Oryctolagus cuniculus (domestic rabbit)
C)species: Oryctolagus cuniculus (domestic rabbit)
C)species: Oryctolagus cuniculus
C)stacession: A23669
R)Thomas, K.M.; Pyun, H.Y.; Navarro, J.
R) Thomas, K.M.; Pyun, H.Y.; Navarro, J.
A) Reference number: A23669; MUID:91056034; PMID:1700779
A) Title: Molecular cloning of the fMet-Leu-Phe receptor from neutrophils.
A) Reference number: A23669; MUID:91056034; PMID:1700779
A) Residues: 1-354 < THO>
C) Superfamily: Vertebrate rhodopsin
C) Superfamily: Vertebrate rhodopsin
C) Keywords: G protein-coupled receptor; glycoprotein; membrane protein; neutrophil
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Accession: 31-Mar. 1992 #text_change 05-Nov-1999
C;Accession: JQ1231; A46483
R;Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyma
Biochem. Biophys. Res. Commun. 179, 784-789, 1991
A;Title: Molecular characterization of the interleukin-8 receptor.
A;Reference number: JQ1231; MUID:91378994; PMID:1898400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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C;Keywords: G protein-coupled receptor; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 2;
Pred. No. 5.5;
2; Mismatches
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Pred. No. 5.5;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.4%;
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Best Local Similarity 61.5%;
Matches 8; Conservative
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Best Local Similarity 61.5
Matches 8; Conservative
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A;Molecule type: mRNA
A;Residues: 1-355 <LEE>
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B97185
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Biochem. Biophys. Res. Commun. 251, 41-48, 1998

A;Title: Cloning of the murine interferon-inducible protein 10 (IP-10) receptor and its A;Reference number: JE0349; MUID: 99009219; PMID: 9790904

A;Resign: JE0349

A;Molecule type: mRNA

A;Residues: 1-367 <TAM>
A;Residues: 1-367 <TAM>
C;Cross-references: DDBJ;AB003174; NID: 93798731; PIDN: BAA34045.1; PID: 93798732

C;Comment: This protein is important for lymphocyte trafficking to lymphoid organs.
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A55735
A55735
G; Decien-coupled receptor EBI1 - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999
C; Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999
C; Accession: A55735
A; R; Schweickart, V. L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B. Genomics 23, 643-650, 1994
A; Title: Cloning of human and mouse EBII, a lymphoid-specific G-protein-coupled receptor A; Reference number: A55735
A; Reference number: A55735
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E.; Navarrc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interleukin-8 receptor (clone 5Bla) - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: A53752
R;Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Nava:
A;Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Nava:
A;Pritle: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.
A;Reference number: A53752; MuID:94230294; PMID:8175642
A;Accession: A53752
A;Acturus preliminary
A;Retule: preliminary
A;Residues: 1-358 <-PRA>
A;Cessiues: 1-358 <-PRA>
A;Cessiues: 1-358 <-PRA>
A;Cessiues: GB:LZ4445; NID:9437661; PIDN:AAA31378.1; PID:9437662
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
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A,Residues: 1-378 <SCH>
A,Cross-references: GB131580; NID:g468340; PIDN:AAA74232.1; PID:g468341
C,Superfamily: vertebrate rhodopsin
C,Keywords: G protein-coupled receptor
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                                                                                                                                                                                                                                                                                                Length 367;
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                                                                                                                                                                                                                                                                                             50.5%; Score 48; DB 2; 50.0%; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 47; DB 2;
Pred. No. 3.8;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 YAFVGVKFREQMWMLFTR 334
                                                                                                                                                                                                                                                                                                                                                                                                                    1 YAFVGEKFRNYLLVFFQK 18
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69.2%;
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Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                        9; Conservative
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Best Local Similarity
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A; Kesatques; 1-3-9; FURE.

A; Kresatques; 1-3-9; FURE.

A; Kresatques; 1-3-9; FURE.

A; Experimental source: lymphocyte

B; Bersgman, D.G.; Ellis, C.; Kumar, C.; Nuthulaganti, P.; Kersten, H.; Elshourbagy, N.; G;

B; Bersgman, D.G.; Ellis, C.; Kumar, C.; Nuthulaganti, P.; Kersten, H.; Elshourbagy, N.; G;

B; Cochem. Biophys. Res. Commun. 183, 999-995, 1982

A; Title: Cloning and characterization of a human angiotensin II type 1 receptor.

A; Reference number: JH0574

A; Molecule type: mRNA

A; Residues 1-359 CBER.

A; Experimental source: liver

B; A; Experimental source: liver

B; A; Experimental source: liver

B; A; Efference number: JH0267; MUD:9198490; PMID:1559596

A; Title: Molecular cloning, sequence analysis and expression of a cDNA encoding human typ.

A; Molecule type: mRNA

A; Residues: 1-359 cTAK>

A; Molecule type: mRNA

A; Reference number: A44014; MUID:92375105; PMID:1508224

A; Reference number: A44014; MUID:92375105; PMID:1508224

A; Reference number: mRNA

A; Reference number: A44014; MUID:92375105; PMID:1508224

A; Reference number: MRNA

A; Reference number: MRNA

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A;Residues: 1-359 «CUR»
A;Cross-references: GB:M93394; NID:g178680; PID:g178681
A;Cross-references: GB:M93394; NID:g178680; PID:g178681
A;Gross-references: GB:M93394; NID:g178680; PID:g178681
A;Gross-references: GB:132359; OMIM:106165
A;Gross-references: GB:132359; OMIM:106165
A;Map position: 3421-3425
A;Map position: 3421-3425
A;Map position: 3421-3425
A;Map position: g1-3425
A;Map position: presented receptor; g1ycoprotein; hormone receptor; transmembrane #status predicted <TM1>
P;65-90/Domain: transmembrane #status predicted <TM2>
P;103-124/Domain: transmembrane #status predicted <TM3>
P;145-167/Domain: 
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C;Species: Canis lupus familiaris (dog)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
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R;Burns, L.; Clark, K.L.; Bradley, J.; Robertson, M.J.; Clark, A.J.L.
FBBS Lett. 343, 146-150, 1994
A;Title: Molecular cloning of the canine angiotensin II receptor. An A;Reference number: $44425, MUID:94222188; PMID:8168620
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F244-264/Domain: transmembrane #status predicted <TM6>
F1201-305/Domain: transmembrane #status predicted <TM7>
F1201-305/Domain: transmembrane #status predicted <TM7>
F14,176,188/Binding site: carbohydrate (Asn) (covalent) #status
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53.8%; Pred. No. 8.2;
iive 3; Mismatches 3; Indels
A;Reference number: JQ1402; MUID:92181475; PMID:1543512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Status: nucleic acid sequence not shown A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-359 < BURN> A; Cross-references: PIDN:AAB30674.1; PID:g546569
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les 7; Conserv
                                                                                                                           A;Molecule type: DNA
A;Residues: 1-359 <FUR>
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Matches
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JN0621
G procein-coupled receptor type B - bovine
G; Species: Bos primigenius taurus (cattle)
G; Species: Bos primigenius taurus (cattle)
G; Species: Bos primigenius taurus (cattle)
G; Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 19-May-2000
C; Accession: JN0621
B; Matsucoka, I; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.
B; Cochem. Biophys. Res. Commun. 194, 504-511, 1993
A; Title: Identification of novel members of G-protein coupled receptor superfamily expre
A; Accession: JN0621
A; Molecule type: mRNA
A; Residues: 1-350 < WAT>
B; Residues: 1-350 < WATO
B;
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JOING4
angiotensin II receptor type 1 - human
NyAlternate names: angiotensin II receptor 1A
CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiSpecies: O-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jul-2000
CiAccession: JC1104, JOI402; JH0574, JH0267; A44014; S18983
RiMauzy, C.A.; Hwang, O.; Egloff, A.M.; Wu, L.H.; Chung, F.Z.
Biochem. Biophys. Res. Commun. 186, 277-284, 1993
A;Title: Cloning, expression, and characterization of a gene encoding the human angioten
A,Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A,Reference number: A96900; MUID:21359325; PMID:21359325
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A,Residues: 1-359 «MMJ»
R;Furuta, H.; Guo, D.F.; Inagami, T.
Biochem. Biophye. Res. Commun. 183, 8-13, 1992
A;Title: Molecular cloning and sequencing of the gene encoding human angiotensin II
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                                                                                                              A.Accession: B97185
A.Status: preliminary
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-377 - KUNA
A.Cross-references: GB:AE001437; PIDN:AAK80269.1; PID:g15025320; GSPDB:GN00168
A.Experimental source: Clostridium acetobutylicum ATCC824
A.Genetics: 
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Pred. No. 8;
5; Mismatches
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Best Local Similarity 47.4%;
Matches 9; Conservative
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Best Local Similarity 38.9
Matches 7; Conservative
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Gaps

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Length 359;

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A; Molecule type: DNA
A; Residues: 1-359 < ELTP.
A; Residues: 1-359 < ELTP.
A; Rote: the authors translated the codon AGC for residue 120 as Thr, GTC for residue 225
A; Kakar, S.S.; Sellers, J.C.; Devor, D.C.; Musgrove, L.C.; Neill, J.D.
B; Chem. Biophys. Res. Commun. 183, 1090-1096, 1992
A; Title: Angiotensin II type-1 receptor subtype cDNAs: differential tissue expression and A; Reference number: JH0578
A; Reference number: JH0578
A; Accession: JH0578
A; Molecule type: mRNA
A; Residues: 1-74, 'L', 76-119,'T', 121-224,'A', 226-359 < KAK>
A; Cross-references: GB: M87003; NID: 9202920; PIDN: AA440739.1; PID: 9202921
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Aug-1992 #sequence revision 17-Aug-1992 #text_change 08-Oct-1999
C;Date: 17-Aug-1992 #sequence revision 17-Aug-1992 #text_change 08-Oct-1999
C;Accession: QQL516; JH0578; PH0850
R;Elron, T.S.; Stephan, C.C.; Taylor, G.R.; Kimball, M.G.; Martin, M.M.; Durand, J.N.;
Biochem: Biochypy Res. Commun. 184, 1067-1073, 1992
A;Title: Isolation of two distinct type 1 angiotensin II receptor genes.
A;Reference number: JQ1516; MUID:92246922; PMID:1575725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Note: sequence extracted from NCBI backbone (NCBIN:100262, NCBIP:100268)
R;Iwai, N.; Inagami, T.
FBSE Lett. 298, 257-260, 257-260, Aspectation of two subtypes in the rat type I angiotensin II receptor. A;Reference number: $20423; MUID:92183879; PMID:1544458
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MyAlternate names: angiotensin II receptor chain B
Cippedes: Ratus norvegius (Norway rat)
Cipacies: Ratus norvegius (Norway rat)
Cipace 04 Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
Cipacession: A42656; 820423
Risandberg, K.; Ji, H.; Clark, A.J.; Shapira, H.; Catt, K.J.
J. Biol. Chem. 267, 9455-9458, 1992
A;Title: Cloning and expression of a novel angiotensin II receptor subtype.
A;Reference number: A42656; MUID:92250585; PMID:1374402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: A42656
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-359 «SAN»
A;Cross-references: GB:M90065; NID:g202801; PIDN:AAA40704.1; PID:g202802
A;Experimental source: adrenal cortex
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C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
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                                                                                         Score 45; DB 2;
Pred. No. 8.2;
3; Mismatches
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3; Mismatches
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Pred. No.
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Best Local Similarity 53.8%;
Matches 7; Conservative 3
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53.88;
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Best Local Similarity 53.8
Matches 7; Conservative
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A; Residues: 1-6.'I', 8-165.'H',167-172,'E',174-204,'V',206-231,'T',233-238,'F',240-359 <8  
A; Cross-references: GB: S37491; NID: 9249947; PIDN: AAB22270.1; PID: 9249948  
A; Cross-references: GB: S37491; NID: 9249947; PIDN: AAB22270.1; PID: 9249948  
A; Cross-roughed receptor; Glycoprotein; PiD: 9249948  
C; Superfamily: vertebrate rhodopsin  
C; Superfamily: vertebrate rhodopsin  
C; Superfamily: vertebrate rhodopsin  
E; Sydo-200 Domain: transmembrane #status predicted <TM1>
F; 50-53 Domain: transmembrane #status predicted <TM3>
F; 147-166 Domain: transmembrane #status predicted <TM5>
F; 147-166 Domain: transmembrane #status predicted <TM6>
F; 141-176, 188 Binding site: carbohydrate (Asn) (covalent) #status predicted F; 331, 338, 348 Binding site: phosphate (Ser) (covalent) #status predicted
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C;Species: Mus musculus (house mouse)
C;Species: To-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 05-Nov-1999
C;Accession: JC1194; JH6622
R;Yoshida, H.; Kakuchi, J.; Guo, D.F.; Furuta, H.; Iwai, N.; van der Meer-de Jong, R.;
Biochem. Biophys. Res. Commun. 186, 1042-1049, 1992
A;Title: Analysis of the evolution of angiotensin II type 1 receptor gene in mammals (m A;Reference number: JC1193; MUID:92359981; PMID:1497638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        angiotensin II receptor type 1 - rabbit
C.Species: Oryctolagus cuniculus (domestic rabbit)
C.Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C.Accession: A48857
R.Burns, K.D.; Inagami, T.; Harris, R.C.
A.M. J. Physiol. 264, F645-F64, 1993
A.Title: Cloning of a rabbit kidney cortex AT1 angiotensin II receptor that is present
A,Reference number: A48857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Residues: 1,255 470S>
;Residues: 1,359 470S>
;Residues: 1,359 470S>
;Assamura, H.; Hein, L.; Krieger, J.E.; Pratt, R.E.; Kobilka, B.K.; Dzau, V.J.
iochem. Biophys. Res. Commun. 185, 253-259, 1992
;Title: Clonhing, characterization, and expression of two angiotensin receptor (AT-1);Reference number: JH0621; MUID:92287102; PMID:1599461
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A;Molecule type: nucleic acid
A;Rosidues: 1-359 <BURN>
A;Residues: 1-359 <BURN>
A;Cesidues: 1-359 <BURN>
A;Cesidues: 1-559 <BURN>
A;Cesidues: 1-550 <BURN>
A;Cesidues: 1-550 <BURN-
A;Chore: sequence extracted from NCBI backbone (NCBIN:129600, NCBIP:129601)
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Pred. No. 8.2;
3; Mismatches 3; Indels
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                                                                    DB 2;
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                                                                    Score 45;
Pred. No.
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C;Superfamily: vertebrate rhodopsin
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53.88;
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                                                                                                 Best Local Similarity
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A,Residues: 1-80,'C',82-108,'T',110-359 <IW2>
A,Cross-references: GB:MY4054; NID:g202918; PIDN:AAA40738.1; PID:g202919
A,Experimental source: kidney
C,Comment: ATI receptor consists of two closely related ATI isoforms of angiotensin II re
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FEBS Lett. 298, 257-260, 1992
ArTitle: Identification of two subtypes in the rat type I angiotensin II receptor.
A;Reference number: S20423; MUID:92183879; PMID:1544458
A;Accession: S20424
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A;Molecule type: mRNA
A;Residues: 1-359 cMURA
A;Cross-references: GB:X62295; NID:g57773; PIDN:CAA44183.1; PID:g57774
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A;Nolecule type: mRNA
A;Nolecule type: mRNA
A;Residues: 1-359 < INNA
R;Iwai, N.; Yamano, Y.; Chaki, S.; Konishi, F.; Bardhan, S.; Tibbetts,
Biochem Biochhys. Res. Commun. 177, 299-304, 1991
A;Tible: Rat angiotensin II receptor: CDNA sequence and regulation of
A;Tible: Rat angiotensin II receptor: CDNA sequence and regulation of
A;Reference number: UQ1055; MUID:91254291; PMID:2043116
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3; Mismatches
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          A; Experimental source: anterior pituitary
Bjochem. Biophye. Res. Commun. 185, 204-210, 1992
Bjochem. Biophye. Res. Commun. 185, 204-210, 1992
A; Title: Characterization of an angiotenain type-1 receptor partial cDNA from rat kidney
A; Reference number: PH0850; MUID:92287094; PMID:1599457
A; Residues: 84-119, 'T', 121-224, 'A', 226-259 < YEM>
A; Residues: 84-119, 'T', 121-224, 'A', 226-259 < YEM>
A; Residues: 84-119, 'T', 121-224, 'A', 226-259 < YEM>
A; Residues: 84-119, 'T', 121-224, 'A', 226-259 < YEM>
A; Residues: B4-119, 'T', 121-224, 'A', 226-259 < YEM>
A; Residues: B4-119, 'T', 121-224, 'A', 226-259 < YEM>
A; Residues: B4-119, 'T', 121-224, 'A', 226-259 < YEM>
A; Residues: B4-119, 'T', 'Annewbrane #status predicted < TWM1>
C; Genetics:
A; Gene
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C; Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C; Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C; Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C; Accession: S15403
R; Sasaki, K.; Yamano, Y.; Bardhan, S.; Iwai, N.; Murray, J.J.; Hasegawa, M.; Matsuda, Y.; Nature 351, 230-233, 1991
A; Title: Cloning and expression of a complementary DNA encoding a bovine adrenal angiote A; Accession: S15403
A; Reference number: S15403
A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-359 - SAS>
A; Cross-references: GB: X62294; NID: 943; PIDN: CAA44182.1; PID: 944
C; Superfamily: vertebrate rhodopsin
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53.8%; Pred. No. 8.2;
iive 3; Mismatches 3; Indels
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us-10-084-813-15.rpr

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A,Molecule type: DNA
A,Residues: 1-311,'T',313-375 <FEN>
A,Cross-references: GB:U77827; NID:g1906591; PIDN:AAC51173.1; PID:g1906592
C,Comment: This protein plays a role in B-cell functions and is involved in endothelial c
         A,Title: Cloning of a novel member of the G protein-coupled receptor family related to per A,Reference number: JC5294; MUID:97224403; PMID:9070864
                                                                                                                                                                                                                                                                                                                                                                                                                               C, Superfamily: Vertebrate rhodopsin
C, Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F, 64-83/Domain: transmembrane #status predicted <TM1>
F, 96-114/Domain: transmembrane #status predicted <TM3>
F, 126-148/Domain: transmembrane #status predicted <TM3>
F, 180-198/Domain: transmembrane #status predicted <TM4>
F, 180-198/Domain: transmembrane #status predicted <TM5>
F, 221-238/Domain: transmembrane #status predicted <TM5>
F, 260-283/Domain: transmembrane #status predicted <TM5>
F, 232, 23, 44/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 2;
Pred. No. 13;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: September 28, 2004, 09:07:11
Job time : 10.925 secs
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ilarity 38.9%;
Conservative
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                          A; Gene: GDB: CMKRL2;
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C, Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; glycoprotein; GTP binding, receptor; transmembra
E; 72-66, Domain: transmembrane #status predicted <TM1>
F; 103-123, Domain: transmembrane #status predicted <TM3>
F; 1047-167, Domain: transmembrane #status predicted <TM4>
F; 147-167, Domain: transmembrane #status predicted <TM5>
F; 147-167, Domain: transmembrane #status predicted <TM5>
F; 240-263, Domain: transmembrane #status predicted <TM7>
F; 278-299, Domain: transmembrane #status predicted <TM7
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NAlternate names: constitutively expressed peptide-like receptor; flow-induced endothel
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1997 #sequence_revision 28-Aug-1998 #text_change 21-Jul-2000
C;Date: 31-Jan-1997 #sequence_revision 28-Aug-1998 #text_change 21-Jul-2000
C;Cspecies: Blay, P.; Nilsson, C.; Lolait, S.J.
Biochem. Biophys. Res. Commun. 228, 285-292, 1996
A;Title: Cloning of human CNNA encoding a novel heptahelix receptor expressed in Burkitt
A;Reference number: JCS069; MUID:97079175; PMID:8920907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Cross-references: GB:Y08162; NID:g1707499; PIDN:CAA69354.1; PID:g1707500
A.Cross-references: GB:Y08162; NID:g1707499; PIDN:CAA69354.1; PID:g1707500
B.Experimental source: B-cell Imphoblast
R.Takada, Y.; Kato, C.; Kondo, S.; Korenaga, R.; Ando, J.
Biochem. Biophys. Res. Commun. 240, 737-741, 1997
Biochem. Cloning of CDNAs encoding G protein-coupled receptor expressed in human endothe A;Reference number: JC5786; MUID:98063308; PMID:9398636
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C, Genetics:
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A;Experimental source: umbilical vein endothelial cell
&;Peng, X; Gregor, P.
Biochem. Biophys. Res. Commun. 231, 651-654, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 24-Nov-1999
C;Accession: GQ2670;
Accession: R.L.; Perlmutter, D.H.
Submitted to the EMBL Data Library, May 1996
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A;Molecule type: mRNA
A;Residues: 1-358 <MCC>
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Pred. No. 8.2;
3; Mismatches
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C,Superfamily: vertebrate rhodopsin
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Best Local Similarity 53.8
Matches 7; Conservative
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A;Accession: G02670
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Best Local Similarity
Matches 7; Conserv
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A; Residues: 1-375 < OWM>
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Residues: 1-375 <TAK>
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EMBL; AB015944; BAA31328.1; -
Interpro; IPR000276; GPCR_Rhodpsn.
PRO0001; 7tm 1; 1.
PRINTS; PR00237; GFCRHODOPSN.
PROSITE; PS00237; G_PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN RECEP_F1_2; 1.
G-protein, coupled receptor; Transmembrane; Glycoprotein; Sulfation;
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DOMAIN
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166.624 Million cell updates/sec
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                                                                                                          September 28, 2004, 08:55:11 ; Search time 5.625 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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CKR3 MOUSE
CKR3 RAT
CKR8 HUMAN
CKR8 MACMU
CKR6 HUMAN
CKR1 HUMAN
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CKR5_MOUSI
CKR2_MOUSI
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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	7	58.		N S	-1	CKR1 MACMU	CMC		P56482	macaca mula	
	38 55	57.9		28	н	CKR3 CAVPO	VPO		Q9z2i3	cavia porce	
	σ	55.		55	Н	CKR1 MOUSE	USE		P51675	mns mnscala	
		55.		26	н	CKRV MO	_MOUSE		P51676	mns musculu	
	41 52	54.		09	-1	CKR4 MOUSE	USE		P51680	mus musculu	
,		54.		78	1	CKR7 HUMAN	MAN		P32248	homo sapien	
•		52.		53	н	IL8B MACMU	DMO.		028519	macaca mula	
		52.		53	-1	IL8B PANTR	NTR		028807	pan troglod	
	45 50	52.		26	н	IL8B_CANFA	NFA		097571	canis famil	
RESULT 1 CKR5_CER ID CKR AC PS6 DT 15-	CKRS_CERAE CKRS_CERAE ID CKRS_CERAE AC P56493; DT 15-JUL-1998	ω ω	STANDARD; (Rel. 36, Cr (Rel. 36, La	RD; Cre	D; Created) Last seg	D; PRT; 352 AF Created) Last sequence update)	352 upda	352 AA. pdate)			
T E	16-OCT-2001 (Rel. 40, L C-C chemokine recentor	ine Ke	1. 40, Poento	r Lag	35 9 9 9	Last annotation update) type 5 (C-C CKR-5) (CC	on up	date)) (CC-CKR-5) (CCR-5) (CCR5).	(CCR-5)	(CCR5).	
l g	CCR5 OR CMKBR5.	KBR5.			4						
SO	Cercopithecus aethiops (Green monkey) (Grivet).	cus a	ethiop	i S	3ree	en monke	y) (G	rivet).			
ز	Bulkaryota.	Moto	. 404	7	404	inery.	utu.	Rikaryota, Metazos, Chordata, Craniata, Vertebrata, Enteleostomi,	ייירם (פרוני		

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-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or

differentiation.
-!- SUBCELIULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors. and mice Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Cercopithecus. TISSUE=Kidney;

MEDILTE-89001387; PubMed=9343222;

KUMMAIN S.E., Platt E.J., Kozak S.L., Kabat D.;

"Polymorphisms in the CCR5 genes of African green monkeys and mic implicate specific amino acids in infections by simian and human immunodeficiency viruses.";

J. Virol. 71:8642-8656(1997). Murayama Y., Matsunaga S., Inoue-Murayama M., "CDNA sequence of African green monkey CCR-5 chemokine receptor SEQUENCE FROM N.A.

EXTRACELLULAR (POTENTIAL)

30

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062745, 062746,
15.DEC-1998 (Rel. 37, Created)
15.DEC-1998 (Rel. 37, Last sequence update)
16.DEC-1998 (Rel. 37, Last sequence update)
16.OEC-2001 (Rel. 40, Last annocation update)
16.CC-chemoxine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
            PROSITE; PRO0237; G PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G_Protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN
1 30 EXTRACELULAR (POTENTIAL).
TRANSMEM 31 58 (POTENTIAL).
DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                       6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTARY.)
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SULFATION (BY SIMILARITY)
SULFATION (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
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100.0%; Pred. No. 6.9e-09;
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 GPCRRHODOPSN.
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nes 18; Conservative
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15
352 AA;
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CKR5_CERTO
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDITIES 9935215; PubMed=10408730; Miller-Truttwin M.C., Corbet S., Hansen J., Georges-Courbot M.-C., Muller-Truttwin M.C., Corbet S., Hansen J., Georges-Courbot M.-C., Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.; Mutations in CCRS-coding sequences are not associated with SIV carrier status in African nonhuman primates."; AIDS Res. Hum. Retroviruses 15:31-391(1999).
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.
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ID CKR5_CERPY

C9TV42;

DT 15-MAR-2004 (Rel. 43, Created)

DT 15-MAR-2004 (Rel. 43, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DT 5-MAR-2004 (Rel. 43, Last annotation update)

DT 5-MAR-2004 (Rel. 43, Last annotation update)

DT 6-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cercopithecus pygerythrus (Vervet monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 95; DB 1; Length 352; 100.0%; Pred. No. 6.9e-09; ive 0; Mismatches 0; Indels
                                                                                              EXTRACELLULAR (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

7 (POTENTIAL).

7 (POTENTIAL).

7 (POTENTIAL).

7 (POTENTIAL).

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8 INILARITY.

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8 ULFATION (BY SIMILARITY).

8 ULFATION (BY SIMILARITY).

8 ULFATION (BY SIMILARITY).
                     2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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                                                                 3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                CYTOPLASMIC (POTENTIAL).
 (POTENTIAL)
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 CCRS OR CMKBRS.
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Best Loc Matches

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RESULT 2

MOD

EMBL, AF035222; AAD44015.1; -. InterPro; IPR000276; GPCR_Rhodpsn. Pfam; PF00001; 7tm_1; 1.

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Gaps

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Length 352; 0; Indels

(POTENTIAL).

us-10-084-813-15.rsp

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Mismatches
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EMBL; AF051902; AAC39830.1; -.

REMBL; AF051903; AAC39831.1; -.

REMBL; AF051904; AAC39831.1; -.

REMBL; AF051904; AAC39833.1; -.

REMBL; AF051905; AAC39833.1; -.

REMBL; AF051905; AAC39833.1; -.

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REMINES, REMORDER, GEROTEIN RECEP FILLS 1.

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-!-FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANIES and subsequently transduces a signal by
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15-ULL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CRR-5) (CC-CKR-5) (CCRS).
CCRS OR CMKBRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gorilla gorilla gorilla (Lowland gorilla).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Gorilla.
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Y -> D (IN ISOLATE 087).
Y -> G (IN ISOLATE 079).
M -> K (IN ISOLATE 087).
L -> V (IN ISOLATE 089).
V -> G (IN ISOLATE 089).
V -> L (IN ISOLATE 079).
T -> I (IN ISOLATE 079).
T -> I (IN ISOLATE 079).
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SULFATION (BY SIMILARITY).
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Y -> D (IN ISOLATE 079).
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EXTRACELLULAR (POTENTIAL).

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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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nes 18; Conservative
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352 AA;
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increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.
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PS1681; 014692; 014693; 014695; 014696; 014697; 014699; 014699; 014700; 014700; 014700; 014700; 014700; 014700; 014700; 014700; 014700; 014700; 014700; 014700; 014700; 014700; 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 15-MR-044 (Rel. 34, Last annotation update) 15-MR-044 (Rel. 34, Last annotation update) (GC-CRR-5) (CC-CRR-5) (GC-CRR-5) (GCR-5) (GCR
                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 6.9e-09;
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CYTOPLASMIC (POTENTIAL).
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    Raport C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.; "Molecular cloning and functional characterization of a novel human CC chemokine receptor (CRS) for RANTES, MIP-1beta, and MIP-lalpha."; J. Biol. Chem. 271:17161-17166(1996).
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Mummidi S., Abuja S.S., McDaniel B.L., Shuja S.K.;
"The human CC chemotine receptor 5 (CCR5) gene. Multiple transcripts
with 5'-end heterogeneity, dual promoter usage, and evidence for
polymorphisms within the regulacory regions and noncoding exons.";
"Diol. Chem. 272:30662-30671(1997).
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Polymorphisms in the CCRS genes of African green monkeys and mice implicate specific amino acids in infections by simian and human immunodeficiency viruses.";
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                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-96295970; PubMed-8699119;
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"Cloning and functional expression of CC CKRS, a human monocyte chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and RANTES.";
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MCCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
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Gnoj L., Ia Bastide M., Kaplan N., Greco T., Touchman J.,
Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
Watanabe M., Doggett N., Garcia D., Sagripanti J.L.,
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
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Deng H., Liu R., Ellmeier W., Choe S., Unutmaz D., Burkhart M., di Marmon S., Sutton R.E., Hill C.M., Davis C.B., Peiper S.C., Schall T.-d., Littman D.R., Landau N.R.; "Identification of a major co-receptor for primary isolates of
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Magierowska M., Barre-Sinoussi F., Issafras H., Theodorou I.,
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MEDLINE=96260018; PubMed=8649512;
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MEDLINE=98001387; PubMed=9343222;
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                                                      MEDLINE=96291862; PubMed=8663314;
CC-chemokine receptor gene.";
Biochemistry 35:3362-3367(1996)
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                                                                                             Paxton W.A., "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
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-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99189752; PubMed=10089882;
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MEDLINES=99416438; PubMed=10486970;

Zhang Y.-W., Ryder O.A., Zhang Y.-P.;

Zhang Y.-W., Ryder O.A., Zhang Y.-P.;

"Sequence evolution of the CCR5 chemokine receptor gene in primates.";

Mol. Biol. Evol. 16:1145-1134 (1999).

-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

MIP-1-beta and RANTES and subsequently transduces a signal by

increasing the intracellular calcium ions level. May play a role

in the control of granulocytic lineage proliferation or

differentiation.
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30-MAY-2000 (Rel. 39, Last sequence update)
28-RES-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5)
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PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hylobatidae, Hylobates.
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
"Sequence evolution of the CCR5 chemokine receptor gene in primates.";
"Sequence evolution of the CCR5 chemokine Binds to MIP-1-alpha,
III-Ibeta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
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-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5)
                                                                                                                                                                          EMEL; AF075451; AAD19863.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Prim; PF00001; 7tm 1; 1.
PRINTS; PR00237; GFCRHODDPSN.
PROSITE; PS00237; GFROTEIN RECEP_F1_1; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
G-protein 31 $8 1 (POTENITAL).
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"Hyboates moloch (Silvery gibbon).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
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SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
1, 4F8E4F344CEB7C91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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100.0%; Pred. No. 6.9e-09;
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58
68
1102
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2318
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es 18; Conserv
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SEQUENCE FROM N.A.
                                                                                                                                                CCRS OR CMKBRS.
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MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99416438; PubMed=10486970;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
"Sequence evolution of the CCR5 chemokine receptor gene in primates.";
Mol. Biol. Evol. 16:1145-1154(1999).

-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                              EMBL, AF177899; AAK43382.1, -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam: PF00001; 7Tm_1; 1.
PRINTS; PR00137; GFCRHODPSN.
PROSITE; PS00237; GFCRHON RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1.
G_PICCEIN COUPLED receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN : STARGELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
C-C_chemokine_receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           differentiation.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hylobates syndactylus (Siamang) (Symphalangus syndactylus).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hylobatidae, Hylobates.
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                                                                                                                                                                                                                                                                                                                                                                                   Score 95; DB 1; Length 352;
Pred. No. 6.9e-09;
); Mismatches 0; Indels
                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
SULFATION (BY SIMILARITY.
                                                                                                                                                        1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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(BY SIMILARITY).
(BY SIMILARITY).
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9623CA98340CF274 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                             352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9590;
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Q95NCS;
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MOD_RES
SEQUENCE
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CKR5_HYLSY
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                        Gaps
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P79436; 002746;
01-NOV-1997 (Rel. 35, Care ted)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCC-S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macaca mulatta (Rhesus macaque),
Macaca fascioularis (Crab eating macaque) (Cynomolgus monkey), and
Macaca nemestrina (Pig-tailed macaque).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=M.mulatta;

MEDLINE=97184592; PubMed=9032394;

MEDLINE=97184592; PubMed=9032394;

Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,

Newman W., Gerard C., Sodroski J.,

"Utilization of C-C chemokine receptor 5 by the envelope

91ycoproteins of a pathogenic simian immunodeficiency virus,

SIVmac239.",
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N (BY SIMILARITY).
N (BY SIMILARITY).
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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SPECIES=M.mulatta; STRAIN=Indian macaque;
MPDI-INE=97213934; PubMed=9060623;
Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40508 MW;
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NCBI_TaxID=9544, 9541, 9545;
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1es 18; Conservative
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14
352 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                                                           NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                     host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phylogeny.";
                                                                                                                                                                                                                                                                                                                                   SECUENCE
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                                                                                              CKR5_F
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                                                                                                              Interpro; IPR000276; GPCR_Rhodpsn.
PRIM: 1.
PRIMIS: PR00137; GPCRM-HODPSN.
PROSITE; PS00237; GPROTEIN RECEP_FI_1; 1.
PROSITE; PS50362; G_PROTEIN RECEP_FI_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN

30
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
Genetically divergent strains of simian immunodeficiency virus use CRS as a coreceptor for entry."; J. Virol. 71:2705-2714(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
M -> I (IN REF. 3).
I -> M (IN REF. 3).
M, SRB96CGS909FACB2 CRC64;
                                            SPECIES=M.mulatta;
MEDLINE=21354176; PubMed=11461684;
Margulies B.J., Hauer D.A., Clements J.E.;
"Identification and comparison of eleven rhesus macaque chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                 receptors.";
AIDS Res. Hum. Retroviruses 17:981-986(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 (POTENTIAL)
CYTOPLASMIC (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40507 MW;
                                                                                                                                                                                                                                                                                                                                     EMBL; U77672; AAC51109.1; -.
EMBL; U73739; AAC51158.1; -.
EMBL; U96762; AAC34132.1; -.
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1124
1124
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1198
2235
2235
235
237
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3352
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268
241
292
352 AA;
                                                                                                                                                                                                                            differentiation.
                                                                                                           SEQUENCE FROM N.A.
                                      SEQUENCE FROM N.A.
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-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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                                                          Gaps
                                                                                                                                                                                                                                                                                                                                        P56440; 002778;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
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Zacharova V., Zachar V., Goustin A.S.;
"Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M., Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M., Peiper S.C., Parmentier M., Broder C.C., Doms R.W.; "Differential utilization of CCR5 by macrophage and T cell tropic simian immunodeficiency virus strains."; Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "HIV type 1 subtypes, coreceptor usage, and CCRS polymorphism."; AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
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                                                          0; Indels
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Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases
100.0%; Score 95; DB 1; I
100.0%; Pred. No. 6.9e-09;
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                                                             Mismatches
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MEDLINE=97268687; Pubmed=9108095;
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                                                                                                                                                                                        297 YAFVGEKFRNYLLVFFQK 314
                                                                                                                           1 YAFVGEKFRNYLLVFFOK 18
   Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                             EMBL; AF005663; AAB6255711;

R EMBL; U94329; AAB6255711;

R EMBL; AF011542; AA665742.1;

R EMBL; AF011540; AA65740.1;

R EMBL; AF011540; AA65740.1;

R EMBL; AF011540; AA65740.1;

R EMBL; AF011540; AA65740.1;

R EMBL; AF01000277.1;

InterPro; IPR000277.1;

R PF000277; GPCRHODOPSN.

R PROSITE; PS00237; GPCRHODOPSN.

R PROSITE; PS00237; GPCRHODOPSN.

R PROSITE; PS00227; GPCREDFORDESP.

R PROSITE; PS00227; GPCREDFORDESP.

R PROSITE; PS00237; GPCREDFORDESP.

R PROSITE PS00237; GPCREDFORDESP.

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15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCRS OR CMKBRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                    4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

S (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

G (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

T (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.

SULPATION (BY SIMILARITY).

SULPATION (BY SIMILARITY).
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Papio anubis (Olive baboon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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SPECIES=P. hamadryas;
MPDLINE=97268687; PubMed=9108095;
Edinger A., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
3 EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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4A33E698B80FE34C CRC64;
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Mismatches 0;
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Matches 18; Conservative (
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NCBI_TaxID=9557, 9555;
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CKR5_PAPHA
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                                                                                                                                                                                                                                                                                                                                                                    Benton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for a C-C type ochemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or
                                                                                               SEQUENCE FROM N.A.
SPECIES=P, handryas;
MEDLINE=99210133; PubMed=10195758;
SARSENA N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;
"Species-specific changes in the CCR5 gene from African and Asian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           differentiation.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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EMBL, AF105289, AAD20557.1; -...

EMBL, AF105299, AAD20558.1; -...

EMBL, AF105290, AAD20559.1; -...

EMBL, AF0023452; AAG63830.1; -...

InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm_1; 1.

PROSITE; PS00237; GPROTEIN RECEP_F1 1; 1.

PROSITE; PS50262; G_PROTEIN RECEP_F1 2; 1.

PROSITE; PS50262; G_PROTEIN RECEP_F1 2; 1.

DOMALN 3 30 EXTRACELLULAR (POTENTIAL).

TRANSMEM 31 F800237 (POTENTIAL).
"Differential utilization of CCR5 by macrophage and T cell tropic simian immunodeficiency virus strains.";
Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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7 (POTENTIAL).
CYTOPLASHIC (POTENTIAL).
BY SIMILARITY.
SULFATION (BY SIMILARITY).
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N-LINKED (GLCNAC. . .) (PA
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SE1504A9BA1FE8B2 CRC64;
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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Pred. No. 6.9e-09;
; Mismatches 0;
                                                                                                                                                                                                                                      nonhuman primates.";
AIDS Res. Hum. Retroviruses 15:479-483(1999).
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Conservative 0;
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EMBL; AF105287; AAD20556.1; -.
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352 AA;
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Best Local Similarity
Matches 18; Conserv
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1 YAFVGEKFRNYLLVFFOK 18

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297 YAFVGEKFRNYLLVFFQK 314

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                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=99416438; PubMed=10486970;
Zhang Y.-W., Zhyder O.A., Zhang Y.-P.;
"Sequence evolution of the CCR5 chemokine receptor gene in primates.";
Mol. Biol. Evol. 16:1145-1154(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or
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PRINTS; PR00237; GPCRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS0026; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

EXTRACELULAR (POTENTIAL).
                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
38-FRB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCRS OR OMKBRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of Grprotein coupled receptors.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pongo.
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EXTRACELLULAR (POTENTIAL)
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F4E2F47135AF658A CRC64;
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                   352 AA
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                      pygmaeus (Orangutan).
                                                   STANDARD;
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352 AA;
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Best Local Similarity
Matches 18; Conserv
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                                                CKRS PONPY
097881;
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                     CKR5_PONPY
RESULT 12
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Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Zhang Y.-P.;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Mol. Biol. Brol. 16:1145-1154 (1999).
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium tons level. May play a role
in the control of granulocytic lineage proliferation or

SEQUENCE FROM N.A. MEDLINE=99416438; PubMed=10486970;

NCBI_TaxID=61621;

Pygathrix.

differentiation. SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

CCRS OR CMKBRS.
Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;

30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FBB-2003 (Rel. 41, Last amortation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR-5)

A.

352

STANDARD;

CKR5 PYGBI 097880;

297 YAFVGEKFRNYLLVFFQK 314

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Pfam, PR00021; TRN 1.1.
PRINTS; PR00237; GFCRHODDPSN.
PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1.
PROSITE; PS00262; G PROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Transmentane; Glycoprotein; Sulfation.
CAPACATAN (POTENITAL).

G-protein coupled receptor; Transmentane; Glycoprotein; Sulfation.
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SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
4366F142730F938F CRC64;
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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Matches 18; Conserv
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Gaps

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Indels

1 YAFVGEKFRNYLLVFFQK 18

Conservative

1 YAFVGEKFRNYLLVFFOK 18

297 YAFVGEKFRNYLLVFFQK 314

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                                                                                                                                                                                                         MEDLINE=99416438; PubMed=10486970;
MEDLINE=99416438; PubMed=10486970;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Zequence evolution of the CCR5 chemokine receptor gene in primates.";
Mol. Biol. Evol. 16:1145-1154(1999).
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CRR-5) (CC-CRF) (CCR5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF075448; AAD19860.1; -
InterPro; IPR000276; GPCR_Rhodpsn.
Pram; PF00011; 7tm 1; 1.
PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS026237; GPROTEIN RECEP_F1_2; 1.
PROSITE; PS50262; GPROTEIN_RECEP_F1_2; 1.
DOMAIN 31 58 1 (POTENTIAL).
TRANSMEM 31 58 1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CYTOPLASHIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
CYTOPLASHIC (POTENTIAL).
CYTOPLASHIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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FE4F9D98D3B3E861 CRC64;
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
SULFATION (BY SIMILARITY)
                                                                                                               Pygathrix nemaeus (Dove langur)
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Best Local Similarity 100.
Matches 18; Conservative
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PYGNE
                                                                                                                                                              Pygathrix.
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                                                                                                                                                                                                                                                                                                        NEDLINE-99416438; PubMed=10486970;

MEDLINE-99416438; PubMed=10486970;

Zhang Y.-W., Ryder O.A., Zhang Y.-P.;

Saquence evolution of the CCR5 chemokine receptor gene in primates.";

Mol. Biol. Evol. 16:1145-1154 (1999).

-! FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

MIP-1-beta and RAMTES and subsequently transduces a signal by

increasing the intracellular calcium ions level. May play a role

in the control of granulocytic lineage proliferation or

differentiation.

-! SUBCELIULAR LOCATION: Integral membrane protein.

-! SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                           Trachypithecus francoisi (Francois' langur) (Indochinese langur).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
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                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
38-FBH-2003 (Rel. 41, Last annotation update)
C_C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
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InterPro, IPR00276; GPCR_Rhodpsn.
PRAMPRS, PR0001; Trm.1; 1.
PRINTS; PR00237; GPCRFIN RECEP_F1_1; 1.
PROSITE; PS0237; G_PROTEIN_RECEP_F1_2; 1.1
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN : 30
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
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100.0%; Score 95; DB 1; L
Best Local Similarity 100.0%; Pred. No. 6.9e-09;
Matches 18; Conservative 0; Mismatches 0;
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297 YAFVGEKFRNYLLVFFQK 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the buspean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                     Zhang Y.-W., Ryder O.A., Zhang Y.-P., "Sequence evolution of the CCRS chemokine receptor gene in primates."; Mol. Biol. Evol. 16:1145-1154(1999).
                                                                                                                                                                                                                                                                                                                                              Biol. Bvol. 16:1145-1154(1999).
FINCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
Trachypithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Or Sella ...

EMBL, AP075443; AAD19855.1; -.

EMBL, AP075443; AAD19855.1; -.

EMBL, PR000276; GPCR_Rhodpsn.

PRINTS; PR000217 7m 1; 1.

PRINTS; PR00227; GPROTEIN RECEP_F1 1; 1.

PROSITE; PS00237; GPROTEIN RECEP_F1 2; 1.

PROSITE; PS00262; GPROTEIN RECEP_F1 2; 1.

GPROTEIN COUPLED F RECEPTION.

GRANDIAL).

1 (POTENTIAL).
                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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4366F148D3A5938F CRC64;
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (
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MEDLINE=99416438; PubMed=10486970;
                                      297 YAFVGEKFRNYLLVFFOK 314
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             YAFVGEKFRNYLLVFFQK
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                                                                                                                                                                                                                                                               NCBI_TaxID=61618;
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Score 95; DB 1;] Pred. No. 6.9e-09;

100.0%;

Best Local Similarity

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Sprague-Dawley;
MEDLINE=9818173; PubMed=9655467;
Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
Defiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
"Chemokine receptor expression in cultured glia and rat experimental
allergic encephaloweptitis.";
J. Neuroimmunol. 86:1-12(198).
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
Last annotation update)
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EMBL; Y12009; CAA72733.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PR00001; 7tm 1; 1.
PRINTS; PR00237; GPCR4HOODSN.
PROSITE; PS00237; GPROTEIN RECEP_F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1.
G-protein coupled receptor; Transembrane; Glycoprotein.
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Charo I.F.;
"Molecular cloning and functional expression of murine JE (monocyte chemoattractant protein 1) and murine macrophage inflammatory protein lalpha receptors: evidence for two closely linked C-C chemokine receptors on chromosome 9.";
J. Biol. Chem. 271:7551-7558(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=129;
MEDLINE=97404635; PubMed=9261347;
MEDLINE=97404635; PubMed=9261347;
Mang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;
"Two distinct CCRS domains can mediate coreceptor usage by human immunodeficiency virus type 1.";
"Tyrol 71:6205-6314(1999).";
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                 CKKS_MOUSE STANDARD; PRT; 354 AA.
P51682; O35313; O35891; P97308; P97405; Q61867;
01-OCT-1996 (Rel. 34, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (AIP-1 alpha receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CS7BL/6, and NIH Swiss; TISSUB=Kidney, Liver, and Spleen; MEDLINE=98001387; PubMed=9343222, Kaban S.E., Platt E.J., Kozak S.L., Kabat D.; Potymorphisms in the CCRS genes of African green monkeys and mice implicate specific amino acids in infections by simian and human immunodeficiency viruses "; virol. 71:8642-8656 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CS7BL/6 X CBA; TISSUB=Thymus; MEDLINE=96278910; PubMed=8662890; MeDLINE=96278910; PubMed=8662890; MeDLINE=96278910; A.J., Prodefoot A.B.I., Wells T.N.C., Power C.A.; "Cloning and characterization of a novel murine macrophage inflammatory protein-1 alpha receptor."; J. Biol. Chem. 271:14445-14451(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=129/SvJ; TISSUE=Spleen;
MEDLINE=96205938; PubMed=8631787;
Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L.,
                                                                           ·LINKED (GLCNAC. .) (POTENTIAL) 77EDB368AA4C868D CRC64;
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                                                                                                                                       Length 354;
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Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
  EXTRACELLULAR (POTENTIAL)
                  7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
                                                                                                                                   Score 85; DB 1; I
Pred. No. 3.7e-07;
1; Mismatches 1,
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nes 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; V447036; AAC52454.1; -.

DR EMBL; X94151; CAA63867.1; -.

DR EMBL; U83275; AAC533867.1; -.

DR EMBL; U83275; AAC53389.1; -.

DR EMBL; AF022990; AAC53389.1; -.

DR EMBL; AF022990; AAC53389.1; -.

DR EMBL; AF01728, AB57183.1; -.

DR EMBL; AF01782; Cars.

DR GO; GO: 0016433; F:C-C chemokine receptor activity; IDA.

R GO; GO: 0016433; GFCR Anodpsn.

PRINTS; PR00237; GFCRAPODPSN.

PROSITE; PS00237; GPROTEIN RECEP F1_1; 1.

DR PROSITE; PS00243; G-PROTEIN RECEP F1_2; 1.

PROMAIN: 33 G I (POTENTIAL).
Guo B., Kuno K., Harada A., Mateushima K.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
-!- FUNCTION: Receptor for and subsequently transduces a signal by
increasing the intracellular calcium ions level.
-!- SUBCELJULAR LOCATION: Integral membrane protein.
-!- SUBCELJULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
but not in nonhematopolatic cell lines.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
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2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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Gaps

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Score 80; DB 1; Length 354; Pred. No. 2.7e-06; Mismatches 1; Indels

84.2%; Score 80; 83.3%; Pred. No.

2; Mismatches

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Matches
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CKR2_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,
A Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,
A Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,
Post T.W., Gerard C., Dorf M.E.;
Transcriptase-polymerase chain reaction does not detect mRNA for the
KC or new MCP-1 receptor.";
J. Neurosci. Res. 45:382-391(1996).
J. Neurosci. Res. 45:382-391(1996).
J. PUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
Cohemickines. Transduces a signal by increasing the intracellular
Calcium ions level.
Calcium ions level.
J. SUBCELLULAR LOCATION: Integral membrane protein.
J. TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
Dut not in nonhematopoletic cell lines.
Chemistry: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning and functional expression of murine JE (monocyte chemoattractant protein 1) and murine macrophage inflammatory protein lalpha receptors: evidence for two closely linked C-C chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U47035; AAC52453.1; -.
EMBL; U47035; AAC52557.1; -.
EMBL; U51717; AAC525784.1; -.
MGD; MGI:106185; Ccr2.
GO; GO:0016483; F:C-C chemokine receptor activity; IDA.
GO; GO:0019955; F:Cycokine binding; IPI.
GO; GO:0018066; P:cellular defense response (sensu Vertebrata); IMP.
GO; GO:0016806; P:hemopoleáis; IMP.
GO; GO:0016899; P:humoral immune response; IMP.
GO; GO:0016899; P:humoral immune response; IMP.
                                                                                                                             P51683, Q61172,
01-0CT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
C-C chemokine receptor 141, Last annotation update)
C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CC-CCR-2)
(JEF)FIC receptor) (MCP-1 receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kurihara T., Bravo R.;
Cloning and functional expression of mCCR2, a murine receptor for
the C-C chemokines JE and FIC. ";
J. Biol. Chem. 271:11603-11606(1996).
                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=96205938; PubMed=8631787;
Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L.,
                                                                                                                    373 AA
                                                                                                                                                                                                                                                                                                                                                                                                              receptors on chromosome 9.";
J. Biol. Chem. 271:7551-7558(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BALB/c;
MEDLINE=96216064; PubMed=8662823;
                                  299 YAFVGEKFRSYLSVFFRK 316
                 1 YAFVGEKFRNYLLVFFOK 18
                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR2).
CCR2 OR CMKBR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               macrophages.
-!- INDUCTION: In animals in which experimental allergic
encephalomyelitis (EAB) has been induced.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 78; DB 1; Length 373
Pred. No. 6.4e-06;
!; Mismatches 2; Indels
                                                                                                                                                                                                                    4 (POTENTIAL).
EXTRACELULAR (POTENTIAL).
5 (POTENTIAL).
                                                                                                           EXTRACELLUIAR (POTENTIAL)

1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
                                                                                                                                                           2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                       39 Y -> H (IN REF. 1).

184 A -> G (IN REF. 1).

54 V -> G (IN REF. 1).

42782 MW, PAO12C10F4C9325A CRC64;
                                                                                                                                                                                                                                                                                          6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                         5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                     7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
GO, GO:0030334; P:regulation of cell migration; IMP.
InterPro; IPR002276; GPCR_Rhodpsn.
PRN1TS; PR00237; GPCRRHODDPSN.
PROSITE; PS00237; GPCRRHODDPSN.
PROSITE; PS502627; GPCRRHODPSN.
G-protein coupled receptor; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 77.8
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055193;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
Transduces a signal by increasing the intracellular calcium ions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Last sequence update)

8-PEB-2003 (Rel. 41, Last annotation update)

C-C chemokine receptor type 2 (C-C CRR-2) (CCR-2) (CCR2)

(Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
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-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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Margulies B.J., Hauer D.A., Clements J.E.;
"Identification and comparison of eleven rhesus macaque chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
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Pred. No. 6.4e-06;
2; Indels
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Event=Alternative splicing; Named isoforms=2;
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                                                                                                                                                       PERMY, PERODO1, 7tm 1, 1.

PRINTS, PRO0237, GPCREHODOPON, PROSITE, PSO0237, G PROTEIN RECEP F1 1; 1.

PROSITE; PSSO262, G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                         EMBL; U77349; AAC03242.1; -. InterPro; IPR000276; GPCR_Rhodpsn.
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Macaca mulatta (Rhesus macaque)
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77.8%;
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Best Local Similarity
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018793;
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CKR2 MACMU
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  A PART A
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the Buropean Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SOL N., Treboute C., Gomas E., Ferchal F., Alizon M.;
Submitted (UUL-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                             EMBL; AF013958; AAD11572.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
PR 17 1. 1.
PR 18 1. 1.
PROSTIE; PS00237; GFCRHODOPSN.
PROSTIE; PS00237; GFCRHODOPSN.
PROSTIE; PS00237; G_PROTEIN RECEP_F1 1; 1.
PROSTIE; PS00262; G_PROTEIN_RECEP_F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mamallai, Eutheria, Primates, Cararrhini, Cercopithecidae, Cercopithecinae, 
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
SULPATION (BY SIMILARITY).
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Pred. No. 1.4e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         305 YAFVGEKFRRYLSMFFRK 322
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77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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P51677; Q15748; Q86WD2; Q9ULX8;
01-0CT-1996 (Rel. 34, Created)
1-0CT-1996 (Rel. 34, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR-3) (CCR3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96235004; PubMed=8642344; Daugherty B.L., Siciliano S.J., Demartino J.A., Malkowitz L., Sirclinano S.J., Demartino J.A., Malkowitz L., Sirclina A., Springer M.S.; Sirclina A., Springer M.S.; Cloning, expression, and characterization of the human eosinophil eotaxin receptor."; J. Exp. Med. 183:2349-2354(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 65, DB 1; Length 355;
Pred. No. 0.0011;
2; Mismatches 4; Indels
                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).

1 (POTENTIAL).

2 (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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5 (POTENTIAL).
...AGMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                               PROSITE; PS00237; G PROTEIN RECEP F1 1; 1. PROSITE; PS50262; G PROTEIN RECEP F1 2; 1. G-protein coupled receptor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC
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                 entities requires a license agreement (
or send an email to license@isb-sib.ch)
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 statement is not
                                                              EMBL, Y13775, CAA74106.1; -.
IllacePro; IPR000275; GECR_Rhodpsn.
Pfam; PF0001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
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MEDLINE=95348056; PubMed=7622448;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               40830 MW;
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66.7%;
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les 12; Conserv
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CKR3 HUNAN
ID CRR3 HUNAN
ID 01-0CT-
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                                                                                                                    MEDLINE=21354176; PubMed=11461684;
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Query Match
Best Local Similarity 66...,
Best 12; Conservative
                         Cercopithecinae; Macaca
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                                                                                                  SEQUENCE FROM N.A.
                                                   NCBI_TaxID=9544;
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                          MIM; 6010268; -.
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0004950; F:chemokine receptor activity; TAS.
GO; GO:00005950; F:chemokine receptor activity; TAS.
GO; GO:00005958; P:cell adhesion; TAS.
GO; GO:00005935; P:chemotaxis; TAS.
GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
GO; GO:0007188; P:G-protein signaling, coupled to cAMP nucleo. .; TAS.
GO; GO:0000125; P:intvasive growth; TAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)
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Macaca mulatta (Rhesus macaque).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELULAR (POTENTIAL).
5 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
C -> S 'ro?
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S -> T (IN REF. 4 AND 5).
E95DCD7A6C643874 CRC64;
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CYTOPLASMIC (POTENTIAL).
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                                                                                            EMBL, U51241; AAB16831.1; --
EMBL, AF026515; AAB0726.1; --
EMBL, AF026515; AAB0286.1; --
EMBL, AB02887; BAA86964.1; --
EMBL, AB023887; AAB85194.1; --
EMBL, AY221092; AAB85194.1; --
EMBL, BC033514; AAB3514.1; --
EMBL, AY221092; AA065970.2; --
EMBL, GC03514; AAB33514.1; --
EMBL, BC031514; ABB33514.1; --
EMBL, BC031514; ABB3514.1; --
EMBL, BC031514; ABB3514.1; --
EMBL, BC031514; ABB3514.1; --
EMBL, BC031514; ABB3514.1; --
EMBL, BC031514; ABB3514; --
EMBL, BC031514; --
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355 AA; 41043 MW;
                                                                        EMBL; U28694; AAC50469.1; -. EMBL; U51241; AAB16831.1; -.
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CKR3 MACMU
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                                                                                      Gaps
Margulies B.J., Hauer D.A., Clements J.E.; "Identification and comparison of eleven rhesus macaque chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
EXTRACELLUTAR (POTENTIAL).
S (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLUTAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
EXTRACELLUTAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
6 (POTENTIAL).
7 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K -> E (IN REF. 2),
K -> R (IN REF. 2).
E271F1E694970D9F CRC64;
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
                                                                     AIDS Res. Hum. Retroviruses 17:981-986(2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
GOPINO COUPLED receptor; Transmembrane.
DOM:
TRANSMEM 35 62 1 (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                      Zingoni A., Soto H., Hedrick J.A., Stoppacciaro A., Storlazzi C.T., Sinigaglia F., D'Ambrosio D., O'Garra A., Robinson D., Rocchi M., Santoni A., Zlotnik A., Napolitano M.; "The chemokine receptor CCR8 is preferentially expressed in Th2 but not Th1 cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .) (POTENTIAL)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FSB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 8 (C-C CKR-8) (CC-CKR OR CMKBR8 OR TER1.
                                                                                                                                                                                                                                                                  Zaballos A., Goya I.I., Gutierrez J., Varona R., Marquez G., Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 298206; CAB10896.1; -.

R EMBL; Z98205; CAB10895.1; -.

R EMBL; AF001277; AAC97589.1; -.

R GO; GO:0016493; F:C- Chemokine receptor activity; IDA.

GO; GO:0005515; F:protein binding; IPI.

R GO; GO:0005915; F:protein binding; IPI.

R InterPro; IPR004068; CC = receptor.

R InterPro; IPR004068; CC = receptor.

R Pfam; PF00001; 7tm 1; 1.

R PRINTS; PR00137; GPCRRHODOPSN.

R PROSITE; PS00237; G-PROTEIN RECEP_F1 1; 1.

R G-Protein coupled receptor; Transmembrane; Glycoprotein.

R G-Protein coupled receptor; Transmembrane; Glycoprotein.

R DOMAIN 62 71 (POTENTIAL).

R DOMAIN 62 71 (CYTOPLENTIAL).
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EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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N-LINKED (GLC)
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98334001; PubMed=9670926;
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Best Local Similarity 61.15
Matches 11, Conservative
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1127
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                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                   NCBI_TaxID=10090;
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                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3) (CCR3) (CKR3) (Macrophage inflammatory protein-1 alpha receptor-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gao J. L., Murphy P.M.;

"Cloning and differential tissue-specific expression of three mouse "Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.";

J. Blol. Chem. 270:17494-17501(1995).

-I. FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin, MCP-3, MCP-4 and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level.

-I. SUBCELLULAR LOCATION: Integral membrane protein.

-I. TISSUE SPECIFICITY: Detected in skeletal muscle and in trace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular characterization of two murine eosinophil beta chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amounts in Leukocytes.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96072806; PubMed=7594543;
Post I.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
                                                                                                                                                                    359 AA
                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Immunol. 155:5299-5305(1995).
298 YAFIGEKFKKHLMDVFQK 315
                                                                                                                                                                                                                                                                                                                                                      2) (MIP-1 alpha RL2).
CCR3 OR CMKBR3 OR CMKBR1L2.
                                                                                                                                                                    STANDARD;
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64
68
95
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133
150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                    MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptors
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1 YAFVGEKFRNYLLVFFOK 18
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61.1%;
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                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor-like genes.";
                                                                                                                                 265
289
310
164
359 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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TRANSMEM
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CKR8_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
STRAIN=Wistar; TISSUE=Spleen;
MEDLINE=98118173; Pubmed=9659467;
Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
Defiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
"Chemokine receptor expression in cultured glia and rat experimental
                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Wistar; TISSUE=Spleen;
Harrington P.M., Newton D.J., Coleman J.W., Flanagan B.F.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Expressed in spleen but not in astrocytes or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)
                                                                                                                                                         .
0
                                                                                                                                 Length 359;
                                                                                                                                 Score 64; DB 1; Length 359
Pred. No. 0.0016;
!; Mismatches 3; Indels
          5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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InterPro; IPR000276, GPCR_Rhodpsn.
Pfam; PF00001, 7tm 1; 1. ..
PROSITE; PS00237; GFCRHODOPSN.
PROSITE; PS00237; GFROTEIN_RECEP_F1_1; 1.
PROSITE; PS0262; GFROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane.
DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
 EXTRACELLULAR (POTENTIAL)
                                                                                              -> S (IN REF. 2).
AC11ED66E283CEAF CRC64;
                                                                                                                                                                                                                                                                   359 AA.
                                                                                 BY SIMILARITY.
R -> S (IN REI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  allergic encephalomyelitis.";
J. Neuroimmunol. 86:1-12(1998).
                                                                                                                                                                                                       305 YAFVGERFRKHÍRLFFHR 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF003954; AAC03337.1; -.
                                                                                                                                                                                 1 YAFVGEKFRNYLLVFFQK 18
                                                                                                           41825 MW;
                                                                                                                                  67.48;
                                                                                                                                                         11; Conservative
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 2201
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2243
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                                                                                                          359 AA;
                                                                                                                                              Local Similarity
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054814; 055169;
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01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 8 (C-C CKR-8) (CC-CKR-8) (GPR-CY6)
(GPRCY6) (Chemokine receptor-like 1) (CKR-L1) (TER1) (CMKBRL2) (CC-CHEMOKINE receptor CHEMR1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=97351133; PubMed=9207005;
Tiffany H.L., Lautens L.L., Gao J.-L., Pease J., Locati M.,
Combadiere C., Modi W., Bonner T.I., Murphy P.M.;
"Identification of CCR8: a human monocyte and thymus receptor for the
CC chemokine I.309.",
J. Exp. Med. 186:165-170(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDILINE-99129363; PubMed=9469461;
MEDILINE-99129363; PubMed=9469461;
MEDILINE-99129363; PubMed=9469461;

"Identification of CCR8 as the specific receptor for the human beta-chemokine I-309: cloning and molecular characterization of murine to Immunol. 160:1975-1981 [1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Eur. J. Immunol. 26:301-3028 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE=97040707; PubMed=8886020;
Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;
"Molecular cloning and RNA expression of two new human chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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MEDILINE=97111825; PubMed=8977299;
Sanson M., Stordeur P., Labbe O., Soularue P., Vassart G.,
Parmentler M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 64; DB 1; Length 359
Pred. No. 0.0016;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        -> L (IN REF. 2).
880F682984F501DA CRC64;
                                                                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
POTENTIAL.
                                                                                                                                                                                                                                                                                                           POTENTIAL.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                    CYTOPLASMIC (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
F -> L (IN REF. 2).
                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
POTENTIAL. (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptors.";
AIDS Res. Hum. Retroviruses 17:981-986(2001).
-!- FUNCTION: Receptor for the chemokines SCYA1/I-309, SCYA4/MIP-1-beta and SCYA1/T/TARC. May regulate monocyte chemotaxis and thymic cell line apoptosis (By similarity).
-!- SUBCELIUTAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Spleen;
Marghines1154176; PubMed=11461684;
Margulines2154176; Hauer D.A., Clements J.E.;
"Identification and comparison of eleven rhesus macaque chemokine
ö
                                                                                                                                                                                                                                      CKR8 MACMU STANDARD; PRT; 356 AA.
097655;
16-0CT-2011 (Rel. 40, Created)
16-0CT-2011 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 8 (C-C CKR-8) (CCR-8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AF100205; AAC72403.1; -
InterPro; IPR004068; CC 8 receptor.
InterPro; IPR004068; CC 8 receptor.
InterPro; IPR00001; Twm 1; 1.
PRINTS; PR00237; GFRRHODOPSN.
PROSITE; PS00237; GFRRHODOPSN.
PROSITE; PS00237; GFRRHODOPSN.
PROSITE; PS00237; GFRRHODOPSN.
PROSITE; PS00262; GPROTEIN RECEP F1 1; 1.
G-protein coupled receptor; Transmenbrane; Glycoprotein.
DOMAIN 36 63 1 (POTENTIAL).
TRANSMEM 36 63 1 (POTENTIAL).
TRANSMEM 74 93 CYTOPLASMIC (POTENTIAL).
DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).
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Pred. No. 0.0024;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
     4.
  Mismatches
                                                                                                      300 YAFVGEKFKKHLSEIFOK 317
                                                                                                                                                                                                                                                                                                                                                                                                                                   Macaca mulatta (Rhesus macaque)
  5,
                                                   1 YAFVGEKFRNYLLVFFQK 18
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12; Conservative
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356 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9544;
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  Matches
                                                                                                                                                                                      RESULT 29
                                                                                                                                                                                                                                                                         -! SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:005887; C:integral to plasma membrane; TAS.
GO; GO:0015026; P:chemokine receptor activity; TAS.
GO; GO:0015026; P:coreceptor activity; TAS.
GO; GO:00071502; P:coreceptor activity; TAS.
GO; GO:000716; P:chemotaxis; TAS.
GO; GO:0007204; P:cyteoslic calcium ion concentration elevation; TAS.
GO; GO:0007186; P:Cyteoslic calcium ion concentration elevation; TAS.
GO; GO:0007186; P:Cyteoslic calcium ion concentration elevation; TAS.
InterPro; PRROMOGNE; CR. Receptor.
InterPro; IPROMOGNE; GPCR. Rhodpsn.
PFGm; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                             "Identification of the CC chemokines TARC and macrophage inflammatory protein-1 beta as novel functional ligands for the CCR8 receptor.";
Eur. J. Immunol. 28:582-588(1998).
-!- FUNCTION: Receptor for the chemokines SCYA1/I-309, SCYA4/MIP-1-beta and SCYA1/7TARC. May regulate monocyte.chemotaxis and thymic cell line apoptosis. Alternative coreceptor with CD4 for HIV-1
                                                                                                                             LIGAND BINDING.
MEDLINE=98180363; PubMed=9521068;
Bernardini G., Hedrick J., Sozzani S., Luini W., Spinetti G.,
Welss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; if it.

PEAM: PRO001; 7tm 1; i.

PRINTS; PRO1330; CHEMOKINER8.

PRINTS; PRO0137; GPERHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS00262; G PROTEIN RECEP F1 1; 1.

FROM PROFITE F1 1; 1.

FROM PROFITE F1 1; 1.

PROSITE F1 1; 1.

PROSITE F1 1; 1.

PROSITE F1 1; 1.

FROM PROFITE F1 1; 1.

FROM PROFITE F1 1; 1.

PROSITE F1 1; 1.

P
                      SEQUENCE FROM N.A.
Nakajima T., Yoshida R., Harada S.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U45983; AAB61962.1; --
EMBL; U62556; AAB05542.1; --
EMBL; Z79782; CAB02142.1; --
EMBL; Y08456; CAA69712.1; --
EMBL; AF005210; AA865877.1; --
PIR; JC5067; JC5067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40844 MW;
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106
355 AA;
                                                                                                                                                                                                                                            Napolitano M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                   infection.
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Gaps

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66.7%;

12; Conservative

Matches

Score 63; DB 1; Length 355; Pred. No. 0.0024;

66.38;

Query Match Best Local Similarity

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SEQUENCE FROM N.A.

MIDLINE=22935763; PubMed=14574404;

MIDGAIL A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,

MINDAIL A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,

MILLING L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,

Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscough R.,

Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,

Babbage A.K., Bagguldy C.L., Bailey J., Banerjee R., Barker D.J.,

Babbage A.K., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,

Barlow K.F., Bares X., Brook J., Brown J.Y.,

Burford D.C., Burrill W., Burcon J., Brown J.Y.,

Burford D.C., Burrill W., Burkon J., Carder C., Carter N.P.,

Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,

Culley K.M., Dhami P., Davies J., Dunn M., Barthrowl M.E.,

Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND FUNCTION.
MEDLINE=97313465; PubMed=9169459;
Babba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,
Nomiyama H., Yoshie O.;
"Identification of CRG6, the specific receptor for a novel
"Imphocyte-directed CC Chemokine LARC.";
Jumphocyte-directed CC Chemokine LARC.";
J. Biol. Chem. 272:14893-14898(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                 C-C chemokine receptor type 6 (C-C CKR-6) (CC-CKR-6) (CCR-6) (LARC receptor) (GPR-CY4) (GPRCY4) (Chemokine receptor-like 3) (CKR-L3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97224503; PubMed=9070937; Jaco F., Lee H.-H., Parber J.M., Parlor T.M., Lee H.-H., Parlor J.M., Parlo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.; "Molecular cloning and RNA expression of two new human chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Warren C.N., Aronstam R.S., Sharma S.V.;
"cDNA clones of human proteins involved in signal transduction
sequenced by the Guthrie cDNA resource center (www.cdna.org).";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lautens L.L., Modi W., Bonner T.I.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
McCoy R., Perlmutter D.H.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor-like genes.";
Biochem. Biophys. Res. Commun. 227:846-853(1996).
                                                                                                                                                                                                                                            CKR6 HUMAN STANDARD; FR1.
PS1684; P78553; Q92846;
D1-CCT-1996 (Rel. 34, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCR6 OR CMKBR6 OR STRL22 OR GPR29 OR CKRL3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=97040707; PubMed=8886020;
                                                                    301 YAFVGEKFKKHLSEIFQK 318
                                  YAFVGEKFRNYLLVFFOK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomics 40:175-180(1997)
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Gilby Law Cilliann C. J. Giltheno R. J., Grathan D. D., Grant M.,

And Cilliann C. J. Giltheno R. J., Grathan D. D., Heathoott R.,

And Cilliann C. J., Giltheno R. J., Grathan D. M., Heathoott R.,

Hammond S. J., Hander D. J., Hart E. A., Heath D. D., Heathoott R.,

Hammond S. J., Hander D. J., Hart E. M., Heath D. D., Heathoott R.,

Hammond S. J., Hander D. J., Hart E. M., Heath D. D., Heathoott R.,

Hammond S. J., Hander D. J., Hart E. M., Hard G. M., Langford C.,

Hammond S. J., Hamphries M.D., Hart R. M., Milke M. Land G. M., Langford C.,

Hammond S. J., Hamphries M.D., Hart R. M., Milke M. Land G. M., Langford C.,

Hammond S. J., Hamphries M.D., Hart R. M., Milke M. Land G. M., Mickerson T.,

Making G. L., Martheos L., Milkelland M. M., Milkelland C. M., Mickerson T.,

Mentrad G. L., Martheos L., Wall M. M. M. M., Milkelland C., Milkelland C., Milkels M.,

Barte R. M., Sherddan B., Rucce M.D., Milke S. M., Milkels S., Plumb B.,

Barte R. M., Mallis J. M., West A. P., Milkel S. J., Whitehead S. L., Third J. M., Mast A. M.,

Barte R. M., Mallis J. M., West A. P., Milker C. M., Bood J. M., Nkay D. M.,

Mill M., Millis J. M., West A. P., Milke S. S., Milkehead S. L., Berk G. M.,

Mill M., Millis J. M., West A. P., Milke S. S., Milkehead S. L., Mart M. M.,

Mill M., Millis J. M., West A. P., Milke S. S., Milkehead S. L., Mill M.,

Mill M., Millis J. M., West A. P., Milke S. S., Milkehead S. L., Millis S. M.,

Mill M., Millis J. M., West A. P., Milke S. S., Milkehead S. L., Millis S. M.,

Mill M., Millis J. M., West A. P., Milke S. S., Milkehead S. L., Millis S. M.,

Mill M., Millis J. M., West A. P., Milke S. S., Milkehead S. L., Shanger M., J., Bender S. J.,

Mill M., Millis J. M., West A. P., Milke S. S., Milkehead S. L., Shanger L., Milkelland R., Groune E. H., Derge J., G., Milkelland S. M., Milkelland M., Milkelland M., Wilkelland M., Milkel

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                       [3]
SEQUENCE FROM N.A.
                                                        SEQUENCE FROM N.A.
                  NCBI_TaxID=9606;
   THE FEET TO BE AND BEAR AND BE
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01-0CT-1993 (Rel. 27, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
16-C chemokine receptor type 1 (CC CKR-1) (CC-CKR-1) (CCR-1)
(Macrophage inflammatory protein-1 alpha receptor) (MIP-lalpha-R)
(RANTES-R) (HM145) (LD78 receptor).
CCR1 OR CKRB1 OR CKR31.
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
                                                               GO: GO: 0005387; C:integral to plasma membrane; TAS. GO: 0004950; E:chemokine receptor activity; TAS. GO: 0004950; E:chemokine receptor activity; TAS. GO: GO: 0004872; E:receptor activity; TAS. GO: GO: 00065928; P:receptor activity; TAS. GO: GO: 00065928; P:cell motility; TAS. GO: GO: 00065928; P:cellular defense response; TAS. GO: GO: 0006593; P:chemotaxis; TAS. GO: GO: 0007204; P:cytosolic calcium ion concentration elevation; TAS. GO: GO: GO: 0006593; P:humoral immune response; TAS. GO: GO: 0007165; P:signal transduction; TAS. InterPro; IPR004067; CC. 6 receptor. InterPro; IPR00407; GPR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL)
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Y -> N (IN REF. 4)

S -> T (IN REF. 5)

C -> T (IN REF. 5)

Q -> L (IN REF. 4)

E -> V (IN REF. 4)

B -> V (IN REF. 4)

C -> IN REF. 4)

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C -> T (IN REF. 4)
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Pred. No. 0.0056;
2; Mismatches 1; Indels
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PRINTS, PROLESS, CHEMOKUNERG.
PROSITE; PSO0237; G-PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G-PROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Transmentane; Glycoprotein.
DOMAIN EXTRACELLULAR (POTENTIAL).
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CYTOPIASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
3 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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6 (POTENTIAL).
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EMBL; BC037960; AAH37960.1;
HSSP; P34996; 1DDD.
Genew; HGNC:1607; CCR6.
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Matches 10; Conserv
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AC P32246;
DT 01-0CT-1993 (
DT 01-0CT-1993 (
DT 15-MAR-2004 (
DE (Acrophage i)

DE (RANTES-R) (
GN CCRI OR CKRB

OS HOMO Sapiens

OC Eukaryota; Me
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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Int. Immunol. 5:1239-1249(1993).

Int. Immunol. 5:1239-1249(1993).

Int. Immunol. 5:1239-1249(1993).

MIP-1 delta, RANTES, and MCP-3 and, less efficiently, to MIP-1-beta or MCP-1 and subsequently transduces a signal by increasing the intracellular calcium ions level. Responsible for affecting stem cell proliferation.

-I-SUBCELLULAR LOCATION: Integral membrane protein.

-I-TISUE SPECIFFICITY: Widely expressed in different hematopoietic
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601005887; C:integral to plasma membrane; TAS.
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0007155; P:chemoxine receptor activity; TAS.
GO; GO:0007155; P:cell adhesion; TAS.
GO; GO:0007267; P:cell signaling; TAS.
GO; GO:0006935; P:chemotaxis; TAS.
GO; GO:0007267; P:cytosolic calcium ion concentration elevation; TAS.
GO; GO:0007267; P:cytosolic calcium ion concentration elevation; TAS.
GO; GO:0007267; P:immune response; TAS.
R GO; GO:0006955; P:immune response; TAS.
R GO; GO:0007125; P:intlammatory response; TAS.
R GO; GO:0007125; P:intlammatory response; TAS.
R GO; GO:0007125; P:intlammatory response; TAS.
R InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                            [2]
SQUENCE FROM N.A.
MEDLINE-93240122; PubMed=7683036;
Gao J.-L., Kuhns D., Tiffany H.L., McDermott D., Li X., Francke U.,
Murphy P.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                   "Structure", Structional expression of the human macrophage inflammatory protein 1 alpha/RANTES receptor."; J. Exp. Med. 177:1421-1427(1993).
MEDLINE=93161416; PubMed=7679328;
Neote K., Digregorio D., Mak J.Y., Horuk R., Schall T.J..
"Molecular cloning, functional expression, and signaling
characteristics of a C-C chemokine receptor.";
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PROSITE; PSO262; G PROTEIN RECEP F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein.

DOMAIN 35 60 1 (POTENTIAL).

TRANSMEM 55 91 2 (POTENTIAL).

TRANSMEM 65 91 2 (POTENTIAL).

TRANSMEM 92 107 EXTRACELLULAR (POTENTIAL).

TRANSMEM 92 107 EXTRACELLULAR (POTENTIAL).

TRANSMEM 120 12 (POTENTIAL).

DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
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PRINTS; PR00237; GPCRRHODOPSN.
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EMBL; L10918; AAA36543.1; -.
EMBL; D10925; BAA01723.1; -.
BFIR; A45177; A45177.
Genew; HGNC:1602; CCR1.
                                                                                                                                                                     Cell 72:415-425(1993).
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EMBL, U04808; AAB87093.1; -.
PIR, I58186; I58186.
InterPro; IPR005387; Fractalkiner.
ROSITE; PS50262; G_PROTEIN_
-protein coupled receptor;
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nes 9; Conservative
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367 AA;
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SEQUENCE FROM N.A.
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C3X1_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99077268; PubMed=9862452; Martin P., Roncal F., Varona R., Zaballos A., Gutierrez J., Martin P., Roncal F., Albar J.P., Ardavin C., Marquez G.; Molecular cloning, functional characterization and mRNA expression analysis of the murine chemokine receptor CCR6 and its specific ligand mnp-setha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEBS Lett. 440:188-194(1998).
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-3-alpha/LakC and subsequently transduces a signal by increasing the intracellular calcium ions level.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 6 (C-C CKR-6) (CC-CKR-6) (KY411)
                 EXTRACELLULAR (POTENTIAL).

S (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLONAC. ..) (POTENTIAL).

BY SIMILARITY.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                         63.2%; Score 60; DB 1; Length 355; llarity 61.1%; Pred. No. 0.0079; Conservative 2; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                         337 E -> D (IN REF. 3).
41172 MW; B2C100FFED275985 CRC64;
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PRINTS; PRO1527; GPCRAHODOPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.
          (POTENTIAL)
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EMBL, AJ22714; CAA10956.1; -.
MGD; MG11333797; Ccf6.
GO; GO:0005515; F:protein binding; IPI.
INTERPRO; IPR004067; CC 6_receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
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tes 11; Conserv
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=Sprage Dawley; TISSUE-Spinal cord;

MEDLINE=94323113; PubMed=804728;

MEDLINE=94323113; PubMed=804728;

MEDLINE=94323113; PubMed=804728;

"CDMA cloning of a G-protein-coupled receptor expressed in rat spinal cord and brain related to chemokine receptors.";

Neurosci. Lett. 169:85-89(1994).

-I FUNCTION: Receptor for the CX2C chemokine fractalkine and mediates both its adhesive and migratory functions.

-I SUBCELDIAR LOCATION: Integral membrane protein.

-I TISSUE SPECIFICITY: Most abundant in adult spinal cord, brain, kidney, gut, uterus and testes.

-I PTM: This protein is not N-glycosylated which is unusual for G-
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
30-MR-2000 (Rel. 39, Last annotation update)
CX3C Chemotine receptor 1 (G-X3-C CRR-1) (CX3CR1) (Fractalkine receptor) (GPR13) (RBS11).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLUIAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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PROTEIN RECEP_F1_2; 1.
sceptor; Transmembrane; Glycoprotein.
39 BXTRACELDULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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Pred. No. 0.012;
3; Mismatches
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42102 MW;
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69.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CZech II; TISSUE=Mammary gland; MEDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.L., Wang J., Haich F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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30-WAY-2000 (Rel. 39, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
CX3C chemokine receptor 1 (C-X3-C CKR-1) (CX3CR1) (Fractalkine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 58; DB 1; Length 354;
Pred. No. 0.017;
1; Mismatches 6; Indels
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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1 (POTENTIAL).
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                                                                                                                 PROSITE; PS00237; G PROTEIN RECEP F1 1; 1. PROSITE; PS50262; G PROTEIN RECEP F1 2; 1. G-protein coupled receptor; Transmembrane.
                                                                                                                                                                                                                                                                     CYTOPLASMIC
InterPro, IPR000276; GPCR_Rhodpsn
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                            Pfam; PF00001; 7tm 1; 1.
PRINTS; PR01562; FRACTALKINER.
PRINTS; PR00237; GPCRRHODOPSN.
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nes 11; Conservative
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Q9Z0D9;
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RA BOSAK S.A., Usguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA BOSAK S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J., BOSAK S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Villalon D.K., Muzny D.M., Soderren B.J., Lu X., Glibbs R.A., Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mitting M., Madan J.W., Colfigues S., Sanchez A., Mitting M., Madan J.W., Dickson M.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rablerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R. "Generation and initial analysis of more than 15,000 full-length RT Muman and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

C. -- SUBCELLULAR LOCATION: Integral membrane protein.

C. -- SUBCELLULAR LOCATION: Integral membrane protein.

C. -- PTM: This protein is not N-glycosylated which is unusual for G-protein-coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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PRINTS; PR01337; GPCRRHODOPSN.
PROGITE; PS0237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PROSIES; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane.
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
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P49238;
01-FEB-1996 (Rel. 33, Created)
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les 11; Conservative
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C3X1 HUMAN
ID C3X1 HI
AC P49238
DT 01-FEB-
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1 YAFVGEKFRNYLLVFFOK 18
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A trausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A trausher R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Ebbat N.K.,

A placchenko L., Marusina R., Farmer A.A., Rubin G.M., Hong L.,

B Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gibbs R.A.,

Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., García A.M., Gabbs R.A.,

Richards S., Worley K.C., Hale S., García A.M., Gabbs R.A.,

Richards S., Worley W.C., Sodergren E.J., Lu K., Gibbs R.A.,

Richards S., Worley W., Sodergren E.J., Lu K., Gibbs R.A.,

Richards S., Worley W., Sodergren E.J., Lu K., Gibbs R.A.,

Rabesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Rodriguez A.C., Grimwood J., Shaltska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

"Generation and mouse cDNA sequences",

I Meman and mouse cDNA sequences",

I Human and wouse cDNA sequences",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98050927; PubMed=9390561; Imai T., Hieshimura M., Nagira M., Nishimura M., Kakizaki M., Takagi S., Nomiyama H., Schall T.J., Yoshie O.; Takagi S., Nomiyama H., Schall T.J., Yoshie O.; "Identification and molecular characterization of fractalkine receptor CX3CR1, which mediates both leukocyte migration and adhesion."; [5]
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDAME=7590284; MEDAMESTRE-5601651; PubMed=7590284; MEDIATE-56011651; PubMed=7590284; MEDAMEDIATE-56011651; Decoupled to the sequent C.J., Schweickart V.L., Eddy R.L. Jr., Shows T.B., Gray P.W.; "The orphan G-protein-coupled receptor-encoding gene V28 is closely related to genes for chemokine receptors and is expressed in lymphoid and neural tissues "; gene 163:295-299(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murphy P.M.;
"Identification of CX3CR1. A chemotactic receptor for the human CX3C chemokine fractalkine and a fusion coreceptor for HIV-1.";
J. Biol. Chem. 273:23799-23804(1998).
01-FEB-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annocation update)
CX3C chemokine receptor 1 (C-X3-C CKR-1) (CX3CR1) (FractalKine receptor) (GPR13) (V28) (Beta chemokine receptor-like 1) (CMK-BRL-1)
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MEDLINE-20195025; PubMed=10731151;
Faure S., Meyer L., Costagliola D., Vaneensberghe C., Genin E.,
Autran B., Delfraissy J.-F., McDermott D.H., Murphy P.M., Debre P.,
Theodorou L., Combadiere C.;
"Rapid progression to AlDS in HIV+ individuals with a structural
variant of the chemokine receptor CX3CR1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98395093; PubMed-9726990;
Combadiere C., Salzwedel K., Smith E.D., Tiffany H.L., Berger E.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=95374679; PubMed=7646814;
MEDLINE=95374679; PubMed=7646814;
"Clombadiere C., Ahuja S.K., Murphy P.M.;
"Cloning, chromosomal localization, and RNA expression of a human beta chemokine receptor-like gene.";
DNA Cell Biol, 14:673-680(1995).
                                                                                                                                                Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                           (CMKBLKI).
CX3CR1 OR GPR13
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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R MIM; 60470; -.

R GO; GO:0005887; C:integral to plasma membrane; TAS.

GO; GO:0005887; C:chemokine receptor activity; TAS.

R GO; GO:0006989: P:cell adhesion; TAS.

R GO; GO:0006981; P:cellular defense response; TAS.

R GO; GO:0006981; P:cellular defense response; TAS.

R GO; GO:000186; P:cellular defense response; TAS.

R GO; GO:000186; P:G-protein coupled receptor protein signalin. ..;

R InterPro; IPR000277; Fractalkiner.

DR RINTS; PR00017; 7tm 1; 1.

DR PRINTS; PR001527; FRACTALKINER.

DR PRINTS; PR001237; GPRCHEHODOPEN.

DR PROSITE; PS00237; GPRCHEHODOPEN.

DR ROSITE; PS00237; GPRCHEN RECEP FI 1; 1.

DR ROSITE; PS00246; GPROTEIN RECEP FI 2; 1.

R G-protein coupled receptor; Transmembrane; POIENTIAL).
Science 287:2274-2277(2000).

-!- FUNCTION: Receptor for the CX3C chemokine fractalkine and media both its adhesive and migratory functions. Acts as co-receptor with CD4 for HTV-1 virus envelope protein (in vitro).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUB SPECIFICITY: Expressed in lymphoid and neural tissues.
-!- DISEASE: Increased susceptibility to HIV infection and rapid progression to AIDS are associated with the Ile-249/Met-280 haplotype.
                                                                                                                                                                                                                                                            -!- SIMILARÎTY: Belongs to family 1 of G-protein coupled receptors.
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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C59DC5F4C4312F22 CRC64;
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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EMBL; U28934; AAAB7032.1; -.
EMBL; BC028078; AAH28078.1; -.
PIR; JC4304; JC4304.
Genew; HGNC:2558; CX3CR1.
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Best Local Similarity 61.1%;
Matches 11; Conservative
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Inngjerdingen M., Damaj B., Maghazachi A.A.;
"Human NK cells express CC chemokine receptors 4 and 8 and respond to thymus and activation-regulated chemokine, macrophage-derived chemokine, and I-309.";
J. Immunol. 164:4048-4054(2000).
--- FUNCTION: High affinity receptor for the C-C type chemokines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: High affinity receptor for the C-C type chemokines TARC/SCYA17 and MDC/SCYA22. The activity of this receptor is mediated by G(i) proteins which activate a phosphatidylinositol-
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIANE-95370289; PubMed-7642614;

Power C.A., Meyer A., Nemeth K., Bacon K.B., Hoogewerf A.J.,

Proudfoot A.E.I., Wells T.N.C.;

"Mollecular cloning and functional expression of a novel CC chemokine
receptor cDNA from a human basophilic cell line.";

J. Biol. Chem. 270:19495-19500(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99394604; PubMed=10466728; Campbell J.J., Qin S., Ponath P., Andrew D.P., Warnke R., Ruffing N., Kassam N., Wu L., Butcher B.C.; The chemokine receptor CCR4 in vascular recognition by cutaneous but intestinal memory T cells."; Nature 400:776-780(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A., AND VARIANTS VAL-130 AND SER-178.
MEDLINE=21040311; PubMed=11196669;
Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki Hirai K., Tokunaga K.;
"New variations of human CC-chemokine receptors CCR3 and CCR4.";
"New variations of human CC-chemokine receptors CCR3 and CCR4.";
                                                                                                       CKR4 HUMAN STANDARD; PRT; 360 AA.

901LY6; Q9ULX7;
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor type 4 (C-C CKR-4) (CCR-4) (CCR4)
(KS-5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97313486, PubMed=9169480;
Imai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yoshie O.,
Imai T., Baba M. Lander M., Kakizaki M., Takagi S., Yoshie O.,
Imai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yoshie O.,
Diological Indiand for CC chemokine receptor 4.",
J. Biol. Chem. 272:15036-15042(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98104168; PubMed=9430724; mod C.L., Nishimura M., Godiska Manai T., Chantry D., Raport C.J., Wood C.L., Nishimura M., Godiska Yoshie O., Gray P.W.; Macrophage-derived chemokine is a functional ligand for the CC "Macrophage-derived chemokine is a functional ligand for the CC
                                                                                                                                                                                                                                                   CCR4 OR CMKBR4.
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Kopatz S.A., Aronstam R.S., Sharma S.V.,
"CDNA clones of human proteins involved in signal transduction
sequenced by the Guthrie cond. resource center (www.cdna.org).";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION, TISSUE SPECIFICITY, AND PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chemokine receptor 4.";
J. Biol. Chem. 273:1764-1768(1998)
      293 YAFAGEKFRYLYHLYGK 310
                                                                                                                                                                                                                                                                                                                                                                                   FROM N.A.
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                        CKR4 HUMAN
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calculudate second messaging is specification and configuration mediate of correceptor for some primary HIV-2 isolates. In the CNS, could mediate hippocampal-neuron survival.

-!- SUBCELLUDAR LOCATION: Integral membrane protein.
-!- SUBCELLUDAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Predominantly expressed in the thymus, in peripheral blood Leukcoytes, including T cells, mostly odds cells, and in monocytes. Detected also in macrophages, IL-2-activated and in monocytes. Detected also in macrophages, IL-2-activated natural killer cells and skin-homing memory T cells, mostly the ones expressing the cutaneous lymphocyte antigen (CLA). Expressed in brain microvascular and coronary artery endothelial cells.
-- PTM: IN NATURAL KILLER CELLS, SCYA22 BINDING INDUCES
-- PTM: IN NATURAL KILLER CELLS, SCYA22 BINDING INDUCES
-- PTM: BY BETA-ADRENERGIC RECEPTOR KINASES 1 AND 2.
-- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM) 604836; --
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005850; F:chemokine receptor activity; TAS.
GO; GO:0006935; P:chemokans; TAS.
GO; GO:0006935; P:chemotans; TAS.
GO; GO:0006955; P:immune response; TAS.
GO; GO:0006954; P:inflammatory response; TAS.
FILE-PRO: IPRO00276; GPCR_Rhodpsn.
PF00001; 7tm_1; 1.
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
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PROSITE; PS00237; GPROTEIN RECEP_F1_1; 1.
PROSITE; PS02626; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Phosphorylation; Polymorphism.
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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EMBL, AB02389; BAA86966.1; --
EMBL, AB023891; BAA86967.1; --
EMBL, AB023891; BAA86968.1; --
EMBL, AB023892; BAA86969.1; --
EMBL, AB023892; BAA86969.1; --
PMBL, AB71667, AB7160.
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Mismatches

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Conservative

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1 YAFVGEKFRNYLLVFFOK 18
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                                                                                           RESULT 38
CKR3_CAVPO
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                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                        AIDS Res. Hum. Retroviruses 17:981-986 (2001).

-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, RANTES. MCP-3 AND, LESS BFFICIENTLY, TO MIP-1-BETA OR MCP-1 AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCHUM IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL PROLIFERATION.
                     Gaps
                                                                                                                                                              15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 1 (C-C CKR-1) (CC-CKR-1) (CCR-1)
                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=21354176; PubMed=11461684; Margulies B.J., Hauer D.A., Clements J.B.; "Identification and comparison of eleven rhesus macaque chemokine
                                                                                                                                                                                                        Macaca mulatta (Rhesus macaque).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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Pred. No. 0.039;
                     Indels
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                     4,
        Pred. No. 0.026;
; Mismatches
                                                                                                                             355 AA.
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                                                                                                                            PRT;
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
58.8%; Pie.
                                                         | |:||||| |:|
304 YFFLGEKFRKYILQLFK 320
                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                          1 YAFVGEKFRNYLLVFFQ 17
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                    Conservative
                                                                                                                            STANDARD;
                                                                                                                                                                                                                                              Cercopithecinae; Macaca.
NCBL_TaxID=9544;
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146
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       Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
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28-FEB-2003
                                                                                                                                                                                                                                                                                                                                receptors."
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P56482;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]—SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEDINE=99049845; PubMed=9834099;
Sabroe I., Conroy D.M., Gerard N.P., Li Y., Collins P.D., Post T.W., Jose P.J., Williams T.J., Gerard C.J., Ponath P.D.;
"Cloning and characterization of the guinea pig eosinophil ectaxin receptor, C-C chemokine receptor-3: blockade using a monoclonal antibody in vivo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Immunol. 161:6139-6147(1998).

-!- FUNCTION: Receptor for a C-C type chemokine. Binds to ectaxin, MCP-3, MCP-4 and RANTES and subsequently transduces a signal by increasing the intracellular calcum ions level (By similarity)
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
10-CPT-2003 (Rel. 42, Last sequence update)
C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR-3)
                                                                                                                                                                                                                                                                                                                                                                           Cavia porcellus (Guinea pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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7873FAB7A38C3670 CRC64;
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CYTOPLASMIC (POTENTIAL).
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfan, PF00001, 7tm 1; 1.
PRINTS; PR00037; GPCREHODOSSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane.
TRANSMEM 44 64 POTENTIAL.
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301 YAFAGERFRKYLROLFHR 318
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                                                                                                                                                 STANDARD;
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358 AA;
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                                                                                                                                                                                                                                                                                                                                                   CCR3 OR CMKBR3.
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Q9Z2I3;
30-MAY-2000 (
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TRANSMEM
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TIESUBEBERGARE,

KM EDLINE=22388257; PubMed=12477932;

KA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Back S.M., Moran R.D., Moran D.M., Hong L.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R. Helton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Batesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

R. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

R. Chancraiton and initial analysis of more than 15,000 full-length

R. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

PROBLIFFRANTON: RESEPPOR ROR A.C. TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,

RAMINES, AND LESS EFFICIBRILY. TO MIP-1-BETA OR RCELL

PROFILERDATION TRANSDUCES A SIGNAL BY INCREASING THE INTRACELULIAR

C. CALCUIN IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Detected in the heart, spleen, lung,
peritoneal exudate cells and leukocytes.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                       PSI675; Q91VP9; 01-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) C-C chemokine receptor type 1 (C-C CKR-1) (CC-CKR-1) (CC-L) (MIP-lalpha-R) (Macrophage inflammatory protein-1 alpha receptor) (MIP-lalpha-R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular characterization of two murine ecsinophil beta chemokine
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRANI-129/Sv. TISSUE-Peritoneal macrophage;
MEDLINE-96072806; PubMed=1594543;
Post I.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gao J.-L., Murphy P.M.;
"Cloning and differential tissue-specific expression of three receptor-like genes, including the gene for a beta chemokane receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor."; J. Biol. Chem. 270:17494-17501(1995).
                                                                                                                                   355 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=129/SvJ;
MEDLINE=95340546; PubMed=7542241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptors.";
J. Immunol. 155:5299-5305(1995).
304 YAFVGERFOKYLRHFLHR 321
                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                      CCR1 OR CMKBR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gerard C.;
                                                                                                                                      MOUSE
                                                                                                                                                                                                                                                                                                     (RANTES-R)
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ö the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). Gaps Gao J.-L., Murphy P.M.; "Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090; 01-OCT-1996 (Rel. 34, Last sequence update)
BFRBE.2003 (Rel. 41, Last annotation update)
C-C chemokine receptor 1-like protein 1 (Macrophage inflammatory protein-1 alpha receptor-like 1). . 0 55.8%; Score 53; DB 1; Length 355; 55.6%; Pred. No. 0.13; ive 2; Mismatches 6; Indels EMBL; BC011092; AAH11092.1; -..
EMBL; BC011092; AAH11092.1; -..
MGI; 1493139; 1493139.
GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0005954; P:inflammatory response; IMP.
GO; GO:0030099; P:inflammatory response; IMP.
InterPro; IPR000276; GPC; Abodpsn.

PFG0001; 77m_1; 11. 6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
M -> V (IN REF. 3).
L -> P (IN REF. 3).
H -> Q (IN REF. 3). 3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL). -> Q (IN KEF: 3). FCE9FFF70E6F38B1 CRC64; EXTRACELLULAR (POTENTIAL) 2 (POTENTIAL). EXTRACELLULAR (POTENTIAL) 1 (POTENTIAL). CYTOPLASMIC (POTENTIAL). Ā PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane.
DOMAIN 34 1 34 1 (POTENTIAL). 356 MEDLINE=95340546; PubMed=7542241; 301 YVFVGERFWKYLRQLFQR 318 1 YAFVGEKFRNYLLVFFOK 18 40901 MW; EMBL; U29678; AAA86119.1; -. EMBL; U28404; AAA89153.1; -. Query Match Best Local Similarity 55.6 Matches 10; Conservative STANDARD; Mus musculus (Mouse) 278 355 AA; SEQUENCE FROM N.A. STRAIN=129/SvJ; 61 65 108 130 172 198 CKRV MOUSE P51676; DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEM CONFLICT TRANSMEM DOMAIN TRANSMEM DISULFID CONFLICT TRANSMEM DOMAIN DOMAIN CKRV MOUSE ઠે 셤

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functional macrophage inflammatory protein-1 alpha receptor.";
J. Biol. Chem. 270:17494-17501(1995).
--- FUNCTION: Probable receptor for a C-C type chemokine.
---- SUBCELLULAR LOCATION: Integral membrane protein.
---- TISSUE SPECIFICITY: Detected in the spleen, liver and leukocytes.
---- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                  55.8%; Score 53; DB 1; Length 356; 50.0%; Pred. No. 0.13; tive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                     4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

S (POTENTIAL).

C YTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

7 (POTENTIAL).

7 (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

8 SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58C01ABA8D7D4B06 CRC64;
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Best Local Similarity 50.vv
Best Local 9, Conservative
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356 AA;
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Search completed: September 28, 2004, 09:04:08
Job time : 6.625 secs

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Gaps ò

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014694
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014694
  014664 homo sapien

09tuq7 erythrocebu

09un24 homo sapien

09un25 homo sapien

09ub17 homo sapien

09ub17 homo sapien

09ub19 homo sapien

09ub19 homo sapien

09tub19 homo sapien

09tub2 homo sapien

09tub2 homo sapien

09tub3 homo sapien

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                                                                                 (without alignments)
197.199 Million cell updates/sec
                                                                      September 28, 2004, 08:56:16; Search time 28.8 Seconds
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                                                                                                                                                                                                        1017041
           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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95
1 YAFVGEKFRNYLLVF
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Maximum DB seq length: 200000000
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The state of the s ö Gaps Homo sapiens (Human). Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; .; 0 Length 333; Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 333 333 333 333 AA; 38174 MW; AEFBA07A67893AEB CRC64; 01-03A1-1998 (TrEMBLrel. 05, Created) 01-03AN-1998 (TrEMBLrel. 05, Last sequence update) 01-03AN-2003 (TrEMBLrel. 24, Last annotation update) CCR5 receptor (Fragment). 333 AA PRT; 1 YAFVGEKFRNYLLVFFQK 18 PRELIMINARY; Receptor. NON TER SEQUENCE

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014694 0990024 0990024 0990023 0990025 0990026 0990028 0990028 0990028 0990028 0990028

278 YAFVGEKFRNYLLVFFQK 295

В

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EMBL; AF162049; AAD47804.1; -..., GO; GO: 0016021; C:integral to membrane; IEA.

GO; GO: 0004802; F: riceeptor activity; IEA.

GO; GO: 0001584; F: rindopsin-like receptor activity; IEA.

GO; GO: 0007186; P:G-protein coupled receptor protein signalin. .; IEA.
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EMBL; AF161919; AAD47676.1; -.

EMBL; AF161919; AAD47676.1; -.

EMBL; AF161919; AAD47676.1; -.

EMBL; AF161919; AAD47676.1; -.

EMBL; C: integral comprane; IEA.

GO; GO:0001584; F: thodopain-like receptor activity; IEA.

GO; GO:0001586; P:G-protein coupled receptor protein signalin. . .; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                   Erythrocebus patas (Red guenon) (Hussar).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Erythrocebus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinkey S.; "Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 95; DB 6; Length 334; 100.0%; Pred. No. 1.1e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                species.";
Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 AA; 38460 MW; B19D0CEC667B69F0 CRC64;
                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
C-C. chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                334 AA
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PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G-PROTEIN RECEP_F1 1; 1.
PROSITE; PS50262; G-PROTEIN RECEP_F1_2; 1.
                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9538;
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Q9UN24;
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EMBL, AF161916; AAD47673.1; ...
GO; GO:0016872; E::receptor activity; IEA.
GO; GO:0001584; F::receptor activity; IEA.
GO; GO:0001584; F::receptor activity; IEA.
GO; GO:0001584; F::rhodopsin-like receptor activity; IEA.
InterPro; IPR000276; PGPCR. Rhodopsn.
Ffam; PF00001; 7tm.1; 1.
PRINTE; PR00237; GPROTEIN RECEP. 11; 1.
PROSITE; PS50257; GPROTEIN RECEP. 11; 1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kulken C., Marx P., Wolinksy S.;

"Sequences of the CCR5 genes from diverse simian and prosimian
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                                                                                                                                             100.0%; Score 95; DB 4; Length 339; 100.0%; Pred. No. 1.18-07; tive 0; Mismatches 0; Indels
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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339 339
339 AA, 39066 MW, 8BAF02E19423BF79 CRC64;
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339 339
339 AA, 39162 MW, A56369FE0529F4AB CRC64;
                                                                                                                                                                                                                                                                                                                       Q9UNZ6;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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                                                                                                                                                                                                                                                                                                              339 AA
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            Pfam; PF00001; 7tm 1; 1. —
PRNTYS; PR00237; GPCRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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InterPro; IPR000276; GPCR_Rhodpsn
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                                                                                                                                                           Local Similarity 100.
Les 18; Conservative
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                                                                     Receptor.
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Homo sapiens (Human)

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Query Match
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Submitted (UUL-1999) to the EMBL/GenBank/DDBU databases.
EMBL; ARI-1920, AAD4767.1.; ...
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor protein signalin. ..; IEA.
InterPro; IRRO0276; GPCR_Rhodopsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GFCRAHODOPSN.
PROSITE; PS00237; GFROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
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Kunstran K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pilai S., Kuiken C., Marx P., Wolinksy S.;

Shibata R., Yoder A., Pilai S., Kuiken C., Marx P., Wolinksy S.;

"Sequences of the CCR5 genes from diverse simian and prosimian species.";

"Species.";

Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF161921; AAD47678.1; -.

EMBL; AAD476778.1; 
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                SEQUENCE FROM N.A.
Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.
"Sequences of the CCRS genes from diverse simian and prosimian
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339 339
339 AA, 39115 MW, 3C6369F922C91AA7 CRC64;
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Matches 18; Conservative
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EMBL; AF161918; AAD47675.1; Co. the combrane; IEA.

GO; GO:00168072; F:receptor activity; IEA.

GO; GO:000188; P:rhodopsin-like receptor activity; IEA.

GO; GO:000188; P:rhodopsin-like receptor protein signalin. ..; IEA.

InterPro; IPR000276; GPCR_Rhodpsn.
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCR5 genes from diverse simian and prosimian
species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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100.0%; Pred. No. 1.1e-07;
tive 0; Mismatches 0; Indels
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EMBL; AF161914; AAD47671.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
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339 339
339 AA; 39146 MW; 10FE05FE5371D4B3 CRC64;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                  0.7.MAY-2000 (TrEMBLrel. 13, Created)
0.1.MAY-2000 (TrEMBLrel. 13, Last sequence update)
01.JUAY-2003 (TrEMBLrel. 24, Last annotation update)
C-C Chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    339 AA
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PROSTI: PRO0237; GPCRRADODSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
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                                290 YAFVGEKFRNYLLVFFQK 307
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1 YAFVGEKFRNYLLVFFOK 18
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es 18; Conservative
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RESULT 9

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EMBL; AF162024; AAD47779.1; --
EMBL; AF162024; AAD47746.1; --
EMBL; AF161889; AAD47646.1; --
EMBL; AF161889; AAD47646.1; --
GO; GO:00016021; C:integral to membrane; IEA.
GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor protein signalin. . .;
InterPro; IPR000276; GPCR_Rhodopsn.
                                                                                                                                                                                                                                                                                            species.";
Submitted (ULL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (ULL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161913; AAD47670.1;
GO; GO:0016812; C:integral to membrane; IEA.
GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor protein signalin..
Interpro; IPR000276; GPCR_Rhodpsn.
PRGNOTIS; PR000237; GPCREHDOOPSN.
PROSITE; PS00237; GPCREHDOOPSN.
PROSITE; PS500262; G_PROTEIN_RECEP_F1_1; 1.
                                                                                                                             Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hylobatidae, Hylobates.
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K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                    Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy N
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 95; DB 4; Length 339; 100.0%; Pred. No. 1.1e-07; Aztive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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339 339
339 AA; 39183 MW; 56C819F92D6DB1A6 CRC64;
01-WAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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                                                                                                                (Human)
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Best Local Similarity
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                Homo sapiens
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EMBL; AF161905; AAD47666.1; -
EMBL; AF161909; AAD47667.1; -
EMBL; AF161911; AAD47668.1; -
EMBL; AF161911; AAD47668.1; -
EMBL; AF161912; AAD47668.1; -
EMBL; AF161912; AAD47669.1; -
EMBL; AF161912; Frieceptor activity; IEA.
GO; GO:0016021; Frieceptor activity; IEA.
GO; GO:0001684; Frieceptor activity; IEA.
GO; GO:000186; Frieceptor activity; IEA.
GO; GO:0001786; Frieceptor activity; IEA.
GO; GO:0001786; Frieceptor activity; IEA.
GO; GO:0001786; Frieceptor activity; IEA.
    GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm l1, 7tm l1, PRINTS; PR00037; GPCRHODPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCR5 genes from diverse simian and prosimian
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                                                                                                                                                                                                                                                         Length 339;
                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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339 339
339 AA; 39086 MW; 88AD8B44E2CB4EC2 CRC64;
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339 AA; 39114 MW; 3C6369F92C29F4A7 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
C-C Chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                       100.0%; Score 95; DB 4; Lv
100.0%; Pred. No. 1.1e-07;
rative 0; Mismatches 0;
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PRNUTS; PR00237; GPCRHODOSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN_RECEP_F1_2; 1.
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Matches 18; Conserv
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                                                                                                                                                   Receptor.
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RESULT 10 Q9UN28 ID Q9UN2: AC Q9UN2:

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Length 339;

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species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF161948; AAD47704.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004812; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor protein signalin. . .; IEA.
InterPro: IPR000276; GPCR_Rhodopsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHODOSN.
PROSITE; PS00237; GPCRHODOSN.
PROSITE; PS00237; GPCRHODOSN.
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161894; AAD47651.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0001884; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
InterPro; IPR000276; PGCR_Rhodopsin.
FR00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gorilla gorilla gorilla (Lowland gorilla).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Gorilla.
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Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy & "Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 95; DB 6; Length 33
100.0%; Pred. No. 1.1e-07;
tive 0; Mismatches 0; Indels
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339 339
339 AA, 39015 MW, 6D1A91546270F70D CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UIN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339 AA
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PROSITE; PSO0237; G PROTEIN RECEP F1 1;
PROSITE; PS50262; G PROTEIN RECEP F1 2;
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Best Local Similarity 100.
Matches 18; Conservative
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF161887; AAD47644.1;
GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016842; F:receptor activity; IEA.

GO; GO:0001884; F:receptor activity; IEA.

GO; GO:0001886; F:receptor activity; IEA.

GO; GO:0001886; F:receptor activity; IEA.

GO; GO:0001886; F:receptor activity; IEA.

FINTERPROPORTITE: PFOOGOL: TRM 1: 1.

PRINTS; PRO00237; GFORRHODORN.

PROSITE; PSO0237; GPRRHODORN.

PROSITE; PSO0237; GPRRHODORN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hylobates concolor (crested gibbon).
Wataryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hylobatidae, Hylobates.
NCBI_TaxID=29089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae, Cercopithecinae, Cercopithecus.
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
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                                                                         Query Match 100.0%; Score 95; DB 6; Length 339; Best Local Similarity 100.0%; Pred. No. 1.1e-07; Matches 18; Conservative 0; Mismatches 0; Indels
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39075 MW; 09257FBFB834C4AE CRC64;
     339
39036 MW; 5555FEAF2614D35C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C_chemokine receptor 5 (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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100.0%; Pred. No. 1.1e-07;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 18; Conservative
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339 33
339 AA;
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339 3
339 AA;
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097UX1
DD 01-MA
DT 01-MA
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DR 00, G
DR 00,
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QOTUUD
AC
DDT QOTUUD
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ö Gaps ö Length 339; 100.0%; Score 95; DB 6; Length 33 100.0%; Pred. No. 1.1e-07; iive 0; Mismatches 0; Indels 339 339 MW; A4A79753DA2F7AAF CRC64;

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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                                                                                                                       Query Match
Best Local Similarity 100.
Matches 18; Conservative
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Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161979; AAD47734.1;
GO; GO:0016201; C:integral to membrane; IEA.
GO; GO:0001524; F:racceptor activity; IEA.
GO; GO:0001524; F:racceptor activity; IEA.
GO; GO:0001546; F:racceptor activity; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR00027; GPCR.Rhodpsn.
PROSITE; PS00037; GPCR.RHODPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_1; 1.
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                                                                                                                                                          Macaca nemestrina (Pig-tailed macaque).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bammalia; Butheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                         Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hylobates concolor (crested gibbon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hylobatidae, Hylobates.
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339 339
339 AA, 39092 MW, 84B51B9548B0703C CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                            %1-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C Chemokine receptor 5 (Fragment).
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                       PRELIMINARY;
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109 TUW
AC 09 TUW
AC 09 TUW
DT 01-MA
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CC C
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OC NOBIL
RA SEQUE
RA SEQUE
RA SHIDA
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                                                                                                                                                        Gaps
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SQUENCE FROM N.A.
Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Kunstman R., Chen Z., Fillai S., Kuiken C., Marx P., Wolinksy S.;
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCR5 genes from diverse simian and prosimian
"Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cercopithecus diana (Diana monkey).

Bukaryota, Metacoa; Chordata, Oraniata, Vertebrata, Euteleostomi;

Mammalia, Butheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cercopithecus aethiops (Green monkey) (Grivet).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
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                                                                                               100.0%; Score 95; DB 6; Length 339;
100.0%; Pred. No. 1.1e-07;
tive 0; Mismatches 0; Indels
1 1
339 339 339 WW, EC4CE48DEEEF107E CRC64;
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01-MAY-2000 (TrEMBirel. 13, Last sequence update)
01-UNA-2003 (TrEMBirel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MX-2000 (TrEMBLrel. 13, Created)
01-MXY-2000 (TrEMBLrel. 13, Last sequence update)
01-UJN-2003 (TrEMBLrel. 24, Last annotation update)
0-C Chemokine receptor 5 (Fragment).
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A Subbarce FROM N.A.

A Shibara R., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

A Shibara R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;

T. Sequences of the CCR5 genes from diverse simian and prosimian

species..;

Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

E. Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

R MAD47660.1;

R MAD47660.1;

R MO; GO:0016021;

C:integral to membrane; IEA.

GO; GO:0018872;

F:receptor activity; IEA.

GO; GO:0001884;

F:hadopsin-like receptor protein signalin. .; II

R Pfam; PF00001;

R Pfam; PF00001;

R Pfam; PF0001;

R PROSTIE;

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Cercopithecus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 95; DB 6; Length 339;
100.0%; Pred. No. 1.1e-07;
tive 0; Mismatches 0; Indels
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EMBL; AF162047; AAD47802.1; -.
EMBL; AF162042; AAD47797.1; -.
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                         339 AA
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                                                                           290 YAFVGEKFRNYLLVFFQK 307
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                                   1 YAFVGEKFRNYLLVFFQK 18
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Pan troglodytes (Chimpanzee).
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nes 18; Conservative
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                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                         Q9TUW4
Q9TUW4;
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                                                                                                                                                                                                                                                           Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF161905; AAD47652.1; -.

EMBL; AF161908; AAD47655.1; -.

EMBL; AF161904; AAD47658.1; -.

EMBL; AF161904; AAD47658.1; -.

EMBL; AF161904; AAD47661.1; -.

EMBL; AF161904; AAD47658.1; -.

EMBL; AF161904; AAD47661.1; -.

EMBL; AF161904; AAD47658.1; -.

EMBL; AF161904; AAD47661.1; -.

EMBL; AF161904; AAD47658.1; -.

GO; GO:0001687; F:receptor activity; IEA.

GO; GO:0001786; P:rhodopsin-like receptor activity; IEA.

GO; GO:0007186; P:rhodopsin-like receptor protein signalin. .; IEA.
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                                                                SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; "Sequences of the CCR5 genes from diverse simian and prosimian species.";
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCR5 genes from diverse simian and prosimian species.";
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
NCBI_TaxID=9598;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 95; DB 6; Length 339; 100.0%; Pred. No. 1.1e-07; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                             Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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339 339
339 AA, 39049 MW, 6D1A93F66270F3ED CRC64;
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PROSITE; PS00237; G PROTEIN RECEP_F11; 1.
PROSITE; PS50262; G PROTEIN RECEP_F12; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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Pan troglodytes (Chimpanzee)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
nes 18; Conservative
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NCBI_TaxID=36224;
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Q9TQW4;
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
BNBL; AF162015, AAD4770.1;
GO; GO:0016621; C:integral to membrane; IEA.
GO; GO:001862; F:receptor activity; IEA.
GO; GO:000186; F:rhodopsin-like receptor activity; IEA.
InterPro; IPR00276; GPCR_Rhodpsin.
PFGM; PF00001; Tem_1.
PRINTS; PR00017; Tem_1.
PROSITE; PS00237; GPCRRHODPSN.
PROSITE; PS00237; GPCRRHODPSN.
PROSITE; PS00237; GPCRHODPSN.
Receptor.
InterPro; IPR00017; GPROTEIN_RECEP_F1_2; 1.
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Eukaryota, Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
NCBI_TaxID=100754;
                                                                                                                                                                                                              Macaca mulatta (Rhesus macaque).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    species.;

Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AFIG1961, AAA7716.1,

GO, GO:0016021, C:integral to membrane; IEA.

GO; GO:0018472; F:receptor activity; IEA.

GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001884; F:rhodopsin-like receptor protein signalin.

Interpro; IPR000276; GPCR-Rhodpsn.

Pfam; PF00001, 7cm 1, 1.

PRINTS; PR00237; GPCRHODOPSN.

PROSITE; PS00237; G-RROTEIN RECEP_F1_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. Kurber B., Oprondek J., Stanton J., Agy P. Kunseman K., Chen Z., Korber B., Kuiken C., Marx P., Wolinksy Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy N
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
"Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 95; DB 6; Length 339; 100.0%; Pred. No. 1.1e-07; trive 0; Mismatches 0; Indels
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339 AA; 39121 MW; AFB6E3EE4D6D3484 CRC64;
    01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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les 18; Conservative
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NON TER
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SEQUENCE
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Q9TUR9;
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Q9TUR9
             SO THE STATE OF TH
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EMBL; AF162044; AAD47799.1; -. membrane; IEA.
GO; GO:0016812; C:integral activity; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001186; P:G-protein coupled receptor protein signalin. . .; IEA.
InterPro; IPR000275; GPCR_Rhodpsn.
PRINTS; PR00237; GPRHODOPSN.
PROSITE; PS00237; GPRHODOPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_FI_2; 1.
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RUBGUENCE FROM N.A.

RUBSTAGE A., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shinstan K., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; T. Schainteed (Jul. 1999) to the EMBL/GenBank/DDBJ databases.

Rubi, AP162054; AAA47809.1; -
DR GO; GO:00046021; C:integral to membrane; IEA.

GO; GO:0004872; F:receptor activity, IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001586; P:rhodopsin-like receptor activity; IEA.

DR GO; GO:0001186; P:rhodopsin-like receptor protein signalin. . ; I

DR Fam; PF00011, 7tm 1; 1.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mamalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Erythrocebus.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339 AA; 39150 MW; 847D5F92BB03E6E2 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          339 AA
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PRINTS, PR00237; GPCRHODDSN,
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       290 YAFVGEKFRNYLLVFFQK 307
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les 18; Conserv
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Q9TUU3
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AC Q9TUU3;
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Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mamanlai, Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species.";
Submitted (ULL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF161954, AAD47710.1;
EMBL, AF161952, AAD47706.1;
EMBL, AF161952, AAD47708.1;
EMBL, AF161952, AAD47708.1;
EMBL, AF161952, AAD47708.1;
EMBL, AF161952, AAD47708.1;
EMBL, FREGOROUS CONDISORS, ENCOPPER ACTIVITY, IEA.
GO, GO:0001684; F:rhodopsin-like receptor activity; IEA.
GO, GO:0001584; F:rhodopsin-like receptor protein signalin.
FILESPEC, IPRO00275, GPCR. Rhodopsn.
FERML, PF00001; 74m_1; 1.
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                                                                Length 339;
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                                                           100.0%; Score 95; DB 6; Length 33
100.0%; Pred. No. 1.1e-07;
tive 0; Mismatches 0; Indels
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39097 MW; C576E7AA492D7080 CRC64;
  339 339 39063 MW; 78BCE7A84B877085 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
0CC chemokine receptor 5 (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN3-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                               339 AA.
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PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                          Conservative
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339 3
339 AA;
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Best Local Similarity
Matches 18; Conserv
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae;
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EMBL, AF161953, AA047709.1, ...

GO, GO:0016621; C:integral to membrane; IEA.

GO, GO:001684; F:receptor activity; IEA.

GO, GO:0001884; F:rhodopsin-like receptor activity; IEA.

GO, GO:0001886; F:rhodopsin-like receptor protein signalin...

InterPro; IPR000276; GERRHOOPSH.

PROMINE; PR00237; GERRHOOPSN.

PROSITE; PS00237; GERRHOOPSN.

PROSITE; PS00262; GERRHOOPSN.
                                                                                                                   Species.";
Submitted (ULL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161972. AAD47727.1;
GO; GO:0016021; Cantegral to membrane; IEA.
GO; GO:0014872; F:receptor activity; IEA.
GO; GO:000188; F:rhodopsin-like receptor activity; IEA.
GO; GO:000188; F:rhodopsin-like receptor protein signalin. InterPro; IPR000276; GPCR-Rhodpsn.
FRAM: PR00011, 7tm 1; 1.
PRINTS; PR000237; GFCRHODOPSN.
PROSITE; PS00237; GFCRHODOPSN.
PROSITE; PS00237; GFCRHODOPSN.
PROSITE; PS00237; GFRHODOPSN.
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SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
"Sequences of the CCRS genes from diverse simian and prosimian
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy P
Kunstman K., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
"Sequences of the CCR5 genes from diverse simian and prosimian
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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339 339
339 AA, 39067 MW, SBFCBCS5BA96C2F9E CRC64,
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-TAX-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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Best Local Similarity 100.
Matches 18; Conservative
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NCBI_TaxID=9541;
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EMBL; AF162003; AAD47758.1; -.
EMBL; AF162004; AAD47759.1; -.
EMBL; AF162004; AAD47759.1; -.
EMBL; AF162004; AAD47759.1; -.
EMBL; AF162004; AAD47759.1; -.
EMBL; C:integral to membrane; IEA.
GO; GO:0001681; F:receptor activity; IEA.
GO; GO:0001188; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001186; P:rhodopsin-like receptor protein signalin. .; IEA.
InterPro; IPR000276; GPCR Rhodpsn.
PRINTS; PR00217; GPCRHODOPSN.
PROSITE; PS00237; GPCRHODOPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_FI_2; 1.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
"Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 95; DB 6; Length 339; 100.0%; Pred. No. 1.1e-07; ive 0; Mismatches 0; Indels
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
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SEQUENCE FROM N.A.
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Matches
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Q9TUW6
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GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0004882; F:rhodopsin-like receptor activity; IEA.
GO, GO:0007186; P:rhodopsin-like receptor protein signalin. ..; IEA.
InterPro; IPR00276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1.
PRINTS; PR00237; GPCRRHODDSN.
PROSITE; PS00237; G_PCRRHODDSN.
PROSITE; PS00237; G_PCRRHODDSN.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae, Colobinae,
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                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates; Catarrhini, Cercopithecidae, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCR5 genes from diverse simian and prosimian
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Submitter.";
Submit AF162005, AAD47760.1; -.
EMBL; AF162000; AAD47755.1; -.
EMBL; AF162001; AAD47755.1; -.
EMBL; AF162001; AAD47756.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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339 339
339 AA, 39178 MW; 9DF2A6F446C55AED CRC64;
                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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               YAFVGEKFRNYLLVFFQK 307
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                                                                                                                                                                                                                                                                                                                                                                              Cercopithecus aethiops vervet.
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Les 18; Conservative
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SEQUENCE FROM N.A.
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Q9TUR6
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species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                      339 AA; 39103 MW; 4038C132D024C5A4 CRC64;
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339 339 NW; F0132E8BC44EF829 CRC64;
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                                                                                                                                                           1 YAFVGEKFRNYLLVFFOK 18
                                                                                                  Local Similarity 100.
les 18; Conservative
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nes 18; Conservative
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NCBI_TaxID=9542;
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339
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Q9TUR2;
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161951; AAD47707.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0001894; F:rhocoptor activity; IEA.
GO; GO:0001896; F:rhocoptor activity; IEA.
GO; GO:0007186; P:rhocoptor ocupled receptor protein signalin. . .; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                Cercopithecus mona.
Wakaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Cercopithecus.
                                                                                                                                                                                                                    SEQUENCE FROM N.A. Kunstman K., Oprondek J., Stanton J., Agy M., Stnibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S.; Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S.; "Sequences of the CCR5 genes from diverse simian and prosimian
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                                                                                                                                                                                                                                                                                                    species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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339 339
339 AA; 39019 MW; 7176F940AF11F3ED CRC64;
  01-MAY-2000 (TrEMBLrel. 13, Created)
11-MAY-2000 (TrEMBLrel. 13, Last sequence update)
11-UN-2003 (TrEMBLrel. 24, Last annotation update)
12-C chemokine receptor 5 (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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PROSITE, PS00237, G PROTEIN RECEP FI 1, 1.
PROSITE; PS50262, G PROTEIN RECEP FI 2, 1.
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Best Local Similarity
Matches 18; Conserv
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O9TSN3
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ID Q9TSN3
AC Q9TSN
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
NCBI_TaxID=9538;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Fillai S., Kulken C., Marx P., Wolinkey S.;
"Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
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GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0007186; F:rhodopsin-like receptor activity; IEA.

GO; GO:0007186; F:rhodopsin-like receptor protein signalin.

InterPro; IPR00276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRHODOPSN.

PROSITE; PS00237; GPCRHODOPSN.

PROSITE; PS00237; GPROTEIN RECEP_F1_1; 1.
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  Length 339;
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100.0%; Pred. No. 1.1e-07;
tive 0; Mismatches 0; Indels
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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100.0%; Score 95; DB 6; I
100.0%; Pred. No. 1.1e-07;
                                                                                                                                                                                                                                                                                 339 AA
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                                                Mismatches
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290 YAFVGEKFRNYLLVFFQK 307

SEQUENCE FROM N.A.

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SEQUENCE FROM N.A.
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Q9TUU6;
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Submitted (ULL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (ULL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161989; AAD47744.1; -..
EMBL; AF161988; AAD47743.1; -..
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001886; P:G-protein coupled receptor protein signalin. .;
InterPro; IPR000276; GPCR_Rhodopsn.
                   Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; "Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotā, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF162013, AAD47189.1; --
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001586; F:G-protein coupled receptor protein signalin.
InterPro; IPR000276; GPCR.Rhodopsn.
FROMITS; PR000277; GFCRRHODOSN.
FROMITS; PR00237; G-PRRHODOSN.
FROSITE; PS502237; G-PROTEIN RECEP_F1_1; 1.
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Pred. No. 1.1e-07;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 339;
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339 339
339 AA; 39113 MW; 7£9803EAOEOAF9ED CRC64;
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339 339 339 WW, AD31455EBBC69499 CRC64;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 95; DB 6; L 100.0%; Pred. No. 1.1e-07; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339 AA
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Best Local Similarity 100.0
***rhes 18; Conservative
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nes 18; Conservative
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161956; AAD4712.1;
GO; GO:00016021; C:integral to membrane; IEA.
GO; GO:0001884; F:receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.
InterPro; IPR000276; GFCR Rhodopsn.
InterPro; IPR000276; GFCR Rhodopsn.
Pfam; PF00001; 7tm 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                       Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; "Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; "Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cercopithecus nictitans (white-nosed guenon).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,

Cercopithecinae, Cercopithecus.
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF162046; AAD4779811, 1.
EMBL; AF062043; AAD47798811, -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:integral to methorane; IEA.
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                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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O9TQUS,
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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Pred. No. 1.1e-07;
; Mismatches 0;
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                               PRT;
                                                                                                                                                                                                                    Macaca fuscata (Japanese macaque)
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es 18; Conservative
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Best Local Similarity
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                                                                                   NCBI_TaxID=9598
                                                                                                                                                                                                         species.";
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GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
InterPro; IPR000276; GPGR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPGRHODOPSN.
PROSITE; P800237; GPROTEIN RECEP F1 1; 1.
PROSITE; P850262; G_PROTEIN_RECEP F1_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Papio papio (Guinea baboon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates; Catarrhini, Cercopithecidae,
Cercopithecinae, Papio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CGR5 genes from diverse simian and prosimian
species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
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333 339 339 WW, 84EB018085DC0A62 CRC64;
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339 339 339 378 MW; 847F8F936B00E6E2 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C_chemokine receptor 5 (Fragment).
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PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Best Local Similarity 100.
Matches 18; Conservative
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Q9TUS7
ID Q9TUS
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Q9TUW7
ID Q9TUW
AC Q9TUW
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                                                                                                                                SEQUENCE FROM N.A.

K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; "Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCR5 genes from diverse simian and prosimian
Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                             Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF16.1899; AAD47656.1; -

EQ, GO:0016.100.1 Cintegral to membrane; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor protein signalin.

InterPro; IPR00027; GPCRAPODPSN.

PRINTS; PR00027; GPCRAPODPSN.

PROSITE; PS00027; GPROTEIN RECEP F1 1; 1.

PROSITE; PS500262; G_PROTEIN RECEP_F1_2; 1.
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Local Similarity 100.0%; Score 95; DB 6; Length 33
Local Similarity 100.0%; Pred. No. 1.1e-07;
es 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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339 339
339 AA; 39157 MW; 4A9EBAD183E8E72D CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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Pred. No. 1.1e-07;
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39103 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pongo pygmaeus (Orangutan)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
```

0;

0; Gaps

Matches 18; Conservative 0; Mismatches 0; Indels

\$ Q

Search completed: September 28, 2004, 09:06:20 Job time : 28.8 secs